(12) STANDARD PATENT (11) Application No. **AU 2018266711 B2**
(19) AUSTRALIAN PATENT OFFICE

(54) Title
Anti-CD3-binding domains and antibodies comprising them, and methods for their generation and use

(51) International Patent Classification(s)
C07K 16/28 (2006.01) ***C07K 16/18*** (2006.01)
A61K 39/00 (2006.01) ***C07K 16/30*** (2006.01)
A61K 39/395 (2006.01) ***C07K 16/32*** (2006.01)

(21) Application No: **2018266711** (22) Date of Filing: **2018.05.08**

(87) WIPO No: **WO18/208864**

(30) Priority Data

(31) Number	(32) Date	(33) Country
62/503,315	**2017.05.08**	**US**

(43) Publication Date: **2018.11.15**
(44) Accepted Journal Date: **2025.02.06**

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(56) Related Art
WO 2004/106380 A2
WO 2015/095392 A1

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
15 November 2018 (15.11.2018)

WIPO | PCT

(10) International Publication Number
WO 2018/208864 A1

(51) International Patent Classification:
A61K 39/00 (2006.01) *C07K 16/28* (2006.01)
A61K 39/395 (2006.01) *C07K 16/30* (2006.01)
C07K 16/18 (2006.01) *C07K 16/32* (2006.01)

(21) International Application Number:
PCT/US2018/031705

(22) International Filing Date:
08 May 2018 (08.05.2018)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
62/503,315 08 May 2017 (08.05.2017) US

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(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JO, JP, KE, KG, KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM,

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

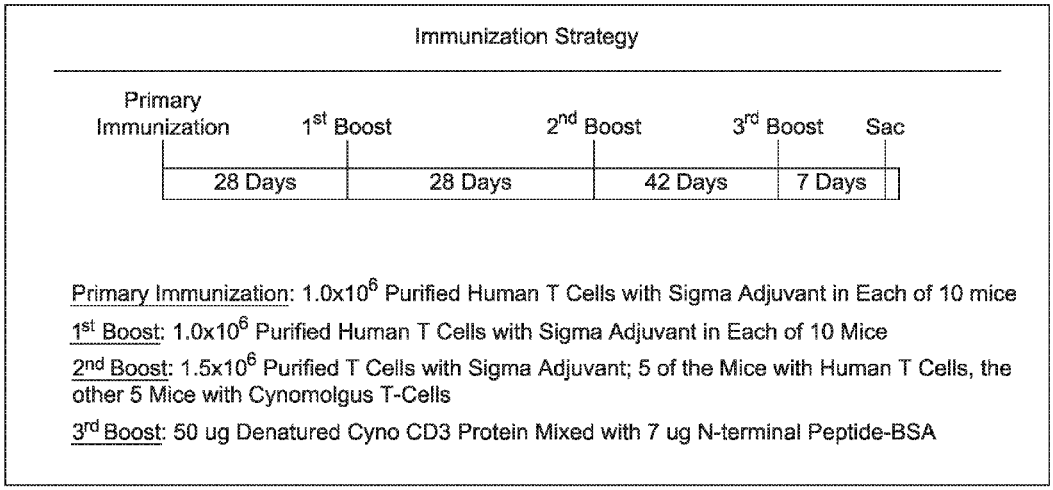


Figure 1

(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.

WO 2018/208864 A1

[Continued on next page]

TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Published:

— *with international search report (Art. 21(3))*
— *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments (Rule 48.2(h))*
— *with sequence listing part of description (Rule 5.2(a))*

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 $\leq$1 μM, $\leq$100 nM, $\leq$10 nM, $\leq$1 nM, $\leq$0.1 nM, $\leq$0.01 nM, or $\leq$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), PlG61, 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: QDGNEEMGGITQTPYKVSISGTTVILTCPQYPGSEILWQHNDKNIGGDEDDKNIGSDEDH LSLKEFSELEQSGYYVCYPRGSKPEDANFYLYLRARVCENCMEMDGGSDKTHTCPPCP APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 6716); and the second polypeptide chain comprises the following amino acid sequence: FKIPIEELEDRVFVNCNTSITWVEGTVGTLLSDITRLDLGKRILDPRGIYRCNGTDIYKDKE STVQVHYRMCQSCVELDGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK (SEQ ID NO: 6717). In certain embodiments the first polypeptide of the heterodimeric CD3 fusion protein comprises the following amino acid sequence: QDGNEEMGSITQTPYQVSISGTTVILTCSQHLGSEAQWQHNGKNKEDSGDRLFLPEFSE MEQSGYYVCYPRGSNPEDASHHLYLKARVCENCMEMDGGSDKTHTCPPCPAPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY ASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 6718); and the second polypeptide chain comprises the following amino acid sequence: FKIPVEELEDRVFVKCNTSVTWVEGTVGTLLTNNTRLDLGKRILDPRGIYRCNGTDIYKD KESAVQVHYRMCQNCVELDPGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL

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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.

[81A] Any discussion of documents, acts, materials, devices, articles or the like which has been included in the present specification is not to be taken as an admission that any or all of these matters form part of the prior art base or were common general knowledge in the field relevant to the present disclosure as it existed before the priority date of each of the appended claims.

Detailed Description of the Invention

[82] 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.).

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

[83A] Throughout this specification, except where the context implies or requires otherwise, the word "comprise", or variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated element or feature, but not to preclude the presence of any further element or feature.

[84] “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

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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.

[85] 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., IgG1,

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 lim ited 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), PlG61, 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, 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.

[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, BIyS, 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 2.6×10^4 (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 $(Gly4Ser)_N$ 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 CD3εδFc 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 $2x10^5$ 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.

[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 x 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^{7-8} 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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTAACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGAACAGTTATGTATCCTGGTTTGCTTATTGG GGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-16606 LAD2189_P03_F02	Heavy chain variable region ("HC") nucleic acid sequence
Ab 1	2	EVQLLESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACAGTTATGTATCCTG GTTTGCTTAT	ADI-16606 LAD2189_P03_F02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 1	9	CAGACTGTGGTGACCCAGGAGCCATCGTTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTAGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCG GCACAAACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGATGATGAATCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-16606 LAD2189_P03_F02	Light chain variable region("LC") nucleic acid sequence
Ab 1	10	QTVVTQEPSFSVSPGGTVTLTCRSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTNKRAPGVPDRFSGSLLGDKAALTITG AQADDESDYYCALWYSNLWVFGGGTKLTVL	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	AGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-20587 SAD5519_P01_B02	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 2	18	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-20587 SAD5519_P01_B02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 2	25	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCGGTGTC CCCTGGAGGGACAGTCACACTCACTTGTAGATCAAGCAC TGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCCGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAATCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-20587 SAD5519_P01_B02	Light chain variable region("LC") nucleic acid sequence
Ab 2	26	QTVVTQEPSLSVSPGGTVTLTCRSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDESDYYCALWYSNLWVFGGGTKLTVL	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	AGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-20588 SAD5520_P01_E08	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 3	34	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-20588 SAD5520_P01_E08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 3	41	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTAGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAAACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-20588 SAD5520_P01_E08	Light chain variable region("LC") nucleic acid sequence
Ab 3	42	QTVVTQEPSLSVSPGGTVTLTCRSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTNKRAPGVPDRFSGSLLGDKAALTITG AQADDEADYYCALWYSNLWVFGGGTKLTVL	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	AGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGGCTCTCCTGTGCAGCCTCT GGATTCACCTTTAACACATATGCCATGAATTGGGTCCGC CAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGA TTAGGTCCAAGTATAACAATTACGCTACATACTACGCAG ACTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATT CCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGA GCCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAG TAACTTCGGGAACGGTTATGTATCCTGGTTTGCTTACTG	ADI-20589 SAD5519_P02_D03	Heavy chain variable region ("HC") nucleic acid sequence

		GGGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 4	50	EVQLLESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHSNFGNGYVSWFAYWGQG TLVTVSS	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	AGGATTAGGTCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACAGTAACTTCGGGAACGGTTATGTATCCTG GTTTGCTTAC	ADI-20589 SAD5519_P02_D03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 4	57	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCGGTGTC CCCTGGAGGGACAGTCACACTCACTTGTAGATCAAGCAC TGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCCGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAATCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-20589 SAD5519_P02_D03	Light chain variable region("LC") nucleic acid sequence
Ab 4	58	QTVVTQEPSLSVSPGGTVTLTCRSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDESDYYCALWYSNLWVFGGGTKLTVL	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	AGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-20590 SAD5519_P05_C08	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 5	66	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKST LYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGGT	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	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-20590 SAD5519_P05_C08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 5	73	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCGGTGTC CCCTGGAGGGACAGTCACACTCACTTGTAGATCAAGCAC TGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCCGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAATCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-20590 SAD5519_P05_C08	Light chain variable region("LC") nucleic acid sequence
Ab 5	74	QTVVTQEPSLSVSPGGTVTLTCRSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDESDYYCALWYSNLWVFGGGTKLTVL	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	AGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-20594 SAD5523_P02_D07	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 6	82	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-20594 SAD5523_P02_D07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 6	89	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTAGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGATCCAG CAGACCCCAGGCCAGGCCCCGCGCGGACTCATCGGCGG CACAAACAAGCGCGCTCCTGGGGTCCCTGATCGCCTCTC TGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCAC GGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGTG CGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGGG ACCAAGCTGACCGTCCTA	ADI-20594 SAD5523_P02_D07	Light chain variable region("LC") nucleic acid sequence
Ab 6	90	QTVVTQEPSLSVSPGGTVTLTCRSSTGAVTTSNYANWIQQ TPGQAPRGLIGGTNKRAPGVPDRLSGSLLGDKAALTITGA QADDEADYYCALWYSNLWVFGGGTKLTVL	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	AGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCGGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACGTACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTACCTGCAAATAAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-20596 SAD5519_P03_E05	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAGCCCTGGTCACCGTCTCCTCA		
Ab 7	98	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQINSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQGA LVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACGTACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-20596 SAD5519_P03_E05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 7	105	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCGGTGTC CCCTGGAGGGACAGTCACACTCACTTGTAGATCAAGCAC TGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCCGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAATCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-20596 SAD5519_P03_E05	Light chain variable region("LC") nucleic acid sequence
Ab 7	106	QTVVTQEPSLSVSPGGTVTLTCRSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDESDYYCALWYSNLWVFGGGTKLTVL	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	AGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-20599 SAD5522_P03_C02	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 8	114	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-20599 SAD5522_P03_C02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 8	121	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCGGTGTC CCCTGGAGGGACAGTCACACTCACTTGTAGATCAAGCAC TGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCCGGGGTCCCTGAGCGCTTC TCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATC ACGGGGGCCCAGGCAGAGGATGAATCTGATTATTACTG TGTGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAG GGACCAAGCTGACCGTCCTA	ADI-20599 SAD5522_P03_C02	Light chain variable region("LC") nucleic acid sequence
Ab 8	122	QTVVTQEPSLSVSPGGTVTLTCRSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPERFSGSLLGDKAALTITGA QAEDESDYYCVLWYSNLWVFGGGTKLTVL	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	AGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-20605 SAD5522_P01_E11	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 9	130	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-20605 SAD5522_P01_E11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 9	137	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCGGTGTC CCCTGGAGGGACAGTCACACTCACTTGTAGATCAAGCAC TGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCCGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTCGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAATCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-20605 SAD5522_P01_E11	Light chain variable region("LC") nucleic acid sequence
Ab 9	138	QTVVTQEPSLSVSPGGTVTLTCRSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDESDYYCALWYSNHWVFGGGTKLTVL	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	AGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGT AACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-20607 SAD5520_P02_C11	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 10	146	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKST LYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-20607 SAD5520_P02_C11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 10	153	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTAGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAAACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-20607 SAD5520_P02_C11	Light chain variable region("LC") nucleic acid sequence
Ab 10	154	QTVVTQEPSLSVSPGGTVTLTCRSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTNKRAPGVPDRFSGSLLGDKAALTITG AQADDEADYYCALWYSNLWVFGGGTKLTVL	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	AGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTCTGCCACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACAGTCACGTATCCTGGTTTGCTCATTGG	ADI-20608 SAD5520_P06_G02	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 11	162	EVQLLESGGGLVQPGGSLRLSCAASGFTSATYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNSHVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACAGTCACGTATCCTG GTTTGCTCAT	ADI-20608 SAD5520_P06_G02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 11	169	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTAGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAAACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-20608 SAD5520_P06_G02	Light chain variable region("LC") nucleic acid sequence
Ab 11	170	QTVVTQEPSLSVSPGGTVTLTCRSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTNKRAPGVPDRFSGSLLGDKAALTITG AQADDEADYYCALWYSNLWVFGGGTKLTVL	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	AGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTAACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCCGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACAGTTATGTATCCTGGTTTGCTTCTTGG	ADI-20609 SAD5521_P01_E04	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 12	178	EVQLLESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKN TLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFASWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACAGTTATGTATCCTG GTTTGCTTCT	ADI-20609 SAD5521_P01_E04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 12	185	CAGACTGTGGTGACCCAGGAGCCATCGTTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGCTCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGATGATGAATCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-20609 SAD5521_P01_E04	Light chain variable region("LC") nucleic acid sequence
Ab 12	186	QTVVTQEPSFSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQADDESDYYCALWYSNLWVFGGGTKLTVL	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	GGCTCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-21943 LAD4204_P01_E02	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 13	194	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-21943 LAD4204_P01_E02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 13	201	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-21943 LAD4204_P01_E02	Light chain variable region("LC") nucleic acid sequence
Ab 13	202	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGA QADDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-21944 LAD4204_P01_E05	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 14	210	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-21944 LAD4204_P01_E05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 14	217	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGTCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-21944 LAD4204_P01_E05	Light chain variable region("LC") nucleic acid sequence
Ab 14	218	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG VQADDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-21945 LAD4204_P01_D06	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 15	226	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-21945 LAD4204_P01_D06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 15	233	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCGC TGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GTGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-21945 LAD4204_P01_D06	Light chain variable region("LC") nucleic acid sequence
Ab 15	234	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQADDEADYYCVLWYSNLWVFGGGTKLTVL	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	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGC CAAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-21946 LAD4204_P01_F06	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 16	242	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-21946 LAD4204_P01_F06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 16	249	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCGC TGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-21946 LAD4204_P01_F06	Light chain variable region("LC") nucleic acid sequence
Ab 16	250	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQADDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGC CAAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-21947 LAD4204_P01_H07	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 17	258	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-21947 LAD4204_P01_H07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 17	265	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAATAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-21947 LAD4204_P01_H07	Light chain variable region("LC") nucleic acid sequence
Ab 17	266	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQADDEADYYCALWYNNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGT AACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-21948 LAD4206_P01_D10	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 18	274	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKST LYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-21948 LAD4206_P01_D10	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 18	281	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCGC TGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GTGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-21948 LAD4206_P01_D10	Light chain variable region("LC") nucleic acid sequence
Ab 18	282	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQADDEADYYCVLWYSNLWVFGGGTKLTVL	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	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGC CAAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGT AACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-21949 LAD4206_P01_F10	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 19	290	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKST LYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-21949 LAD4206_P01_F10	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 19	297	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCGC TGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-21949 LAD4206_P01_F10	Light chain variable region("LC") nucleic acid sequence
Ab 19	298	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQADDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGC CAAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGT AACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-21950 LAD4206_P01_D11	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 20	306	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKST LYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-21950 LAD4206_P01_D11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 20	313	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAATAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-21950 LAD4206_P01_D11	Light chain variable region("LC") nucleic acid sequence
Ab 20	314	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQADDEADYYCALWYNNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-21951 LAD4204_P02_F04	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 21	322	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-21951 LAD4204_P02_F04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 21	329	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GTGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-21951 LAD4204_P02_F04	Light chain variable region("LC") nucleic acid sequence
Ab 21	330	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCVLWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-21952 LAD4204_P02_B05	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 22	338	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-21952 LAD4204_P02_B05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 22	345	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-21952 LAD4204_P02_B05	Light chain variable region("LC") nucleic acid sequence
Ab 22	346	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-21953 LAD4204_P02_F01	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 23	354	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-21953 LAD4204_P02_F01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 23	361	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCGC TGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-21953 LAD4204_P02_F01	Light chain variable region("LC") nucleic acid sequence
Ab 23	362	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGA QADDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGC CAAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-21954 LAD4204_P02_D03	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 24	370	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-21954 LAD4204_P02_D03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 24	377	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCGC TGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAATAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-21954 LAD4204_P02_D03	Light chain variable region("LC") nucleic acid sequence
Ab 24	378	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQADDEADYYCALWYNNLWVFGGGTKLTVL	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	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGC CAAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGT AACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-21955 LAD4206_P02_G01	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 25	386	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKST LYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-21955 LAD4206_P02_G01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 25	393	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCGC TGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-21955 LAD4206_P02_G01	Light chain variable region("LC") nucleic acid sequence
Ab 25	394	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGA QADDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGC CAAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGT AACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-21956 LAD4206_P02_D03	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 26	402	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKST LYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-21956 LAD4206_P02_D03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 26	409	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCGC TGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAATAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-21956 LAD4206_P02_D03	Light chain variable region("LC") nucleic acid sequence
Ab 26	410	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQADDEADYYCALWYNNLWVFGGGTKLTVL	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	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGC CAAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACGCTTATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACGATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-23629 LAD4692_P01_A06	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 27	418	EVQLLESGGGLVQPGGSLRLSCAASGFTFDAYAMNWVRQ APGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACGATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-23629 LAD4692_P01_A06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 27	425	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTGATCTGTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-23629 LAD4692_P01_A06	Light chain variable region("LC") nucleic acid sequence
Ab 27	426	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSDLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-23632 LAD4695_P01_E09	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 28	434	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-23632 LAD4695_P01_E09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 28	441	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTGATCTGTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-23632 LAD4695_P01_E09	Light chain variable region("LC") nucleic acid sequence
Ab 28	442	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSDLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-23633 LAD4773_P02_A05	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 29	450	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-23633 LAD4773_P02_A05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 29	457	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-23633 LAD4773_P02_A05	Light chain variable region("LC") nucleic acid sequence
Ab 29	458	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGGAAGGTTACGTATCCTGGTTTGCTCATTGG	ADI-23634 LAD4774_P02_C06	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 30	466	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGEGYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGGAAGGTTACGTATCCTG GTTTGCTCAT	ADI-23634 LAD4774_P02_C06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 30	473	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-23634 LAD4774_P02_C06	Light chain variable region("LC") nucleic acid sequence
Ab 30	474	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGGAAGGTTACGTATCCTGGTTTGCTCATTGG	ADI-23635 LAD4775_P02_F07	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 31	482	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHGNFGEGYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGGAAGGTTACGTATCCTG GTTTGCTCAT	ADI-23635 LAD4775_P02_F07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 31	489	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-23635 LAD4775_P02_F07	Light chain variable region("LC") nucleic acid sequence
Ab 31	490	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACGCTCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-23636 LAD4776_P01_C01	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 32	498	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNALRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-23636 LAD4776_P01_C01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 32	505	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-23636 LAD4776_P01_C01	Light chain variable region("LC") nucleic acid sequence
Ab 32	506	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGAACGCTTACGTATCCTGGTTTGCTCATTGG	ADI-23637 LAD4777_P01_A02	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 33	514	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNAYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGCTTACGTATCCTG GTTTGCTCAT	ADI-23637 LAD4777_P01_A02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 33	521	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-23637 LAD4777_P01_A02	Light chain variable region("LC") nucleic acid sequence
Ab 33	522	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACGCTCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACGCTTACGTATCCTGGTTTGCTCATTGG	ADI-23638 LAD4778_P01_A03	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 34	530	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNALRAEDTAVYYCVRHGNFGNAYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGCTTACGTATCCTG GTTTGCTCAT	ADI-23638 LAD4778_P01_A03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 34	537	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-23638 LAD4778_P01_A03	Light chain variable region("LC") nucleic acid sequence
Ab 34	538	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-24388 BAD24629_C01	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 35	546	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-24388 BAD24629_C01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 35	553	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-24388 BAD24629_C01	Light chain variable region("LC") nucleic acid sequence
Ab 35	554	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-24389 BAD24629_G01	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 36	562	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-24389 BAD24629_G01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 36	569	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-24389 BAD24629_G01	Light chain variable region("LC") nucleic acid sequence
Ab 36	570	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-24390 BAD24629_A02	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 37	578	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-24390 BAD24629_A02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 37	585	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-24390 BAD24629_A02	Light chain variable region("LC") nucleic acid sequence
Ab 37	586	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-24391 BAD24629_A03	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 38	594	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-24391 BAD24629_A03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 38	601	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-24391 BAD24629_A03	Light chain variable region("LC") nucleic acid sequence
Ab 38	602	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-24392 BAD24629_H03	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 39	610	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-24392 BAD24629_H03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 39	617	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-24392 BAD24629_H03	Light chain variable region("LC") nucleic acid sequence
Ab 39	618	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-24393 BAD24629_A04	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 40	626	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-24393 BAD24629_A04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 40	633	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-24393 BAD24629_A04	Light chain variable region("LC") nucleic acid sequence
Ab 40	634	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACTCATAC TCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCC AAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGC CGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTA ACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGGG	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	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-24394 BAD24702_A01	Light chain variable region("LC") nucleic acid sequence
Ab 41	650	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-24395 BAD24629_B05	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 42	658	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-24395 BAD24629_B05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 42	665	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-24395 BAD24629_B05	Light chain variable region("LC") nucleic acid sequence
Ab 42	666	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-24396 BAD24629_E05	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 43	674	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-24396 BAD24629_E05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 43	681	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-24396 BAD24629_E05	Light chain variable region("LC") nucleic acid sequence
Ab 43	682	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-24397 BAD24629_B06	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 44	690	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-24397 BAD24629_B06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 44	697	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-24397 BAD24629_B06	Light chain variable region("LC") nucleic acid sequence
Ab 44	698	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-24398 BAD24734_D01	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 45	706	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-24398 BAD24734_D01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 45	713	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-24398 BAD24734_D01	Light chain variable region("LC") nucleic acid sequence
Ab 45	714	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-24399 BAD24702_F02	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 46	722	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-24399 BAD24702_F02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 46	729	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-24399 BAD24702_F02	Light chain variable region("LC") nucleic acid sequence
Ab 46	730	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-24400 BAD24629_G07	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 47	738	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-24400 BAD24629_G07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 47	745	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGTTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-24400 BAD24629_G07	Light chain variable region("LC") nucleic acid sequence
Ab 47	746	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-24401 BAD24629_A08	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 48	754	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-24401 BAD24629_A08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 48	761	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-24401 BAD24629_A08	Light chain variable region("LC") nucleic acid sequence
Ab 48	762	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-24402 BAD24629_E08	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 49	770	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-24402 BAD24629_E08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 49	777	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-24402 BAD24629_E08	Light chain variable region("LC") nucleic acid sequence
Ab 49	778	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGTGTCTGGAGTGGGTCGCAAGGATT AGATCCAAGTATAACAATTACGCTACATACTACGCAGAC TCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCC AAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGC CGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTA ACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGGG	ADI-24419 BAD24630_D05	Heavy chain variable region ("HC") nucleic acid sequence

		GCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 50	786	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-24419 BAD24630_D05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 50	793	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCTGTGG GACCAAGCTGACCGTCCTA	ADI-24419 BAD24630_D05	Light chain variable region("LC") nucleic acid sequence
Ab 50	794	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGCGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGTGTCTGGAGTGGGTCGCAAGGATT AGATCCAAGTATAACAATTACGCTACATACTACGCAGAC TCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCC AAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGC CGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTA ACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGGG	ADI-24420 BAD24630_E05	Heavy chain variable region ("HC") nucleic acid sequence

		GCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 51	802	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-24420 BAD24630_E05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 51	809	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCTGTGG GACCAAGCTGACCGTCCTA	ADI-24420 BAD24630_E05	Light chain variable region("LC") nucleic acid sequence
Ab 51	810	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGCGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGTGTCTGGAGTGGGTCGCAAGGATT AGATCCAAGTATAACAATTACGCTACATACTACGCAGAC TCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCC AAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGC CGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTA ACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGGG	ADI-24421 BAD24630_D06	Heavy chain variable region ("HC") nucleic acid sequence

		GCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 52	818	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-24421 BAD24630_D06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 52	825	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCTGTGG GACCAAGCTGACCGTCCTA	ADI-24421 BAD24630_D06	Light chain variable region("LC") nucleic acid sequence
Ab 52	826	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGCGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGTGTCTGGAGTGGGTCGCAAGGATT AGATCCAAGTATAACAATTACGCTACATACTACGCAGAC TCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCC AAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGC CGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTA ACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGGG	ADI-24422 BAD24702_D07	Heavy chain variable region ("HC") nucleic acid sequence

		GCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 53	834	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-24422 BAD24702_D07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 53	841	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCTGTGG GACCAAGCTGACCGTCCTA	ADI-24422 BAD24702_D07	Light chain variable region("LC") nucleic acid sequence
Ab 53	842	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGCGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGTGTCTGGAGTGGGTCGCAAGGATT AGATCCAAGTATAACAATTACGCTACATACTACGCAGAC TCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCC AAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGC CGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTA ACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGGG	ADI-24423 BAD24702_C08	Heavy chain variable region ("HC") nucleic acid sequence

		GCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 54	850	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-24423 BAD24702_C08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 54	857	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCTGTGG GACCAAGCTGACCGTCCTA	ADI-24423 BAD24702_C08	Light chain variable region("LC") nucleic acid sequence
Ab 54	858	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGCGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGTGTCTGGAGTGGGTCGCAAGGATT AGATCCAAGTATAACAATTACGCTACATACTACGCAGAC TCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCC AAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGC CGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTA ACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGGG	ADI-24424 BAD24630_E07	Heavy chain variable region ("HC") nucleic acid sequence

		GCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 55	866	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-24424 BAD24630_E07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 55	873	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCTGTGG GACCAAGCTGACCGTCCTA	ADI-24424 BAD24630_E07	Light chain variable region("LC") nucleic acid sequence
Ab 55	874	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGCGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGTGTCTGGAGTGGGTCGCAAGGATT AGATCCAAGTATAACAATTACGCTACATACTACGCAGAC TCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCC AAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGC CGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTA ACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGGG	ADI-24425 BAD24630_C08	Heavy chain variable region ("HC") nucleic acid sequence

		GCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 56	882	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-24425 BAD24630_C08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 56	889	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCTGTGG GACCAAGCTGACCGTCCTA	ADI-24425 BAD24630_C08	Light chain variable region("LC") nucleic acid sequence
Ab 56	890	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGCGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGTGTCTGGAGTGGGTCGCAAGGATT AGATCCAAGTATAACAATTACGCTACATACTACGCAGAC TCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCC AAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGC CGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTA ACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGGG	ADI-24426 BAD24702_A09	Heavy chain variable region ("HC") nucleic acid sequence

		GCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 57	898	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-24426 BAD24702_A09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 57	905	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCTGTGG GACCAAGCTGACCGTCCTA	ADI-24426 BAD24702_A09	Light chain variable region("LC") nucleic acid sequence
Ab 57	906	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGCGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGTGTCTGGAGTGGGTCGCAAGGATT AGATCCAAGTATAACAATTACGCTACATACTACGCAGAC TCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCC AAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGC CGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTA ACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGGG	ADI-24427 BAD24630_C09	Heavy chain variable region ("HC") nucleic acid sequence

		GCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 58	914	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-24427 BAD24630_C09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 58	921	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCTGTGG GACCAAGCTGACCGTCCTA	ADI-24427 BAD24630_C09	Light chain variable region("LC") nucleic acid sequence
Ab 58	922	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGCGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGTGTCTGGAGTGGGTCGCAAGGATT AGATCCAAGTATAACAATTACGCTACATACTACGCAGAC TCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCC AAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGC CGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTA ACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGGG	ADI-24428 BAD24630_F09	Heavy chain variable region ("HC") nucleic acid sequence

		GCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 59	930	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-24428 BAD24630_F09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 59	937	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCTGTGG GACCAAGCTGACCGTCCTA	ADI-24428 BAD24630_F09	Light chain variable region("LC") nucleic acid sequence
Ab 59	938	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGCGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGTGTCTGGAGTGGGTCGCAAGGATT AGATCCAAGTATAACAATTACGCTACATACTACGCAGAC TCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCC AAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGC CGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTA ACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGGG	ADI-24429 BAD24630_C10	Heavy chain variable region ("HC") nucleic acid sequence

		GCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 60	946	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-24429 BAD24630_C10	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 60	953	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCTCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCTGTGG GACCAAGCTGACCGTCCTA	ADI-24429 BAD24630_C10	Light chain variable region("LC") nucleic acid sequence
Ab 60	954	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDLFSGSLLGDKAALTITGA QAEDEADYYCALWYSNHWVFGCGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGTGTCTGGAGTGGGTCGCAAGGATT AGATCCAAGTATAACAATTACGCTACATACTACGCAGAC TCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCC AAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGC CGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTA ACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGGG	ADI-24430 BAD24702_D09	Heavy chain variable region ("HC") nucleic acid sequence

		GCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 61	962	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-24430 BAD24702_D09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 61	969	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCTGTGG GACCAAGCTGACCGTCCTA	ADI-24430 BAD24702_D09	Light chain variable region("LC") nucleic acid sequence
Ab 61	970	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGCGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGTGTCTGGAGTGGGTCGCAAGGATT AGATCCAAGTATAACAATTACGCTACATACTACGCAGAC TCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCC AAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGC CGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTA ACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGGG	ADI-24431 BAD24702_B11	Heavy chain variable region ("HC") nucleic acid sequence

		GCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 62	978	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-24431 BAD24702_B11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 62	985	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCTGTGG GACCAAGCTGACCGTCCTA	ADI-24431 BAD24702_B11	Light chain variable region("LC") nucleic acid sequence
Ab 62	986	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGCGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGTGTCTGGAGTGGGTCGCAAGGATT AGATCCAAGTATAACAATTACGCTACATACTACGCAGAC TCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCC AAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGC CGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTA ACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGGG	ADI-24432 BAD24630_D12	Heavy chain variable region ("HC") nucleic acid sequence

		GCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 63	994	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-24432 BAD24630_D12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 63	1001	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCTGTGG GACCAAGCTGACCGTCCTA	ADI-24432 BAD24630_D12	Light chain variable region("LC") nucleic acid sequence
Ab 63	1002	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGCGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGTGTCTGGAGTGGGTCGCAAGGATT AGATCCAAGTATAACAATTACGCTACATACTACGCAGAC TCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTCC AAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGC CGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGTA ACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGGG	ADI-24433 BAD24702_C12	Heavy chain variable region ("HC") nucleic acid sequence

		GCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 64	1010	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-24433 BAD24702_C12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 64	1017	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCTGTGG GACCAAGCTGACCGTCCTA	ADI-24433 BAD24702_C12	Light chain variable region("LC") nucleic acid sequence
Ab 64	1018	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGCGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGGGATGTCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-24447 BAD24734_F09	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 65	1026	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGGCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-24447 BAD24734_F09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 65	1033	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCTGTGG GACCAAGCTGACCGTCCTA	ADI-24447 BAD24734_F09	Light chain variable region("LC") nucleic acid sequence
Ab 65	1034	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGCGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGGGATGTCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-24448 BAD24734_A10	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 66	1042	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGGCLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-24448 BAD24734_A10	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 66	1049	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCTTGATCTCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCTGTGG GACCAAGCTGACCGTCCTA	ADI-24448 BAD24734_A10	Light chain variable region("LC") nucleic acid sequence
Ab 66	1050	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVLDLFSGSLLGDKAALTITGA QAEDEADYYCALWYSNHWVFGCGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCCAGGGGTGGTTACGTATCCTGGTTTGCTCATTGG	ADI-26955 LAD5221_P05_A01	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 67	1058	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHGNFQGGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCCAGGGTGGTTACGTATCCTG GTTTGCTCAT	ADI-26955 LAD5221_P05_A01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 67	1065	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26955 LAD5221_P05_A01	Light chain variable region("LC") nucleic acid sequence
Ab 67	1066	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGGGGGGTTACGTATCCTGGTTTGCTTGGTG	ADI-26956 LAD5221_P05_F01	Heavy chain variable region ("HC") nucleic acid sequence

		GGGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 68	1074	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHGNFGGGYVSWFAWWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGGGGGGTTACGTATCCTG GTTTGCTTGG	ADI-26956 LAD5221_P05_F01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 68	1081	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26956 LAD5221_P05_F01	Light chain variable region("LC") nucleic acid sequence
Ab 68	1082	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGCG AACTTCGGGGGCGGGTTACGTATCCTGGTTTGCTCATTGG	ADI-26957 LAD5221_P05_A02	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 69	1090	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHANFGAGYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGCGAACTTCGGGGCGGGTTACGTATCCTG GTTTGCTCAT	ADI-26957 LAD5221_P05_A02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 69	1097	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26957 LAD5221_P05_A02	Light chain variable region("LC") nucleic acid sequence
Ab 69	1098	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGGAAGGTTACGTATCCTGGTTTGCTCATTGG	ADI-26958 LAD5221_P05_E02	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 70	1106	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHGNFGEGYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGGAAGGTTACGTATCCTG GTTTGCTCAT	ADI-26958 LAD5221_P05_E02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 70	1113	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26958 LAD5221_P05_E02	Light chain variable region("LC") nucleic acid sequence
Ab 70	1114	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGAT AACTTCGGGGGCTGGTTACGTATCCTGGTTTGCTCATTGG	ADI-26959 LAD5221_P05_A03	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 71	1122	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHDNFGAGYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGATAACTTCGGGGCTGGTTACGTATCCTG GTTTGCTCAT	ADI-26959 LAD5221_P05_A03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 71	1129	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26959 LAD5221_P05_A03	Light chain variable region("LC") nucleic acid sequence
Ab 71	1130	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGGTTGGTTACGTATCCTGGTTTGCTTCTTGG	ADI-26960 LAD5221_P05_E03	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 72	1138	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHGNFGVGYVSWFASWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGGTTGGTTACGTATCCTG GTTTGCTTCT	ADI-26960 LAD5221_P05_E03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 72	1145	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26960 LAD5221_P05_E03	Light chain variable region("LC") nucleic acid sequence
Ab 72	1146	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACGATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGGAAGGTTACGTATCCTGGTTTGCTCATTGG	ADI-26962 LAD5221_P05_G04	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 73	1154	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHGNFGEGYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACGATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGGAAGGTTACGTATCCTG GTTTGCTCAT	ADI-26962 LAD5221_P05_G04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 73	1161	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26962 LAD5221_P05_G04	Light chain variable region("LC") nucleic acid sequence
Ab 73	1162	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACGATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGAT AACTTCGGGGGCTGGTTACGTATCCTGGTTTGCTCATTGG	ADI-26963 LAD5221_P05_B05	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 74	1170	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHDNFGAGYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACGATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGATAACTTCGGGGCTGGTTACGTATCCTG GTTTGCTCAT	ADI-26963 LAD5221_P05_B05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 74	1177	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26963 LAD5221_P05_B05	Light chain variable region("LC") nucleic acid sequence
Ab 74	1178	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACGATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGGTTGGTTACGTATCCTGGTTTGCTTCTTGG	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	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26964 LAD5221_P05_H05	Light chain variable region("LC") nucleic acid sequence
Ab 75	1194	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACGATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGGGTGCTTACGTATCCTGGTTTGCTCATTGG	ADI-26965 LAD5221_P05_C06	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 76	1202	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHGNFGGAYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACGATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGGGTGCTTACGTATCCTG GTTTGCTCAT	ADI-26965 LAD5221_P05_C06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 76	1209	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26965 LAD5221_P05_C06	Light chain variable region("LC") nucleic acid sequence
Ab 76	1210	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACGCTTATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACGATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGGGGGGTTACGTATCCTGGTTTGGGCATTG	ADI-26966 LAD5221_P05_F06	Heavy chain variable region ("HC") nucleic acid sequence

		GGGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 77	1218	EVQLLESGGGLVQPGGSLRLSCAASGFTFDAYAMNWVRQ APGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHGNFGGGYVSWFGHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACGATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGGGGGGTTACGTATCCTG GTTTGGGCAT	ADI-26966 LAD5221_P05_F06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 77	1225	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26966 LAD5221_P05_F06	Light chain variable region("LC") nucleic acid sequence
Ab 77	1226	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACGCTTATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACGATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACTATGCTGTATCCTGGTTTGCTCATTGG	ADI-26968 LAD5221_P05_F07	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 78	1234	EVQLLESGGGLVQPGGSLRLSCAASGFTFDAYAMNWVRQ APGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHGNFGNYAVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACGATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACTATGCTGTATCCTG GTTTGCTCAT	ADI-26968 LAD5221_P05_F07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 78	1241	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26968 LAD5221_P05_F07	Light chain variable region("LC") nucleic acid sequence
Ab 78	1242	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCCAGGGGTGGTTACGTATCCTGGTTTGCTCATTGG	ADI-26969 LAD5222_P05_A08	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 79	1250	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHGNFQGGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCCAGGGTGGTTACGTATCCTG GTTTGCTCAT	ADI-26969 LAD5222_P05_A08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 79	1257	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26969 LAD5222_P05_A08	Light chain variable region("LC") nucleic acid sequence
Ab 79	1258	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGCG AACTTCGGGGGCGGGTTACGTATCCTGGTTTGCTCATTGG	ADI-26971 LAD5222_P05_A09	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 80	1266	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHANFGAGYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGCGAACTTCGGGGCGGGTTACGTATCCTG GTTTGCTCAT	ADI-26971 LAD5222_P05_A09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 80	1273	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26971 LAD5222_P05_A09	Light chain variable region("LC") nucleic acid sequence
Ab 80	1274	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGGAAGGTTACGTATCCTGGTTTGCTCATTGG	ADI-26972 LAD5222_P05_F09	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 81	1282	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHGNFGEGYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGGAAGGTTACGTATCCTG GTTTGCTCAT	ADI-26972 LAD5222_P05_F09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 81	1289	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26972 LAD5222_P05_F09	Light chain variable region("LC") nucleic acid sequence
Ab 81	1290	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGAT AACTTCGGGGGCTGGTTACGTATCCTGGTTTGCTCATTGG	ADI-26973 LAD5222_P05_E10	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 82	1298	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHDNFGAGYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGATAACTTCGGGGCTGGTTACGTATCCTG GTTTGCTCAT	ADI-26973 LAD5222_P05_E10	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 82	1305	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26973 LAD5222_P05_E10	Light chain variable region("LC") nucleic acid sequence
Ab 82	1306	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGGGTGCTTACGTATCCTGGTTTGCTCATTGG	ADI-26974 LAD5222_P05_A11	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 83	1314	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHGNFGGAYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGGGTGCTTACGTATCCTG GTTTGCTCAT	ADI-26974 LAD5222_P05_A11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 83	1321	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26974 LAD5222_P05_A11	Light chain variable region("LC") nucleic acid sequence
Ab 83	1322	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACGATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGGAAGGTTACGTATCCTGGTTTGCTCATTGG	ADI-26975 LAD5222_P05_F11	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 84	1330	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHGNFGEGYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACGATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGGAAGGTTACGTATCCTG GTTTGCTCAT	ADI-26975 LAD5222_P05_F11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 84	1337	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26975 LAD5222_P05_F11	Light chain variable region("LC") nucleic acid sequence
Ab 84	1338	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACGATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGAT AACTTCGGGGCTGGTTACGTATCATGGTTTGCTCATTGG	ADI-26976 LAD5222_P05_A12	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTATCCTCA		
Ab 85	1346	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHDNFGAGYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACGATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGATAACTTCGGGGCTGGTTACGTATCATG GTTTGCTCAT	ADI-26976 LAD5222_P05_A12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 85	1353	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26976 LAD5222_P05_A12	Light chain variable region("LC") nucleic acid sequence
Ab 85	1354	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACGATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGGTTGGTTACGTATCCTGGTTTGCTTCTTGG	ADI-26977 LAD5222_P05_F12	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 86	1362	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHGNFGVGYVSWFASWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACGATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGGTTGGTTACGTATCCTG GTTTGCTTCT	ADI-26977 LAD5222_P05_F12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 86	1369	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26977 LAD5222_P05_F12	Light chain variable region("LC") nucleic acid sequence
Ab 86	1370	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACGATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGGGTGCTTACGTATCCTGGTTTGCTCATTGG	ADI-26978 LAD5222_P06_A01	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 87	1378	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHGNFGGAYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACGATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGGGTGCTTACGTATCCTG GTTTGCTCAT	ADI-26978 LAD5222_P06_A01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 87	1385	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26978 LAD5222_P06_A01	Light chain variable region("LC") nucleic acid sequence
Ab 87	1386	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACGCTTATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACGATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGGGGGGTTACGTATCCTGGTTTGGGCATTG	ADI-26979 LAD5222_P06_E01	Heavy chain variable region ("HC") nucleic acid sequence

		GGGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 88	1394	EVQLLESGGGLVQPGGSLRLSCAASGFTFDAYAMNWVRQ APGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHGNFGGGYVSWFGHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACGATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGGGGGGTTACGTATCCTG GTTTGGGCAT	ADI-26979 LAD5222_P06_E01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 88	1401	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26979 LAD5222_P06_E01	Light chain variable region("LC") nucleic acid sequence
Ab 88	1402	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACGCTTATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACGATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACGTGGGGGGGTGGTTACGTATCCTGGTTTGCTCATTG	ADI-26980 LAD5222_P06_A02	Heavy chain variable region ("HC") nucleic acid sequence

		GGGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 89	1410	EVQLLESGGGLVQPGGSLRLSCAASGFTFDAYAMNWVRQ APGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHGNVGGGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACGATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACGTGGGGGGTGGTTACGTATCCTG GTTTGCTCAT	ADI-26980 LAD5222_P06_A02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 89	1417	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26980 LAD5222_P06_A02	Light chain variable region("LC") nucleic acid sequence
Ab 89	1418	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACGCTTATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACGATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGAACTATGCTGTATCCTGGTTTGCTCATTGG	ADI-26981 LAD5222_P06_E02	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 90	1426	EVQLLESGGGLVQPGGSLRLSCAASGFTFDAYAMNWVRQ APGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHGNFGNYAVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACGATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACTATGCTGTATCCTG GTTTGCTCAT	ADI-26981 LAD5222_P06_E02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 90	1433	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26981 LAD5222_P06_E02	Light chain variable region("LC") nucleic acid sequence
Ab 90	1434	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCCAGGGGTGGTTACGTATCCTGGTTTGCTCATTGG	ADI-26982 LAD5223_P05_A03	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 91	1442	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHGNFQGGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCCAGGGTGGTTACGTATCCTG GTTTGCTCAT	ADI-26982 LAD5223_P05_A03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 91	1449	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTGATCTGTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26982 LAD5223_P05_A03	Light chain variable region("LC") nucleic acid sequence
Ab 91	1450	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSDLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGGGGGGTTACGTATCCTGGTTTGCTTGGTG	ADI-26983 LAD5223_P05_C03	Heavy chain variable region ("HC") nucleic acid sequence

		GGGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 92	1458	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHGNFGGGYVSWFAWWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGGGGGGTTACGTATCCTG GTTTGCTTGG	ADI-26983 LAD5223_P05_C03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 92	1465	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTGATCTGTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26983 LAD5223_P05_C03	Light chain variable region("LC") nucleic acid sequence
Ab 92	1466	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSDLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGCG AACTTCGGGGGCGGGTTACGTATCCTGGTTTGCTCATTGG	ADI-26984 LAD5223_P05_A04	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 93	1474	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHANFGAGYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGCGAACTTCGGGGCGGGTTACGTATCCTG GTTTGCTCAT	ADI-26984 LAD5223_P05_A04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 93	1481	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTGATCTGTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26984 LAD5223_P05_A04	Light chain variable region("LC") nucleic acid sequence
Ab 93	1482	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSDLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGGAAGGTTACGTATCCTGGTTTGCTCATTGG	ADI-26985 LAD5223_P05_D05	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 94	1490	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHGNFGEGYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGGAAGGTTACGTATCCTG GTTTGCTCAT	ADI-26985 LAD5223_P05_D05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 94	1497	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTGATCTGTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26985 LAD5223_P05_D05	Light chain variable region("LC") nucleic acid sequence
Ab 94	1498	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSDLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGAT AACTTCGGGGGCTGGTTACGTATCCTGGTTTGCTCATTGG	ADI-26986 LAD5223_P05_E04	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 95	1506	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHDNFGAGYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGATAACTTCGGGGCTGGTTACGTATCCTG GTTTGCTCAT	ADI-26986 LAD5223_P05_E04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 95	1513	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTGATCTGTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26986 LAD5223_P05_E04	Light chain variable region("LC") nucleic acid sequence
Ab 95	1514	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSDLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGGTTGGTTACGTATCCTGGTTTGCTTCTTGG	ADI-26987 LAD5223_P05_F05	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 96	1522	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHGNFGVGYVSWFASWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGGTTGGTTACGTATCCTG GTTTGCTTCT	ADI-26987 LAD5223_P05_F05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 96	1529	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTGATCTGTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26987 LAD5223_P05_F05	Light chain variable region("LC") nucleic acid sequence
Ab 96	1530	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSDLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGGGTGCTTACGTATCCTGGTTTGCTCATTGG	ADI-26988 LAD5223_P05_B06	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 97	1538	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHGNFGGAYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGGGTGCTTACGTATCCTG GTTTGCTCAT	ADI-26988 LAD5223_P05_B06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 97	1545	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTGATCTGTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26988 LAD5223_P05_B06	Light chain variable region("LC") nucleic acid sequence
Ab 97	1546	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSDLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACGATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGGAAGGTTACGTATCCTGGTTTGCTCATTGG	ADI-26989 LAD5223_P05_F06	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 98	1554	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHGNFGEGYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACGATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGGAAGGTTACGTATCCTG GTTTGCTCAT	ADI-26989 LAD5223_P05_F06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 98	1561	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTGATCTGTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26989 LAD5223_P05_F06	Light chain variable region("LC") nucleic acid sequence
Ab 98	1562	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSDLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACGATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGAT AACTTCGGGGGCTGGTTACGTATCCTGGTTTGCTCATTGG	ADI-26990 LAD5223_P05_B07	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 99	1570	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHDNFGAGYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACGATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGATAACTTCGGGGCTGGTTACGTATCCTG GTTTGCTCAT	ADI-26990 LAD5223_P05_B07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 99	1577	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTGATCTGTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26990 LAD5223_P05_B07	Light chain variable region("LC") nucleic acid sequence
Ab 99	1578	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSDLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACGATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGGTTGGTTACGTATCCTGGTTTGCTTCTTGG	ADI-26991 LAD5223_P05_E07	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 100	1586	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHGNFGVGYVSWFASWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACGATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGGTTGGTTACGTATCCTG GTTTGCTTCT	ADI-26991 LAD5223_P05_E07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 100	1593	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTGATCTGTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26991 LAD5223_P05_E07	Light chain variable region("LC") nucleic acid sequence
Ab 100	1594	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSDLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACGATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGGGTGCTTACGTATCCTGGTTTGCTCATTGG	ADI-26992 LAD5223_P05_D08	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 101	1602	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHGNFGGAYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACGATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGGGTGCTTACGTATCCTG GTTTGCTCAT	ADI-26992 LAD5223_P05_D08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 101	1609	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTGATCTGTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26992 LAD5223_P05_D08	Light chain variable region("LC") nucleic acid sequence
Ab 101	1610	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSDLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACGCTTATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACGATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGGGGGGTTACGTATCCTGGTTTGGGCATTG	ADI-26993 LAD5223_P05_F08	Heavy chain variable region ("HC") nucleic acid sequence

		GGGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 102	1618	EVQLLESGGGLVQPGGSLRLSCAASGFTFDAYAMNWVRQ APGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHGNFGGGYVSWFGHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACGATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGGGGGGTTACGTATCCTG GTTTGGGCAT	ADI-26993 LAD5223_P05_F08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 102	1625	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTGATCTGTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26993 LAD5223_P05_F08	Light chain variable region("LC") nucleic acid sequence
Ab 102	1626	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSDLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACGCTTATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACGATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACGTGGGGGGGTGGTTACGTATCCTGGTTTGCTCATTG	ADI-26994 LAD5223_P05_A09	Heavy chain variable region ("HC") nucleic acid sequence

		GGGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 103	1634	EVQLLESGGGLVQPGGSLRLSCAASGFTFDAYAMNWVRQ APGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHGNVGGGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACGATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACGTGGGGGGTGGTTACGTATCCTG GTTTGCTCAT	ADI-26994 LAD5223_P05_A09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 103	1641	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTGATCTGTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26994 LAD5223_P05_A09	Light chain variable region("LC") nucleic acid sequence
Ab 103	1642	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSDLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACGCTTATGCCATGAACTGGGTGCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACGATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGAACTATGCTGTATCCTGGTTTGCTCATTGG	ADI-26995 LAD5223_P05_F09	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 104	1650	EVQLLESGGGLVQPGGSLRLSCAASGFTFDAYAMNWVRQ APGKGLEWVARIRSKYNDYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHGNFGNYAVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACGATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACTATGCTGTATCCTG GTTTGCTCAT	ADI-26995 LAD5223_P05_F09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 104	1657	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTGATCTGTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-26995 LAD5223_P05_F09	Light chain variable region("LC") nucleic acid sequence
Ab 104	1658	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSDLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28708 LAD4204_P01_B01	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 105	1666	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-28708 LAD4204_P01_B01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 105	1673	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28708 LAD4204_P01_B01	Light chain variable region("LC") nucleic acid sequence
Ab 105	1674	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGA QADDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28709 LAD4204_P01_E01	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 106	1682	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-28709 LAD4204_P01_E01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 106	1689	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28709 LAD4204_P01_E01	Light chain variable region("LC") nucleic acid sequence
Ab 106	1690	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGA QAEDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28710 LAD4204_P01_A02	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 107	1698	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-28710 LAD4204_P01_A02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 107	1705	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GTGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28710 LAD4204_P01_A02	Light chain variable region("LC") nucleic acid sequence
Ab 107	1706	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGA QADDEADYYCVLWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28711 LAD4204_P01_A03	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 108	1714	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-28711 LAD4204_P01_A03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 108	1721	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGTCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28711 LAD4204_P01_A03	Light chain variable region("LC") nucleic acid sequence
Ab 108	1722	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG VQADDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28712 LAD4204_P01_E03	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 109	1730	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-28712 LAD4204_P01_E03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 109	1737	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCGC TGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGTCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28712 LAD4204_P01_E03	Light chain variable region("LC") nucleic acid sequence
Ab 109	1738	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG VQADDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGC CAAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28713 LAD4204_P01_A04	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 110	1746	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-28713 LAD4204_P01_A04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 110	1753	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGTCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28713 LAD4204_P01_A04	Light chain variable region("LC") nucleic acid sequence
Ab 110	1754	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG VQAEDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28714 LAD4204_P01_H04	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 111	1762	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-28714 LAD4204_P01_H04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 111	1769	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGTCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAATAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28714 LAD4204_P01_H04	Light chain variable region("LC") nucleic acid sequence
Ab 111	1770	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG VQADDEADYYCALWYNNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28715 LAD4204_P01_C05	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 112	1778	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-28715 LAD4204_P01_C05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 112	1785	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGTCCAGGCAGATGATGAAGCTGATTATTACTGT GTGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28715 LAD4204_P01_C05	Light chain variable region("LC") nucleic acid sequence
Ab 112	1786	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG VQADDEADYYCVLWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28716 LAD4204_P01_G05	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 113	1794	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-28716 LAD4204_P01_G05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 113	1801	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCGC TGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28716 LAD4204_P01_G05	Light chain variable region("LC") nucleic acid sequence
Ab 113	1802	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQADDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGC CAAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28717 LAD4204_P01_A07	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 114	1810	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-28717 LAD4204_P01_A07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 114	1817	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAATAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28717 LAD4204_P01_A07	Light chain variable region("LC") nucleic acid sequence
Ab 114	1818	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQADDEADYYCALWYNNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28718 LAD4204_P01_A08	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 115	1826	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-28718 LAD4204_P01_A08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 115	1833	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GTGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28718 LAD4204_P01_A08	Light chain variable region("LC") nucleic acid sequence
Ab 115	1834	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQADDEADYYCVLWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28719 LAD4205_P01_A09	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 116	1842	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKST LYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGGT	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	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28719 LAD4205_P01_A09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 116	1849	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28719 LAD4205_P01_A09	Light chain variable region("LC") nucleic acid sequence
Ab 116	1850	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGA QADDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28720 LAD4205_P01_G09	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 117	1858	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKST LYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGGT	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	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28720 LAD4205_P01_G09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 117	1865	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28720 LAD4205_P01_G09	Light chain variable region("LC") nucleic acid sequence
Ab 117	1866	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGA QAEDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28721 LAD4205_P01_A10	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 118	1874	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKST LYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGGT	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	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28721 LAD4205_P01_A10	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 118	1881	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GTGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28721 LAD4205_P01_A10	Light chain variable region("LC") nucleic acid sequence
Ab 118	1882	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGA QADDEADYYCVLWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28722 LAD4205_P01_E10	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 119	1890	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKST LYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGGT	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	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28722 LAD4205_P01_E10	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 119	1897	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28722 LAD4205_P01_E10	Light chain variable region("LC") nucleic acid sequence
Ab 119	1898	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGA QADDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28723 LAD4205_P01_A11	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 120	1906	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKST LYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGGT	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	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28723 LAD4205_P01_A11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 120	1913	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGTCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28723 LAD4205_P01_A11	Light chain variable region("LC") nucleic acid sequence
Ab 120	1914	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG VQADDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28724 LAD4205_P01_A12	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 121	1922	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKST LYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGGT	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	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28724 LAD4205_P01_A12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 121	1929	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGTCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28724 LAD4205_P01_A12	Light chain variable region("LC") nucleic acid sequence
Ab 121	1930	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG VQAEDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28725 LAD4205_P01_F12	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 122	1938	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKST LYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGGT	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	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28725 LAD4205_P01_F12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 122	1945	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGTCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAATAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28725 LAD4205_P01_F12	Light chain variable region("LC") nucleic acid sequence
Ab 122	1946	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG VQADDEADYYCALWYNNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28726 LAD4205_P02_A01	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 123	1954	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKST LYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGGT	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	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28726 LAD4205_P02_A01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 123	1961	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGTCCAGGCAGATGATGAAGCTGATTATTACTGT GTGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28726 LAD4205_P02_A01	Light chain variable region("LC") nucleic acid sequence
Ab 123	1962	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG VQADDEADYYCVLWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28727 LAD4205_P02_F01	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 124	1970	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKST LYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGGT	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	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28727 LAD4205_P02_F01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 124	1977	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGTCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28727 LAD4205_P02_F01	Light chain variable region("LC") nucleic acid sequence
Ab 124	1978	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG VQADDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28728 LAD4205_P02_A02	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 125	1986	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKST LYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGGT	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	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28728 LAD4205_P02_A02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 125	1993	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCGC TGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28728 LAD4205_P02_A02	Light chain variable region("LC") nucleic acid sequence
Ab 125	1994	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQADDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGC CAAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28729 LAD4205_P02_E02	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 126	2002	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKST LYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGGT	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	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28729 LAD4205_P02_E02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 126	2009	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCGC TGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GTGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28729 LAD4205_P02_E02	Light chain variable region("LC") nucleic acid sequence
Ab 126	2010	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQADDEADYYCVLWYSNLWVFGGGTKLTVL	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	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGC CAAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28730 LAD4205_P02_A03	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 127	2018	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKST LYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGGT	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	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28730 LAD4205_P02_A03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 127	2025	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCGC TGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28730 LAD4205_P02_A03	Light chain variable region("LC") nucleic acid sequence
Ab 127	2026	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQADDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGC CAAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28731 LAD4205_P02_E03	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 128	2034	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKST LYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGGT	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	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28731 LAD4205_P02_E03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 128	2041	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAATAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28731 LAD4205_P02_E03	Light chain variable region("LC") nucleic acid sequence
Ab 128	2042	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQADDEADYYCALWYNNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28732 LAD4205_P02_C04	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 129	2050	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKST LYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGGT	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	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28732 LAD4205_P02_C04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 129	2057	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GTGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28732 LAD4205_P02_C04	Light chain variable region("LC") nucleic acid sequence
Ab 129	2058	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQADDEADYYCVLWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGT AACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28733 LAD4206_P01_D05	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 130	2066	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKST LYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28733 LAD4206_P01_D05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 130	2073	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28733 LAD4206_P01_D05	Light chain variable region("LC") nucleic acid sequence
Ab 130	2074	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGA QADDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGT AACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28734 LAD4206_P01_E05	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 131	2082	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKST LYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28734 LAD4206_P01_E05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 131	2089	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28734 LAD4206_P01_E05	Light chain variable region("LC") nucleic acid sequence
Ab 131	2090	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGA QAEDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGT AACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28735 LAD4206_P01_D06	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 132	2098	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKST LYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28735 LAD4206_P01_D06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 132	2105	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GTGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28735 LAD4206_P01_D06	Light chain variable region("LC") nucleic acid sequence
Ab 132	2106	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGA QADDEADYYCVLWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGT AACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28736 LAD4206_P01_E06	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 133	2114	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKST LYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28736 LAD4206_P01_E06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 133	2121	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28736 LAD4206_P01_E06	Light chain variable region("LC") nucleic acid sequence
Ab 133	2122	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGA QADDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCCGTGTACTACTGCGTCAGGCACAGT AACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28737 LAD4206_P01_A07	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 134	2130	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKST LYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28737 LAD4206_P01_A07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 134	2137	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGTCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28737 LAD4206_P01_A07	Light chain variable region("LC") nucleic acid sequence
Ab 134	2138	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG VQADDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGT AACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28738 LAD4206_P01_F07	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 135	2146	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKST LYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28738 LAD4206_P01_F07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 135	2153	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCGC TGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGTCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28738 LAD4206_P01_F07	Light chain variable region("LC") nucleic acid sequence
Ab 135	2154	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG VQADDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGC CAAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGT AACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28739 LAD4206_P01_D08	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 136	2162	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKST LYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28739 LAD4206_P01_D08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 136	2169	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGTCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28739 LAD4206_P01_D08	Light chain variable region("LC") nucleic acid sequence
Ab 136	2170	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG VQAEDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGT AACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28740 LAD4206_P01_F08	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 137	2178	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKST LYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28740 LAD4206_P01_F08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 137	2185	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGTCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAATAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28740 LAD4206_P01_F08	Light chain variable region("LC") nucleic acid sequence
Ab 137	2186	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG VQADDEADYYCALWYNNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGT AACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28741 LAD4206_P01_A09	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 138	2194	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKST LYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28741 LAD4206_P01_A09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 138	2201	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGTCCAGGCAGATGATGAAGCTGATTATTACTGT GTGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28741 LAD4206_P01_A09	Light chain variable region("LC") nucleic acid sequence
Ab 138	2202	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG VQADDEADYYCVLWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGT AACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28742 LAD4206_P01_E09	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 139	2210	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKST LYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28742 LAD4206_P01_E09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 139	2217	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGTCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28742 LAD4206_P01_E09	Light chain variable region("LC") nucleic acid sequence
Ab 139	2218	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG VQADDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGT AACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28743 LAD4206_P01_B10	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 140	2226	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKST LYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28743 LAD4206_P01_B10	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 140	2233	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCGC TGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28743 LAD4206_P01_B10	Light chain variable region("LC") nucleic acid sequence
Ab 140	2234	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQADDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGC CAAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGT AACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28744 LAD4206_P01_A11	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 141	2242	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKST LYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28744 LAD4206_P01_A11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 141	2249	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAATAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28744 LAD4206_P01_A11	Light chain variable region("LC") nucleic acid sequence
Ab 141	2250	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQADDEADYYCALWYNNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGT AACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28745 LAD4206_P01_A12	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 142	2258	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKST LYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28745 LAD4206_P01_A12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 142	2265	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GTGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28745 LAD4206_P01_A12	Light chain variable region("LC") nucleic acid sequence
Ab 142	2266	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQADDEADYYCVLWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGT AACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28746 LAD4206_P01_F12	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 143	2274	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKST LYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28746 LAD4206_P01_F12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 143	2281	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28746 LAD4206_P01_F12	Light chain variable region("LC") nucleic acid sequence
Ab 143	2282	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQADDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28747 LAD4204_P02_A01	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 144	2290	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-28747 LAD4204_P02_A01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 144	2297	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCA CGGGGGTCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28747 LAD4204_P02_A01	Light chain variable region("LC") nucleic acid sequence
Ab 144	2298	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGV QADDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28748 LAD4204_P02_A02	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 145	2306	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-28748 LAD4204_P02_A02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 145	2313	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAATAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28748 LAD4204_P02_A02	Light chain variable region("LC") nucleic acid sequence
Ab 145	2314	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGA QADDEADYYCALWYNNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28749 LAD4204_P02_E05	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 146	2322	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-28749 LAD4204_P02_E05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 146	2329	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GTGCTGTGGTACAATAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28749 LAD4204_P02_E05	Light chain variable region("LC") nucleic acid sequence
Ab 146	2330	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQADDEADYYCVLWYNNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28750 LAD4205_P03_B07	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 147	2338	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKST LYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGGT	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	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28750 LAD4205_P03_B07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 147	2345	AGACATGTGGTGACCCAGGAGCCATCGCTCTCAGTGTC CCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCA CTGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCC AGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGC GGCCCAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTT CTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCAT CACGGGGGTCCAGGCAGATGATGAAGCTGATTATTACT GTGCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGA GGGACCAAGCTGACCGTCCTA	ADI-28750 LAD4205_P03_B07	Light chain variable region("LC") nucleic acid sequence
Ab 147	2346	RHVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGPDKRAPGVPDRFSGSLLGDKAALIITGV QADDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGT AACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28751 LAD4206_P02_H05	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 148	2354	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKST LYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28751 LAD4206_P02_H05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 148	2361	AGAACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTC CCCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCA CTGGCCGCAGTCACTACTAGTAACTACGCCAACTGGGTCC AGCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGC GGCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTT CTCTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCAT CACGGGGGCCCAGGCAGATGATGAAGCTGATTATTACT GTGTGCTGTGGTACAATAACCTTTGGGTGTTCGGCGGA GGGACCAAGCTGACCGTCCTA	ADI-28751 LAD4206_P02_H05	Light chain variable region("LC") nucleic acid sequence
Ab 148	2362	RTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQADDEADYYCVLWYNNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28752 LAD4204_P02_G02	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 149	2370	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKST LYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGGT	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	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28752 LAD4204_P02_G02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 149	2377	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCGC TGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGTCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28752 LAD4204_P02_G02	Light chain variable region("LC") nucleic acid sequence
Ab 149	2378	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG VQADDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGC CAAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28753 LAD4204_P02_H03	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 150	2386	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-28753 LAD4204_P02_H03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 150	2393	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28753 LAD4204_P02_H03	Light chain variable region("LC") nucleic acid sequence
Ab 150	2394	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28754 LAD4204_P02_B04	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 151	2402	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-28754 LAD4204_P02_B04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 151	2409	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAATAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28754 LAD4204_P02_B04	Light chain variable region("LC") nucleic acid sequence
Ab 151	2410	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYNNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28755 LAD4204_P02_A06	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 152	2418	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-28755 LAD4204_P02_A06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 152	2425	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GTGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28755 LAD4204_P02_A06	Light chain variable region("LC") nucleic acid sequence
Ab 152	2426	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQADDEADYYCVLWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACGGTTACGTATCCTGGTTTGCTCATTGG	ADI-28756 LAD4204_P02_F06	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 153	2434	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACGGTTACGTATCCTG GTTTGCTCAT	ADI-28756 LAD4204_P02_F06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 153	2441	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28756 LAD4204_P02_F06	Light chain variable region("LC") nucleic acid sequence
Ab 153	2442	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQADDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28757 LAD4205_P03_C07	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 154	2450	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKST LYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGGT	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	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28757 LAD4205_P03_C07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 154	2457	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAATAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28757 LAD4205_P03_C07	Light chain variable region("LC") nucleic acid sequence
Ab 154	2458	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQADDEADYYCALWYNNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28758 LAD4205_P03_F07	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 155	2466	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKST LYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGGT	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	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28758 LAD4205_P03_F07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 155	2473	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCGC TGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28758 LAD4205_P03_F07	Light chain variable region("LC") nucleic acid sequence
Ab 155	2474	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGA QADDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGC CAAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28759 LAD4205_P03_B08	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 156	2482	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKST LYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGGT	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	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28759 LAD4205_P03_B08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 156	2489	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAATAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28759 LAD4205_P03_B08	Light chain variable region("LC") nucleic acid sequence
Ab 156	2490	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGA QADDEADYYCALWYNNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28760 LAD4205_P03_F08	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 157	2498	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKST LYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGGT	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	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28760 LAD4205_P03_F08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 157	2505	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCGC TGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28760 LAD4205_P03_F08	Light chain variable region("LC") nucleic acid sequence
Ab 157	2506	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGC CAAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28761 LAD4205_P03_A09	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 158	2514	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKST LYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGGT	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	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28761 LAD4205_P03_A09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 158	2521	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCGC TGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAATAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28761 LAD4205_P03_A09	Light chain variable region("LC") nucleic acid sequence
Ab 158	2522	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQADDEADYYCALWYNNLWVFGGGTKLTVL	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	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGC CAAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28762 LAD4205_P03_E09	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 159	2530	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKST LYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGGT	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	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28762 LAD4205_P03_E09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 159	2537	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28762 LAD4205_P03_E09	Light chain variable region("LC") nucleic acid sequence
Ab 159	2538	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28763 LAD4205_P03_E10	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 160	2546	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKST LYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGGT	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	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28763 LAD4205_P03_E10	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 160	2553	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GTGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28763 LAD4205_P03_E10	Light chain variable region("LC") nucleic acid sequence
Ab 160	2554	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCVLWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28764 LAD4205_P03_A11	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 161	2562	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKST LYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGGT	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	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28764 LAD4205_P03_A11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 161	2569	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28764 LAD4205_P03_A11	Light chain variable region("LC") nucleic acid sequence
Ab 161	2570	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28765 LAD4205_P03_F11	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 162	2578	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKST LYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGGT	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	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28765 LAD4205_P03_F11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 162	2585	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GTGCTGTGGTACAATAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28765 LAD4205_P03_F11	Light chain variable region("LC") nucleic acid sequence
Ab 162	2586	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQADDEADYYCVLWYNNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28766 LAD4205_P03_A12	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 163	2594	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKST LYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGGT	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	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28766 LAD4205_P03_A12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 163	2601	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GTGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28766 LAD4205_P03_A12	Light chain variable region("LC") nucleic acid sequence
Ab 163	2602	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQADDEADYYCVLWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGGTCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAGTGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28767 LAD4205_P03_E12	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 164	2610	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKST LYLQVNSLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGGT	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	GTCAGGCACGGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28767 LAD4205_P03_E12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 164	2617	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28767 LAD4205_P03_E12	Light chain variable region("LC") nucleic acid sequence
Ab 164	2618	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQADDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGT AACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28768 LAD4206_P02_A01	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 165	2626	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKST LYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28768 LAD4206_P02_A01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 165	2633	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCA CGGGGGTCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28768 LAD4206_P02_A01	Light chain variable region("LC") nucleic acid sequence
Ab 165	2634	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGV QADDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGT AACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28769 LAD4206_P02_H01	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 166	2642	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKST LYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28769 LAD4206_P02_H01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 166	2649	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCATCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAATAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28769 LAD4206_P02_H01	Light chain variable region("LC") nucleic acid sequence
Ab 166	2650	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGA QADDEADYYCALWYNNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGT AACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28770 LAD4206_P02_F02	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 167	2658	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKST LYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28770 LAD4206_P02_F02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 167	2665	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCGC TGGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCACGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28770 LAD4206_P02_F02	Light chain variable region("LC") nucleic acid sequence
Ab 167	2666	QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCGCTGGCGCAGTCACTACTAGTAACTACGC CAAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGT AACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28771 LAD4206_P02_E03	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 168	2674	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKST LYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28771 LAD4206_P02_E03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 168	2681	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28771 LAD4206_P02_E03	Light chain variable region("LC") nucleic acid sequence
Ab 168	2682	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGT AACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28772 LAD4206_P02_D04	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 169	2690	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKST LYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28772 LAD4206_P02_D04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 169	2697	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAATAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28772 LAD4206_P02_D04	Light chain variable region("LC") nucleic acid sequence
Ab 169	2698	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYNNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGT AACTTCGGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28773 LAD4206_P02_H04	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 170	2706	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKST LYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28773 LAD4206_P02_H04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 170	2713	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GTGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28773 LAD4206_P02_H04	Light chain variable region("LC") nucleic acid sequence
Ab 170	2714	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCVLWYSNLWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGT AACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28774 LAD4206_P02_A05	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 171	2722	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKST LYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28774 LAD4206_P02_A05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 171	2729	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28774 LAD4206_P02_A05	Light chain variable region("LC") nucleic acid sequence
Ab 171	2730	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCGCCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACAGT AACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG	ADI-28775 LAD4206_P02_A06	Heavy chain variable region ("HC") nucleic acid sequence

		GGCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 172	2738	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFAISRDDSKST LYLQMNSLRAEDTAVYYCVRHSNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACAGTAACTTCGGGAACAGTTACGTATCCTG GTTTGCTCAT	ADI-28775 LAD4206_P02_A06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 172	2745	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GTGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-28775 LAD4206_P02_A06	Light chain variable region("LC") nucleic acid sequence
Ab 172	2746	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQADDEADYYCVLWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	CAGGTACAGCTGCAGCAGTCAGGACCTGAGCTGGTGAA GCCTGGGGCTTCAGTGAGGATATCCTGCAAGGCTTCTG GCTACACCTTCATAAGCTACTATATACACTGGGTGAAGC AGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGATT TATCCTGGAAATGTTAATACTAAGTACAATGAGAAGTTC AAGGCCAAGGCCACACTGACTGCAGACAAATCCTCCAG CACAGCCTACATGCAGCTCAGCAGTCTGACCTCTGAGGA CTCTGCGGTCTATTTCTGTGCAAGAGATGATAACTACTC CTTTGCTTACTGGGGCCAAGGCAACCACGGTCACCGTCT	ADI-15505 SAD4961_P03_F02	Heavy chain variable region ("HC") nucleic acid sequence

		CCTC		
Ab 173	2754	QVQLQQSGPELVKPGASVRISCKASGYTFISYYIHWVKQRP GQGLEWIGWIYPGNVNTKYNEKFKAKATLTADKSSSTAY MQLSSLTSEDSAVYFCARDDNYSFAYWGQGNHGHRLL	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	TGGATTTATCCTGGAAATGTTAATACTAAGTACAATGAG AAGTTCAAGGCC	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	GACATCGTGATGATCCAGTCTCCATCCTCCCTGGCTGTG TCAGCAGGAGAGAAGGTCACTATGAGCTGCAAATCCAG TCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTT GGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAAC TGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCC CTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCA CTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCA GTTTATTACTGCAAGCAATCTTATAATCTTCGGACGTTCG GTGGAGGGACCAAGCTGGAAATAAAA	ADI-15505 SAD4961_P03_F02	Light chain variable region("LC") nucleic acid sequence
Ab 173	2762	DIVMIQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLA WYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLT ISSVQAEDLAVYYCKQSYNLRTFGGGTKLEIK	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	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAA GAACTACTTGGCT	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	GAAGTACAGCTGCAGCAGTCTGGACCTGACCTGGTGAA GCCTGGGGCTTCAGTGAAGATGTCCTGCAAGGCTTCTG GCTACGCCTTCACAAGCTACTATATACACTGGGTGAAGC AGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGATT TATCTTGGAGATGGTAGTACTAACTACAATGAGAAGTTC AAGGGCAAGACCACACTGACTGCAGACAAATCCTCCAG CACAGCCTACATGTTGCTCAGCAGCCTGACCTCTGAGGA CTCTGCGACCTATTTCTGTGCAAGGGATGATTCGTACTA CTTTGACTACTGGGGCCAAGGCACCACGGTCACCGTCTC	ADI-15506 SAD4961_P03_B03	Heavy chain variable region ("HC") nucleic acid sequence

		CTCA		
Ab 174	2770	EVQLQQSGPDLVKPGASVKMSCKASGYAFTSYYIHWVKQ RPGQGLEWIGWIYLGDGSTNYNEKFKGKTTLTADKSSSTA YMLLSSLTSEDSATYFCARDDSYYFDYWGQGTTVTVSS	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	TGGATTTATCTTGGAGATGGTAGTACTAACTACAATGAG AAGTTCAAGGGC	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	GACATTCAGCTCACTCAGTCTCCATCCTCCCTGGCTGTGT CAGCAGGAGAGAAGGTCACTATGAGCTGCAAATCCAGT CAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTT GGCTTGGTACCAACAGAAACCAGGGCAGTCTCCTAAAC TGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCC CTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCA CTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCA GTTTATTACTGCAAGCAATCTTATAGTCTTCGGACGTTCG GTGGAGGGACCAAGCTGGAAATCAAA	ADI-15506 SAD4961_P03_B03	Light chain variable region("LC") nucleic acid sequence
Ab 174	2778	DIQLTQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAW YQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTIS SVQAEDLAVYYCKQSYSLRTFGGGTKLEIK	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	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAA GAACTACTTGGCT	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	CAGGTGAAGCTGGAGGAGTCAGGACCTGAGCTGGTGA AGCCTGGGGCTTCAGTGAGGATATCCTGCAAGGCTTCT GGCTACACCTTCACACGCTACTATATACACTGGGTGAAG CAGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGA TTTATCCTGGAAATGTTAATACTAAATACAATGAGAAGT TCAAGGGCAAGGCCACACTGTCTGCAGACAAATCCTCCA GCACAGCCTACATGCAGCTCAGCAGCCTGACCTCTGAG GACTCTGCGGTCTATTTCTGTGCAAGAGATGGTGATTAC TACTTTGACTACTGGGGCCAAGGCACCACGGTCACCGTC	ADI-15507 SAD4961_P03_G05	Heavy chain variable region ("HC") nucleic acid sequence

		TCCTCA		
Ab 175	2786	QVKLEESGPELVKPGASVRISCKASGYTFTRYYIHWVKQRP GQGLEWIGWIYPGNVNTKYNEKFKGKATLSADKSSSTAY MQLSSLTSEDSAVYFCARDGDYYFDYWGQGTTVTVSS	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	TGGATTTATCCTGGAAATGTTAATACTAAATACAATGAG AAGTTCAAGGGC	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	GACATTCAGCTCACTCAGTCTCCATCCTCCCTGGCTGTGT CAGCAGGAGAGAAGGTCACTATGAGCTGCAAATCCAGT CAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTT GGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAAC TGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCC CTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCA CTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCA GTTTATTACTGCAAGCAATCTTATAATCTTCGGACGTTCG GTGGAGGCACCAAGCTGGAAATCAAA	ADI-15507 SAD4961_P03_G05	Light chain variable region("LC") nucleic acid sequence
Ab 175	2794	DIQLTQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAW YQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTIS SVQAEDLAVYYCKQSYNLRTFGGGTKLEIK	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	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAA GAACTACTTGGCT	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	GAGGTGCAGCTGCAGGAGTCTGGACCTGAGCTGGTGA AACCTGGGGCTTCAGTGAGGATATCCTGCAAGGCTTCT GGCTACACCTTCACAAGCTACTATATACACTGGGTGAAG CAGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGA TTTATCCTGGAAATGTTAATACTAAGTACAATGAGAAGT TCAAGGGCAAGGCCACACTGACTGCAGACAAATCCTCC AGCACAGCCTACATGCAGCTCAGCAGCCTGACCTCTGAG GACTCTGCGGTCTATTTCTGTGCAAGAGATGGTGATTAC TACTTTGACTACTGGGGCCAAGGCACCACGGTCACCGTC	ADI-15508 SAD4961_P03_H08	Heavy chain variable region ("HC") nucleic acid sequence

		TCCTCA		
Ab 176	2802	EVQLQESGPELVKPGASVRISCKASGYTFTSYYIHWVKQRP GQGLEWIGWIYPGNVNTKYNEKFKGKATLTADKSSSTAY MQLSSLTSEDSAVYFCARDGDYYFDYWGQGTTVTVSS	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	TGGATTTATCCTGGAAATGTTAATACTAAGTACAATGAG AAGTTCAAGGGC	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	GACATTCAGCTGACCCAGTCTCCATCCTCCCTGGCTGTG TCAGCAGGAGAGAAGGTCACTATGAGCTGCAAATCCAG TCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTT GGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAAC TGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCC CTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCA CTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCA GTTTATTACTGCAAGCAATCTTATAATCTTCGGACGTTCG GTGGAGGGACCAAGCTGGAGCTGAAA	ADI-15508 SAD4961_P03_H08	Light chain variable region("LC") nucleic acid sequence
Ab 176	2810	DIQLTQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAW YQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTIS SVQAEDLAVYYCKQSYNLRTFGGGTKLELK	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	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAA GAACTACTTGGCT	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	GAGGTCAAGCTGGAGGAGTCAGGACCTGAGCTGGCGA AGCCTGGGGCTTCAGTGAGGATATCCTGCAAGGCTTCT GGCTACACCTTCACAAGCTACTATATACACTGGGTGAAG CAGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGA TTTATCCTGGAAATGTTAATACTAAGTACAATGAGAAGT TCAAGGGCAAGGCCACACTGACTGCAGACACATCCTCC AGCACAGCCTACATGCAGCTCAGCAGCCTGACCTCTGAG GACTCTGCGGTCTATTTCTGTGCAAGAGATGGTAACTAC TTCTTCGATGTCTGGGGCCAAGGCACCACGGTCACCGTC	ADI-15509 SAD4961_P03_D01	Heavy chain variable region ("HC") nucleic acid sequence

		TCCTCA		
Ab 177	2818	EVKLEESGPELAKPGASVRISCKASGYTFTSYYIHWVKQRP GQGLEWIGWIYPGNVNTKYNEKFKGKATLTADTSSSTAY MQLSSLTSEDSAVYFCARDGNYFFDVWGQGTTVTVSS	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	TGGATTTATCCTGGAAATGTTAATACTAAGTACAATGAG AAGTTCAAGGGC	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	GACATCCAGCTGACTCAGTCTCCATCCTCCCTGGCTGTG TCAGCAGGAGAGAAGGTCACTATGAGCTGCAAATCCAG TCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACCT GGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAAC TGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCC CTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCA CTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCA GTTTATTACTGCAAGCAATCTTATAACCTTCGGACGTTCG GTGGAGGGACCAAGCTGGAGCTGAAA	ADI-15509 SAD4961_P03_D01	Light chain variable region("LC") nucleic acid sequence
Ab 177	2826	DIQLTQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAW YQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTIS SVQAEDLAVYYCKQSYNLRTFGGGTKLELK	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	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAA GAACTACCTGGCT	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	GAGGTTCAGCTGGAGGAGTCTGGACCTGAACTGGTGAA GCCTGGGGCTTCAGTGAGGATATCCTGCAAGGCTTCTG GCTACACCTTCACAAGCTACTATATACACTGGGTGAAGC AGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGATT TATCCTGGAAATGTTAATACTAAGTACAATGAGAAGTTC AAGGGCAAGGCCACACTGACTGCAGACAAATCCTCCAG CACAGCCTACATGCAGCTCAGCAGCCTGACCTCTGAGGA CTCTGCAATCTATTTCTGTGCAAGAGATGGTAACTACTTC TTCGATGTCTGGGGCCAAGGCACCACGGTCACCGTCTCC	ADI-15510 SAD4961_P03_H06	Heavy chain variable region ("HC") nucleic acid sequence

		TCA		
Ab 178	2834	EVQLEESGPELVKPGASVRISCKASGYTFTSYYIHWVKQRP GQGLEWIGWIYPGNVNTKYNEKFKGKATLTADKSSSTAY MQLSSLTSEDSAIYFCARDGNYFFDVWGQGTTVTVSS	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	TGGATTTATCCTGGAAATGTTAATACTAAGTACAATGAG AAGTTCAAGGGC	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	GATATCGAGCTGATTCAGTCTCCATCCTCCCTGGCTGTG TCAGCAGGAGAGAAGGTCACTATGAGCTGCAAATCCAG TCAGAATCTGCTCAACAGTAGAACCCGAAAGAACTACTT GGCTTGGTACCGGCAGAAACCAGGGCAGTCTCCTAAAC TGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCC CTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCA CTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCA GTATATTACTGCAAGCAATCTTATAATCTTCGGACGTTC GGTGGAGGGACCAAGCTGGAGCTGAAA	ADI-15510 SAD4961_P03_H06	Light chain variable region("LC") nucleic acid sequence
Ab 178	2842	DIELIQSPSSLAVSAGEKVTMSCKSSQNLLNSRTRKNYLAW YRQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISS VQAEDLAVYYCKQSYNLRTFGGGTKLELK	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	AAATCCAGTCAGAATCTGCTCAACAGTAGAACCCGAAA GAACTACTTGGCT	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	CAGGTAAAGCTGCAGCAGTCTGGACCTGAGCTGGTGAA GCCTGGGGCTTCAGTGAGGATATCCTGCAAGGCTTCTG GCAACACCTTCACAAGCTCCTATATACACTGGGTGAAGC AGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGATT TATCCTGGAAATGTTAATACTAAGTACAATGAGAAGTTC AAGGGCAAGGCCACACTGACTGCAGACAAATCCTCCAG CACAGTCTACATGCAGCTCAGCAGCCTGACCTCTGAGGA CTCTGCGGTCTATTTCTGTGCAAGAGACGGTAGTAGCTA CTACTTTGACTACTGGGGCCAAGGCACCACGGTCACCGT	ADI-15511 SAD4961_P03_D09	Heavy chain variable region ("HC") nucleic acid sequence

		CTCCTCA		
Ab 179	2850	QVKLQQSGPELVKPGASVRISCKASGNTFTSSYIHWVKQR PGQGLEWIGWIYPGNVNTKYNEKFKGKATLTADKSSSTVY MQLSSLTSEDSAVYFCARDGSSYYFDYWGQGTTVTVSS	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	TGGATTTATCCTGGAAATGTTAATACTAAGTACAATGAG AAGTTCAAGGGC	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	GACATCCAGCTGACTCAGTCTCCATCCTCCCTGGCTGTG TCAGCAGGAGAGAAGGTCACTATGAGCTGCAAATCCAG TCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTT GGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAAC TGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCC CTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCA CTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCA GTTTATTACTGCAAGCAATCTTATAATCTTCGGACGTTCG GTGGAGGGACCAAGCTGGAGCTGAAA	ADI-15511 SAD4961_P03_D09	Light chain variable region("LC") nucleic acid sequence
Ab 179	2858	DIQLTQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAW YQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTIS SVQAEDLAVYYCKQSYNLRTFGGGTKLELK	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	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAA GAACTACTTGGCT	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	GAAGTGCAGCTGGAGCAGTCAGGACCTGAGCTGGTGA AGCCTGGGGCTTCAGTGAAGATGTCCTGCAAGGCTTCT GGCTACACCTTCACAAGCTACTATATACACTGGGTGAAG CAGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGA TTTATCCTGGAGATGGTAGTACTAAGTACAATGAGAAGT TCAAGGGCAAGACCACACTGACTGCAGACAAATCCTCC AGCACAGCCTACATGTTGCTCAGCAGCCTGACCTCTGAG GACTCTGCGATCTATTTCTGTGCAAGGGATGGTTCGTAC TACTTTGACTACTGGGGCCAAGGCACCACGGTCACCGTC	ADI-15512 SAD4961_P03_F09	Heavy chain variable region ("HC") nucleic acid sequence

		TCCTCA		
Ab 180	2866	EVQLEQSGPELVKPGASVKMSCKASGYTFTSYYIHWVKQR PGQGLEWIGWIYPGDGSTKYNEKFKGKTTLTADKSSSTAY MLLSSLTSEDSAIYFCARDGSYYFDYWGQGTTVTVSS	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	TGGATTTATCCTGGAGATGGTAGTACTAAGTACAATGAG AAGTTCAAGGGC	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	GACATTCAGCTCACCCAGTCTCCATCCTCCCTGGCTGTGT CAGCAGGAGAGAAGGTCACTATGAGCTGCAAATCCAGT CAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTT GGCTTGGTACCAACAGAAACCAGGGCAGTCTCCTAAAC TGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCC CTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCA CTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCA GTTTATTACTGCAAGCAATCTTATAGTCTTCGGACGTTCG GTGGAGGGACCAAGCTGGAGCTGAAA	ADI-15512 SAD4961_P03_F09	Light chain variable region("LC") nucleic acid sequence

Ab 180	2874	DIQLTQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAW YQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTIS SVQAEDLAVYYCKQSYSLRTFGGGTKLELK	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	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAA GAACTACTTGGCT	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	GAGGTGAAGCTGGAGGAGTCTGGACCTGAGCTGGTGA AGCCTGGGGCTTCAGTGAAGATGTCCTGCAAGGCTTCT GGCTACACCTTCACAAGCTACTATATACACTGGGTGAAG CAGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGA TTTATCCTGGAGATGGTAGTACTAAGTACAATGAGAAGT TCAAGGGCAAGACCACACTGACTGCAGACAAATCCTCC AGCACAGCCTACATGTTGCTCAGCAGCCTGACCTCTGAG GACTCTGCGATCTATTTCTGTGCAAGGGATGGTTCGTAC TACTTTGACTACTGGGGCCAAGGCACCACGGTCACCGTC TCCTCA	ADI-15513 SAD4961_P03_H11	Heavy chain variable region ("HC") nucleic acid sequence
Ab 181	2882	EVKLEESGPELVKPGASVKMSCKASGYTFTSYYIHWVKQRP GQGLEWIGWIYPGDGSTKYNEKFKGKTTLTADKSSSTAYM LLSSLTSEDSAIYFCARDGSYYFDYWGQGTTVTVSS	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	TGGATTTATCCTGGAGATGGTAGTACTAAGTACAATGAG AAGTTCAAGGGC	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	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGGCTGTG TCAGCAGGAGAGAAGGTCACTATGAGCTGCAAATCCAG TCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTT GGCTTGGTACCAACAGAAACCAGGGCAGTCTCCTAAAC TGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCC CTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCA CTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCA GTTTATTACTGCAAGCAATCTTATAGTCTTCGGACGTTCG GTGGAGGGACCAAGCTGGAGCTGAAA	ADI-15513 SAD4961_P03_H11	Light chain variable region("LC") nucleic acid sequence
Ab 181	2890	DIQLTQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAW YQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTIS SVQAEDLAVYYCKQSYSLRTFGGGTKLELK	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	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAA GAACTACTTGGCT	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	GAAGTCAAGCTGCAGGAGTCTGGACCTGAGCTGGTGAA GCCTGGGGCTTCAGTGAAGATGTCCTGCAAGGCTTCTG GCTACACCTTCACAAGCTACTATATACACTGGGTGAAGC AGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGATT TATCCTGGAGATGGTAGTACTAAGTACAATGAGAAGTTC AAGGGCAAGACCACACTGACTGCAGACAAATCCTCCAG CACAGCCTACATGTTGCTCAGCAGCCTGACCTCTGAGGA CTCTGCGATCTATTTCTGTGCAAGGGACTACGGGTACTA CTTTGACTACTGGGGCCAAGGCACCACGGTCACCGTCTC CTCA	ADI-15514 SAD4961_P03_C02	Heavy chain variable region ("HC") nucleic acid sequence
Ab 182	2898	EVKLQESGPELVKPGASVKMSCKASGYTFTSYYIHWVKQR PGQGLEWIGWIYPGDGSTKYNEKFKGKTTLTADKSSSTAY MLLSSLTSEDSAIYFCARDYGYYFDYWGQGTTVTVSS	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	TGGATTTATCCTGGAGATGGTAGTACTAAGTACAATGAG AAGTTCAAGGGC	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	GACATTCAGCTGACCCAGTCTCCATCCTCCCTGGCTGTG TCAGCAGGAGAGAAGGTCACTATGAGCTGCAAATCCAG TCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTT GGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAAC TGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCC CTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCA CTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCA GTTTATTACTGCAAGCAATCTTATAATCTTCGGACGTTCG GTGGAGGGACCAAGCTGGAGCTGAAA	ADI-15514 SAD4961_P03_C02	Light chain variable region("LC") nucleic acid sequence
Ab 182	2906	DIQLTQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAW YQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTIS SVQAEDLAVYYCKQSYNLRTFGGGTKLELK	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	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAA GAACTACTTGGCT	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	GAGGTTAAGCTGGAGGAGTCAGGACCTGAGCTGGTGA AGCCTGGGGCTTCAGTGAGGATATCCTGCAAGGCTTCT GGCTACACCTTCACAAGCTACTATATACACTGGGTGAAG CAGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGA TTTATCCTGGAAATGTTAATACTAAGTACAATGAGAAGT TCAAGGGCAAGGCCACACTGACTGCAGACAAATCCTCC AGCACAGTTTATATGCAGCTCAGCAGCCTGACCTCTGAG GACTCTGCGGTCTATTTCTGTGCAAGAGACTATGGTTAC TACTTTGACTATTGGGGCCAAGGCACCACGGTCACCGTC	ADI-15515 SAD4961_P03_H03	Heavy chain variable region ("HC") nucleic acid sequence

		TCCTCA		
Ab 183	2914	EVKLEESGPELVKPGASVRISCKASGYTFTSYYIHWVKQRP GQGLEWIGWIYPGNVNTKYNEKFKGKATLTADKSSSTVY MQLSSLTSEDSAVYFCARDYGYYFDYWGQGTTVTVSS	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	TGGATTTATCCTGGAAATGTTAATACTAAGTACAATGAG AAGTTCAAGGGC	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	GACATTGTGCTGACCCAGTCTCCATCCTCCCTGGCTGTG TCAGCAGGAGAGAAGGTCACCATGAGCTGCAAATCCAG TCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTT GGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAAC TGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCC CTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCA CTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCA GTTTATTACTGCAAGCAATCTTATAATCTTCGGACGTTCG GTGGAGGGACCAAGCTGGAGCTGAAA	ADI-15515 SAD4961_P03_H03	Light chain variable region("LC") nucleic acid sequence
Ab 183	2922	DIVLTQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAW YQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTIS SVQAEDLAVYYCKQSYNLRTFGGGTKLELK	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	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAA GAACTACTTGGCT	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	GAGGTGCAGCTGGAGGAGTCAGGACCTGAGCTGGTGA GGCCTGGGGCTTCAGTGAGGATATCCTGCAAGGCTTCT GGCTACACCTTCACAAGCTCCTATATACACTGGGTGAAG CAGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGA TTTATCCTGGAAATGTTAATACTAAGTACAATGAGAAGT TCAAGGGCAAGGCCACACTGACTGCAGACAAATCCTCC AGCACAGCCTACATGCACCTCAGCAGCCTGACCTCTGAG GACTCTGCGGTCTATTTCTGTGCAAGAGACTATGGTTAC TACTTTGACTACTGGGGCCAAGGCACCACGGTCACCGTC	ADI-15516 SAD4961_P03_C11	Heavy chain variable region ("HC") nucleic acid sequence

		TCCTCA		
Ab 184	2930	EVQLEESGPELVRPGASVRISCKASGYTFTSSYIHWVKQRP GQGLEWIGWIYPGNVNTKYNEKFKGKATLTADKSSSTAY MHLSSLTSEDSAVYFCARDYGYYFDYWGQGTTVTVSS	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	TGGATTTATCCTGGAAATGTTAATACTAAGTACAATGAG AAGTTCAAGGGC	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	GACATTGTGCTGACCCAATCTCCATCCTCCCTGGCTGTGT CAGCAGGAGAGAAGGTCACTATGAGCTGCAAATCCAGT CAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTT GGCTTGGTACCAGCAGAAAGCAGGGCAGTCTCCTAAAC TGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCC CTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCA CTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCA GTTTATTACTGCAAGCAATCTTATAATCTTCGGACGTTCG GTGGAGGGACCAAGCTGGAGCTGAAA	ADI-15516 SAD4961_P03_C11	Light chain variable region("LC") nucleic acid sequence
Ab 184	2938	DIVLTQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAW YQQKAGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTIS SVQAEDLAVYYCKQSYNLRTFGGGTKLELK	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	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAA GAACTACTTGGCT	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	GAGGTTCAGCTGGAGCAGTCAGGACCTGAGCTGGTGAA GCCTGGGGCTTCAGTGAGGATATCCTGCAAGTCTTCTGG CTACACCTTCACAAGCTACTATATACACTGGGTGAAGCA GAGGCCTGGACAGGGACTTGAGTGGATTGGATGGATTT ATCCTGGAAATGTTAATACTAAATACAATGAGAAGTTCA AGGGCAAGGCCACACTGACTGCAGACAAATCCTCCAGC ACAGCCTACATGCAGCTCAGCAGCCTGACCTCTGAGGAC TCTGCGGTCTATTTCTGTGCAAGAGACTATGGTTACTAC TTTGGCTCCTGGGGCCAAGGCACCACGGTCACCGTCTCC	ADI-15517 SAD4961_P03_H10	Heavy chain variable region ("HC") nucleic acid sequence

		TCA		
Ab 185	2946	EVQLEQSGPELVKPGASVRISCKSSGYTFTSYYIHWVKQRP GQGLEWIGWIYPGNVNTKYNEKFKGKATLTADKSSSTAY MQLSSLTSEDSAVYFCARDYGYYFGSWGQGTTVTVSS	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	TGGATTTATCCTGGAAATGTTAATACTAAATACAATGAG AAGTTCAAGGGC	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	GACATCCAGCTCACCCAGTCTCCATCCTCCCTGGCTGTGT CAGCAGGAGAGAAGGTCACTATGAACTGCAAATCCAGT CAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTT GGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAAT TGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCC CTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCA CTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCA GTTTATTACTGTAAGCAATCTTATAATCTTCGGACGTTCG GTGGAGGCACAAAGCTGGAAATCAAA	ADI-15517 SAD4961_P03_H10	Light chain variable region("LC") nucleic acid sequence
Ab 185	2954	DIQLTQSPSSLAVSAGEKVTMNCKSSQSLLNSRTRKNYLA WYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLT ISSVQAEDLAVYYCKQSYNLRTFGGGTKLEIK	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	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAA GAACTACTTGGCT	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	GAAGTCCAGCTGCAGCAGTCTGGACCTGAGCTGGTGAA GCCTGGGGCTTCAGTGAGGATATCCTGCAAGGCTTCTG GTTACACCTTCACAAGCTACTATATACACTGGGTGAAGC AGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGATT TATCCTGGAAATGTTAATACTAAGTACAATGAGAAGTTC AAGGGCAAGGCCACACTGACTGCAGACAAATCCTCCAG CACAGTCTACATGCAGCTCAGCAGCCTGACCTCTGAGGA CTCTGCGGTCTATTTCTGTGGAAGAGATTACTACGGCTC GTACTACTTTGACAACTGGGGCCAAGGCACCACGGTCA	ADI-15518 SAD4961_P03_C07	Heavy chain variable region ("HC") nucleic acid sequence

		CCGTCTCCTCA		
Ab 186	2962	EVQLQQSGPELVKPGASVRISCKASGYTFTSYYIHWVKQRP GQGLEWIGWIYPGNVNTKYNEKFKGKATLTADKSSSTVY MQLSSLTSEDSAVYFCGRDYYGSYYFDNWGQGTTVTVSS	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	TGGATTTATCCTGGAAATGTTAATACTAAGTACAATGAG AAGTTCAAGGGC	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	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQA PGQGLEWMGWIYPGDGSTKYNEKFKGRVTMTRDTSTST VYMELSSLRSEDTAVYYCARDGSYYFDYWGQGTLVTVSS	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	TGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGA GAAGTTCAAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTC GGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18562 LAD3451_P02_A01	Light chain variable region("LC") nucleic acid sequence
Ab 187	2986	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGTCCTCAGTGAAGGTTTCCTGCAAGGCATCTG GATACACCTTCACCAGCTACTATATACACTGGGTGCGAC AGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGAT CTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAGT TCAAGGGCAGAGTCACCATAACCGCGGACAAGTCCACG AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA GGACACGGCGGTGTACTACTGCGCGAGGGATGGAAGC TATTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACC	ADI-18563 LAD3451_P02_F01	Heavy chain variable region ("HC") nucleic acid sequence

		GTCTCCTCA		
Ab 188	2994	QVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYYIHWVRQA PGQGLEWMGWIYPGDGSTKYNEKFKGRVTITADKSTSTA YMELSSLRSEDTAVYYCARDGSYYFDYWGQGTLVTVSS	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	TGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGA GAAGTTCAAGGGC	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	GCGAGGGGATGGAAGCTATTACTTTGACTAC	ADI-18563 LAD3451_P02_F01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 188	3001	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTC GGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18563 LAD3451_P02_F01	Light chain variable region("LC") nucleic acid sequence
Ab 188	3002	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCT GGATACACCTTCACCAGCTACTATATACACTGGGTGCGA CAGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGGAT CTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAGT TCAAGGGCAGAGTCACCATGACCGCGGACAAGTCCACG AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA GGACACGGCGGTGTACTACTGCGCCAGGGATGGTTCCT ATTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCG	ADI-18564 LAD3451_P03_A01	Heavy chain variable region ("HC") nucleic acid sequence

		TCTCCTCA		
Ab 189	3010	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQA PGQGLEWIGWIYPGDGSTKYNEKFKGRVTMTADKSTSTA YMELSSLRSEDTAVYYCARDGSYYFDYWGQGTLVTVSS	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	TGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGA GAAGTTCAAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTC GGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18564 LAD3451_P03_A01	Light chain variable region("LC") nucleic acid sequence
Ab 189	3018	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCT GGATACACCTTCACCAGCTACTATATACACTGGGTGCGA CAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGA TCTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAG TTCAAGGGCAGAGTCACCATGACCGCGGACAAGTCCAC GAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTG AGGACACGGCGGTGTACTACTGCGCTAGAGATGGCTCA TATTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACC	ADI-18565 LAD3451_P03_A02	Heavy chain variable region ("HC") nucleic acid sequence

		GTCTCCTCA		
Ab 190	3026	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQA PGQGLEWMGWIYPGDGSTKYNEKFKGRVTMTADKSTST AYMELSSLRSEDTAVYYCARDGSYYFDYWGQGTLVTVSS	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	TGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGA GAAGTTCAAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTC GGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18565 LAD3451_P03_A02	Light chain variable region("LC") nucleic acid sequence
Ab 190	3034	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCT GGATACACCTTCACCAGCTACTATATACACTGGGTGCGA CAGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGGAT CTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAGT TCAAGGGCAGAACCACCCTGACCGCGGACAAGTCCACG AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA GGACACGGCGGTGTACTACTGCGCTAGAGACGGATCTT ATTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCG	ADI-18566 LAD3451_P02_A03	Heavy chain variable region ("HC") nucleic acid sequence

		TCTCCTCA		
Ab 191	3042	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQA PGQGLEWIGWIYPGDGSTKYNEKFKGRTTLTADKSTSTAY MELSSLRSEDTAVYYCARDGSYYFDYWGQGTLVTVSS	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	TGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGA GAAGTTCAAGGGC	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	GCTAGAGACGGGATCTTATTACTTTGACTAC	ADI-18566 LAD3451_P02_A03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 191	3049	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTC GGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18566 LAD3451_P02_A03	Light chain variable region("LC") nucleic acid sequence
Ab 191	3050	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGTCCTCAGTGAAGGTTTCCTGCAAGGCATCTG GATACACCTTCACCAGCTACTATATACACTGGGTGCGAC AGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGGATC TACCCTGGTGATGGTAGCACAAAGTACAACGAGAAGTT CAAGGGCAGAACCACCCTGACCGCGGACAAGTCCACGA GCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAG GACACGGCGGTGTACTACTGCGCGAGAGATGGTAGCTA CTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCGT	ADI-18567 LAD3451_P02_E03	Heavy chain variable region ("HC") nucleic acid sequence

		CTCCTCA		
Ab 192	3058	QVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYYIHWVRQA PGQGLEWIGWIYPGDGSTKYNEKFKGRTTLTADKSTSTAY MELSSLRSEDTAVYYCARDGSYYFDYWGQGTLVTVSS	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	TGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGA GAAGTTCAAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCTTAGAACTTTC GGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18567 LAD3451_P02_E03	Light chain variable region("LC") nucleic acid sequence
Ab 192	3066	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCT GGATACACCTTCACCAGCTACTATATACACTGGGTGCGA CAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGA TCTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAG TTCAAGGGCAGAGTCACCATGACCAGGGACACGTCCAC GAGCACAGTCTACATGGAGCTGAGCAGCCTGAGATCTG AGGACACGGCGGTGTACTACTGCGCTAGGGATGGCTCC TACTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACC	ADI-18568 LAD3451_P02_B04	Heavy chain variable region ("HC") nucleic acid sequence

		GTCTCCTCA		
Ab 193	3074	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQA PGQGLEWMGWIYPGDGSTKYNEKFKGRVTMTRDTSTST VYMELSSLRSEDTAVYYCARDGSYYFDYWGQGTLVTVSS	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	TGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGA GAAGTTCAAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTT CGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18568 LAD3451_P02_B04	Light chain variable region("LC") nucleic acid sequence
Ab 193	3082	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYNLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGTCCTCAGTGAAGGTTTCCTGCAAGGCATCTG GATACACCTTCACCAGCTACTATATACACTGGGTGCGAC AGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGAT CTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAGT TCAAGGGCAGAGTCACCATAACCGCGGACAAGTCCACG AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA GGACACGGCGGTGTACTACTGCGCGAGGGATGGAAGC TATTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACC	ADI-18569 LAD3451_P02_E04	Heavy chain variable region ("HC") nucleic acid sequence

		GTCTCCTCA		
Ab 194	3090	QVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYYIHWVRQA PGQGLEWMGWIYPGDGSTKYNEKFKGRVTITADKSTSTA YMELSSLRSEDTAVYYCARDGSYYFDYWGQGTLVTVSS	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	TGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGA GAAGTTCAAGGGC	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	GCGAGGGGATGGAAGCTATTACTTTGACTAC	ADI-18569 LAD3451_P02_E04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 194	3097	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTT CGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18569 LAD3451_P02_E04	Light chain variable region("LC") nucleic acid sequence
Ab 194	3098	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYNLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCT GGATACACCTTCACCAGCTACTATATACACTGGGTGCGA CAGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGGAT CTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAGT TCAAGGGCAGAGTCACCATGACCGCGGACAAGTCCACG AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA GGACACGGCGGTGTACTACTGCGCCAGGGATGGTTCCT ATTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCG	ADI-18570 LAD3451_P02_A05	Heavy chain variable region ("HC") nucleic acid sequence

		TCTCCTCA		
Ab 195	3106	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQA PGQGLEWIGWIYPGDGSTKYNEKFKGRVTMTADKSTSTA YMELSSLRSEDTAVYYCARDGSYYFDYWGQGTLVTVSS	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	TGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGA GAAGTTCAAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTT CGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18570 LAD3451_P02_A05	Light chain variable region("LC") nucleic acid sequence
Ab 195	3114	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYNLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCT GGATACACCTTCACCAGCTACTATATACACTGGGTGCGA CAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGA TCTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAG TTCAAGGGCAGAGTCACCATGACCGCGGACAAGTCCAC GAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTG AGGACACGGCGGTGTACTACTGCGCTAGAGATGGCTCA TATTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACC	ADI-18571 LAD3451_P02_H05	Heavy chain variable region ("HC") nucleic acid sequence

		GTCTCCTCA		
Ab 196	3122	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQA PGQGLEWMGWIYPGDGSTKYNEKFKGRVTMTADKSTST AYMELSSLRSEDTAVYYCARDGSYYFDYWGQGTLVTVSS	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	TGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGA GAAGTTCAAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTT CGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18571 LAD3451_P02_H05	Light chain variable region("LC") nucleic acid sequence
Ab 196	3130	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYNLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCT GGATACACCTTCACCAGCTACTATATACACTGGGTGCGA CAGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGGAT CTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAGT TCAAGGGCAGAACCACCCTGACCGCGGACAAGTCCACG AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA GGACACGGCGGTGTACTACTGCGCTAGAGACGGATCTT ATTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCG	ADI-18572 LAD3451_P02_A06	Heavy chain variable region ("HC") nucleic acid sequence

		TCTCCTCA		
Ab 197	3138	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQA PGQGLEWIGWIYPGDGSTKYNEKFKGRTTLTADKSTSTAY MELSSLRSEDTAVYYCARDGSYYFDYWGQGTLVTVSS	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	TGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGA GAAGTTCAAGGGC	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	GCTAGAGACGGGATCTTATTACTTTGACTAC	ADI-18572 LAD3451_P02_A06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 197	3145	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTT CGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18572 LAD3451_P02_A06	Light chain variable region("LC") nucleic acid sequence
Ab 197	3146	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYNLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGTCCTCAGTGAAGGTTTCCTGCAAGGCATCTG GATACACCTTCACCAGCTACTATATACACTGGGTGCGAC AGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGGATC TACCCTGGTGATGGTAGCACAAAGTACAACGAGAAGTT CAAGGGCAGAACCACCCTGACCGCGGACAAGTCCACGA GCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAG GACACGGCGGTGTACTACTGCGCGAGAGATGGTAGCTA CTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCGT	ADI-18573 LAD3451_P02_G06	Heavy chain variable region ("HC") nucleic acid sequence

		CTCCTCA		
Ab 198	3154	QVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYYIHWVRQA PGQGLEWIGWIYPGDGSTKYNEKFKGRTTLTADKSTSTAY MELSSLRSEDTAVYYCARDGSYYFDYWGQGTLVTVSS	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	TGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGA GAAGTTCAAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTT CGGCGGAGGGACCAAGCTGGAGATCAAA	ADI-18573 LAD3451_P02_G06	Light chain variable region("LC") nucleic acid sequence
Ab 198	3162	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYNLRTFGGGTKLEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCT GGATACACCTTCACCAGCTCCTATATACACTGGGTGCGA CAGGCCCCTGGACAAAGGCTTGAGTGGATGGGATGGAT CTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGTT CAAGGGCAGAGTCACCATAACCAGGGACACGTCCGCGA GCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAG GACACGGCGGTGTACTACTGCGCTAGGGATTATGGCTA CTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCGT	ADI-18574 LAD3452_P02_A07	Heavy chain variable region ("HC") nucleic acid sequence

		CTCCTCA		
Ab 199	3170	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSSYIHWVRQA PGQRLEWMGWIYPGNVNTKYNEKFKGRVTITRDTSASTA YMELSSLRSEDTAVYYCARDYGYYFDYWGQGTLVTVSS	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	TGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAG AAGTTCAAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTC GGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18574 LAD3452_P02_A07	Light chain variable region("LC") nucleic acid sequence
Ab 199	3178	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCT GGATACACCTTCACCAGCTCCTATATACACTGGGTGCGA CAGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGGAT CTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGTT CAAGGGCAGAGCCACCCTGACCGCGGACAAGTCCGCGA GCACAGCCTACATGCACCTGAGCAGCCTGAGATCTGAG GACACGGCGGTGTACTACTGCGCGAGAGACTACGGCTA CTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCGT	ADI-18575 LAD3452_P02_E07	Heavy chain variable region ("HC") nucleic acid sequence

		CTCCTCA		
Ab 200	3186	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSSYIHWVRQA PGQGLEWIGWIYPGNVNTKYNEKFKGRATLTADKSASTAY MHLSSLRSEDTAVYYCARDYGYYFDYWGQGTLVTVSS	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	TGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAG AAGTTCAAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTC GGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18575 LAD3452_P02_E07	Light chain variable region("LC") nucleic acid sequence
Ab 200	3194	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCT GGATACACCTTCACCAGCTCCTATATACACTGGGTGCGA CAGGCCCCTGGACAAAGGCTTGAGTGGATAGGATGGAT CTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGTT CAAGGGCAGAGTCACCATAACCGCGGACAAGTCCGCGA GCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAG GACACGGCGGTGTACTACTGCGCGAGGGATTACGGATA CTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCGT	ADI-18576 LAD3452_P02_A08	Heavy chain variable region ("HC") nucleic acid sequence

		CTCCTCA		
Ab 201	3202	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSSYIHWVRQA PGQRLEWIGWIYPGNVNTKYNEKFKGRVTITADKSASTAY MELSSLRSEDTAVYYCARDYGYYFDYWGQGTLVTVSS	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	TGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAG AAGTTCAAGGGC	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	GCGAGGGGATTACGGATACTACTTTGACTAC	ADI-18576 LAD3452_P02_A08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 201	3209	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTC GGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18576 LAD3452_P02_A08	Light chain variable region("LC") nucleic acid sequence
Ab 201	3210	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCT GGATACACCTTCACCAGCTCCTATATACACTGGGTGCGA CAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGA TCTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGT TCAAGGGCAGAGTCACCATGACCAGGGACACGTCCACG AGCACAGTCTACATGGAGCTGAGCAGCCTGAGATCTGA GGACACGGCGGTGTACTACTGCGCTAGGGACTATGGTT ACTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCG	ADI-18577 LAD3452_P02_G08	Heavy chain variable region ("HC") nucleic acid sequence

		TCTCCTCA		
Ab 202	3218	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSSYIHWVRQA PGQGLEWMGWIYPGNVNTKYNEKFKGRVTMTRDTSTST VYMELSSLRSEDTAVYYCARDYGYYFDYWGQGTLVTVSS	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	TGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAG AAGTTCAAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTC GGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18577 LAD3452_P02_G08	Light chain variable region("LC") nucleic acid sequence
Ab 202	3226	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCT GGATACACCTTCACCAGCTCCTATATACACTGGGTGCGA CAGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGGAT CTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGTT CAAGGGCAGAGTCACCATGACCGCGGACAAGTCCACGA GCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAG GACACGGCGGTGTACTACTGCGCTAGGGACTACGGTTA TTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCGT	ADI-18578 LAD3452_P02_C09	Heavy chain variable region ("HC") nucleic acid sequence

		CTCCTCA		
Ab 203	3234	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSSYIHWVRQA PGQGLEWIGWIYPGNVNTKYNEKFKGRVTMTADKSTSTA YMELSSLRSEDTAVYYCARDYGYYFDYWGQGTLVTVSS	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	TGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAG AAGTTCAAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTC GGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18578 LAD3452_P02_C09	Light chain variable region("LC") nucleic acid sequence
Ab 203	3242	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCT GGATACACCTTCACCAGCTCCTATATACACTGGGTGCGA CAGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGGAT CTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGTT CAAGGGCAGAGCCACCCTGACCGCGGACAAGTCCACGA GCACAGCCTACATGCACCTGAGCAGCCTGAGATCTGAG GACACGGCGGTGTACTACTGCGCGAGGGACTATGGCTA CTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCGT	ADI-18579 LAD3452_P02_E09	Heavy chain variable region ("HC") nucleic acid sequence

		CTCCTCA		
Ab 204	3250	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSSYIHWVRQA PGQGLEWIGWIYPGNVNTKYNEKFKGRATLTADKSTSTAY MHLSSLRSEDTAVYYCARDYGYYFDYWGQGTLVTVSS	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	TGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAG AAGTTCAAGGGC	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	GCGAGGGGACTATGGCTACTACTTTGACTAC	ADI-18579 LAD3452_P02_E09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 204	3257	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTC GGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18579 LAD3452_P02_E09	Light chain variable region("LC") nucleic acid sequence
Ab 204	3258	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCT GGATACACCTTCACCAGCTCCTATATACACTGGGTGCGA CAGGCCCCTGGACAAAGGCTTGAGTGGATGGGATGGAT CTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGTT CAAGGGCAGAGTCACCATAACCAGGGACACGTCCGCGA GCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAG GACACGGCGGTGTACTACTGCGCTAGGGATTATGGCTA CTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCGT	ADI-18580 LAD3452_P02_B10	Heavy chain variable region ("HC") nucleic acid sequence

		CTCCTCA		
Ab 205	3266	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSSYIHWVRQA PGQRLEWMGWIYPGNVNTKYNEKFKGRVTITRDTSASTA YMELSSLRSEDTAVYYCARDYGYYFDYWGQGTLVTVSS	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	TGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAG AAGTTCAAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTT CGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18580 LAD3452_P02_B10	Light chain variable region("LC") nucleic acid sequence
Ab 205	3274	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYNLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCT GGATACACCTTCACCAGCTCCTATATACACTGGGTGCGA CAGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGGAT CTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGTT CAAGGGCAGAGCCACCCTGACCGCGGACAAGTCCGCGA GCACAGCCTACATGCACCTGAGCAGCCTGAGATCTGAG GACACGGCGGTGTACTACTGCGCGAGAGACTACGGCTA CTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCGT	ADI-18581 LAD3452_P02_F10	Heavy chain variable region ("HC") nucleic acid sequence

		CTCCTCA		
Ab 206	3282	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSSYIHWVRQA PGQGLEWIGWIYPGNVNTKYNEKFKGRATLTADKSASTAY MHLSSLRSEDTAVYYCARDYGYYFDYWGQGTLVTVSS	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	TGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAG AAGTTCAAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTT CGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18581 LAD3452_P02_F10	Light chain variable region("LC") nucleic acid sequence
Ab 206	3290	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYNLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCT GGATACACCTTCACCAGCTCCTATATACACTGGGTGCGA CAGGCCCCTGGACAAAGGCTTGAGTGGATAGGATGGAT CTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGTT CAAGGGCAGAGTCACCATAACCGCGGACAAGTCCGCGA GCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAG GACACGGCGGTGTACTACTGCGCGAGGGATTACGGATA CTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCGT	ADI-18582 LAD3452_P02_B11	Heavy chain variable region ("HC") nucleic acid sequence

		CTCCTCA		
Ab 207	3298	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSSYIHWVRQA PGQRLEWIGWIYPGNVNTKYNEKFKGRVTITADKSASTAY MELSSLRSEDTAVYYCARDYGYYFDYWGQGTLVTVSS	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	TGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAG AAGTTCAAGGGC	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	GCGAGGGGATTACGGATACTACTTTGACTAC	ADI-18582 LAD3452_P02_B11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 207	3305	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTT CGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18582 LAD3452_P02_B11	Light chain variable region("LC") nucleic acid sequence
Ab 207	3306	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYNLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCT GGATACACCTTCACCAGCTCCTATATACACTGGGTGCGA CAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGA TCTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGT TCAAGGGCAGAGTCACCATGACCAGGGACACGTCCACG AGCACAGTCTACATGGAGCTGAGCAGCCTGAGATCTGA GGACACGGCGGTGTACTACTGCGCTAGGGACTATGGTT ACTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCG	ADI-18583 LAD3452_P02_E11	Heavy chain variable region ("HC") nucleic acid sequence

		TCTCCTCA		
Ab 208	3314	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSSYIHWVRQA PGQGLEWMGWIYPGNVNTKYNEKFKGRVTMTRDTSTST VYMELSSLRSEDTAVYYCARDYGYYFDYWGQGTLVTVSS	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	TGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAG AAGTTCAAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTT CGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18583 LAD3452_P02_E11	Light chain variable region("LC") nucleic acid sequence
Ab 208	3322	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYNLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCT GGATACACCTTCACCAGCTCCTATATACACTGGGTGCGA CAGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGGAT CTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGTT CAAGGGCAGAGTCACCATGACCGCGGACAAGTCCACGA GCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAG GACACGGCGGTGTACTACTGCGCTAGGGACTACGGTTA TTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCGT	ADI-18584 LAD3452_P02_C12	Heavy chain variable region ("HC") nucleic acid sequence

		CTCCTCA		
Ab 209	3330	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSSYIHWVRQA PGQGLEWIGWIYPGNVNTKYNEKFKGRVTMTADKSTSTA YMELSSLRSEDTAVYYCARDYGYYFDYWGQGTLVTVSS	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	TGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAG AAGTTCAAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTAGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTT CGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18584 LAD3452_P02_C12	Light chain variable region("LC") nucleic acid sequence
Ab 209	3338	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYNLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCT GGATACACCTTCACCAGCTCCTATATACACTGGGTGCGA CAGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGGAT CTACCCTGGTAATGTTAACACAAAGTACAACGAGAAGTT CAAGGGCAGAGCCACCCTGACCGCGGACAAGTCCACGA GCACAGCCTACATGCACCTGAGCAGCCTGAGATCTGAG GACACGGCGGTGTACTACTGCGCGAGGGACTATGGCTA CTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCGT	ADI-18585 LAD3452_P02_H12	Heavy chain variable region ("HC") nucleic acid sequence

		CTCCTCA		
Ab 210	3346	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSSYIHWVRQA PGQGLEWIGWIYPGNVNTKYNEKFKGRATLTADKSTSTAY MHLSSLRSEDTAVYYCARDYGYYFDYWGQGTLVTVSS	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	TGGATCTACCCTGGTAATGTTAACACAAAGTACAACGAG AAGTTCAAGGGC	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	GCGAGGGGACTATGGCTACTACTTTGACTAC	ADI-18585 LAD3452_P02_H12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 210	3353	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTT CGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18585 LAD3452_P02_H12	Light chain variable region("LC") nucleic acid sequence
Ab 210	3354	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYNLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGG ATCGACCCTGAAAATGGTAACACAATCTACGACCCGAA GTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCA CGAGCACAGTCTACATGGAGCTGAGCAGCCTGAGATCT GAGGACACGGCGGTGTACTACTGCGCTAGAGACGGATA TGCAAGGTATTACTTTGACTACTGGGGCCAAGGAACCCT	ADI-18586 LAD3453_P02_D01	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 211	3362	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQGLEWMGWIDPENGNTIYDPKFQGRVTMTRDTST STVYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVT VSS	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	TGGATCGACCCTGAAAATGGTAACACAATCTACGACCCG AAGTTCCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTC GGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18586 LAD3453_P02_D01	Light chain variable region("LC") nucleic acid sequence
Ab 211	3370	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGG ATCGACCCTGAAAATGGTAACACAATCTACGACCCGAA GTTCCAGGGCAGAGTCACCATGACCGCGGACACGTCCA CGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GAGGACACGGCGGTGTACTACTGCGCGAGGGACGGTT ATGCTAGATATTACTTTGACTACTGGGGCCAAGGAACCC	ADI-18587 LAD3453_P02_E01	Heavy chain variable region ("HC") nucleic acid sequence

		TGGTCACCGTCTCCTCA		
Ab 212	3378	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQGLEWIGWIDPENGNTIYDPKFQGRVTMTADTSTS TAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTV SS	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	TGGATCGACCCTGAAAATGGTAACACAATCTACGACCCG AAGTTCCAGGGC	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	GCGAGGGGACGGTTATGCTAGATATTACTTTGACTAC	ADI-18587 LAD3453_P02_E01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 212	3385	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTC GGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18587 LAD3453_P02_E01	Light chain variable region("LC") nucleic acid sequence
Ab 212	3386	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGG ATCGACCCTGAAAATGGTAACACAATCTACGACCCGAA GTTCCAGGGCAGAGCCACCATAACCGCGGACACGTCCA CGAACACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GAGGACACGGCGGTGTACTACTGCGCCAGAGATGGTTA TGCCAGATACTACTTTGACTACTGGGGCCAAGGAACCCT	ADI-18588 LAD3453_P02_B02	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 213	3394	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQGLEWIGWIDPENGNTIYDPKFQGRATITADTSTNT AYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVS S	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	TGGATCGACCCTGAAAATGGTAACACAATCTACGACCCG AAGTTCCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTC GGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18588 LAD3453_P02_B02	Light chain variable region("LC") nucleic acid sequence
Ab 213	3402	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCCCCTGGACAAAGGCTTGAGTGGATGGGATGG ATCGACCCTGAAAATGGTAACACAATCTATGACCCGAAG TTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGC CAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTG AAGACACGGCGGTGTACTACTGCGCGAGAGATGGATAC GCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTG	ADI-18589 LAD3453_P02_E02	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 214	3410	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDPENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTV SS	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	TGGATCGACCCTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTC GGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18589 LAD3453_P02_E02	Light chain variable region("LC") nucleic acid sequence
Ab 214	3418	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCCCCTGGACAAAGGCTTGAGTGGATAGGATGGA TCGACCCTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGTCACCATAACCGCGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCTAGAGACGGTTACG CCAGATATTACTTTGACTACTGGGGCCAAGGAACCCTGG	ADI-18590 LAD3453_P02_A03	Heavy chain variable region ("HC") nucleic acid sequence

		TCACCGTCTCCTCA		
Ab 215	3426	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWIGWIDPENGNTIYDPKFQGRVTITADTSAST AYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVS S	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	TGGATCGACCCTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTC GGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18590 LAD3453_P02_A03	Light chain variable region("LC") nucleic acid sequence
Ab 215	3434	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCCCCTGGACAAAGGCTTGAGTGGATAGGATGGA TCGACCCTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGCCACCATAACCGCGGACACGTCCGCC AACACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGACGGATACG CGAGATACTACTTTGACTACTGGGGCCAAGGAACCCTG	ADI-18591 LAD3453_P02_E03	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 216	3442	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWIGWIDPENGNTIYDPKFQGRATITADTSANT AYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVS S	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	TGGATCGACCCTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTC GGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18591 LAD3453_P02_E03	Light chain variable region("LC") nucleic acid sequence
Ab 216	3450	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGG ATCGACCCTGAAAATGGTAACACAATCTACGACCCGAA GTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCA CGAGCACAGTCTACATGGAGCTGAGCAGCCTGAGATCT GAGGACACGGCGGTGTACTACTGCGCTAGAGACGGATA TGCAAGGTATTACTTTGACTACTGGGGCCAAGGAACCCT	ADI-18592 LAD3453_P02_B04	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 217	3458	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQGLEWMGWIDPENGNTIYDPKFQGRVTMTRDTST STVYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVT VSS	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	TGGATCGACCCTGAAAATGGTAACACAATCTACGACCCG AAGTTCCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTT CGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18592 LAD3453_P02_B04	Light chain variable region("LC") nucleic acid sequence
Ab 217	3466	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYNLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGG ATCGACCCTGAAAATGGTAACACAATCTACGACCCGAA GTTCCAGGGCAGAGCCACCATAACCGCGGACACGTCCA CGAACACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GAGGACACGGCGGTGTACTACTGCGCCAGAGATGGTTA TGCCAGATACTACTTTGACTACTGGGGCCAAGGAACCCT	ADI-18593 LAD3453_P02_C05	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 218	3474	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQGLEWIGWIDPENGNTIYDPKFQGRATITADTSTNT AYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVS S	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	TGGATCGACCCTGAAAATGGTAACACAATCTACGACCCG AAGTTCCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTT CGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18593 LAD3453_P02_C05	Light chain variable region("LC") nucleic acid sequence
Ab 218	3482	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYNLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCCCCTGGACAAAGGCTTGAGTGGATGGGATGG ATCGACCCTGAAAATGGTAACACAATCTATGACCCGAAG TTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGC CAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTG AAGACACGGCGGTGTACTACTGCGCGAGAGATGGATAC GCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTG	ADI-18594 LAD3453_P02_E05	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 219	3490	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDPENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTV SS	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	TGGATCGACCCTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGTGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTT CGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18594 LAD3453_P02_E05	Light chain variable region("LC") nucleic acid sequence
Ab 219	3498	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYNLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCCCCTGGACAAAGGCTTGAGTGGATAGGATGGA TCGACCCTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGTCACCATAACCGCGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCTAGAGACGGTTACG CCAGATATTACTTTGACTACTGGGGCCAAGGAACCCTGG	ADI-18595 LAD3453_P02_D06	Heavy chain variable region ("HC") nucleic acid sequence

		TCACCGTCTCCTCA		
Ab 220	3506	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWIGWIDPENGNTIYDPKFQGRVTITADTSAST AYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVS S	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	TGGATCGACCCTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTT CGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18595 LAD3453_P02_D06	Light chain variable region("LC") nucleic acid sequence
Ab 220	3514	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYNLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCCCCTGGACAAAGGCTTGAGTGGATAGGATGGA TCGACCCTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGCCACCATAACCGCGGACACGTCCGCC AACACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGACGGATACG CGAGATACTACTTTGACTACTGGGGCCAAGGAACCCTG	ADI-18596 LAD3453_P02_F06	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 221	3522	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWIGWIDPENGNTIYDPKFQGRATITADTSANT AYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVS S	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	TGGATCGACCCTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTT CGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18596 LAD3453_P02_F06	Light chain variable region("LC") nucleic acid sequence
Ab 221	3530	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYNLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGG ATCGACCCTGAAAATGGTAACACAATCTACGACCCGAA GTTCCAGGGCAGAGTCACCATGACCGCGGACACGTCCA CGAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GAGGACACGGCGGTGTACTACTGCGCGAGGGACGGTT ATGCTAGATATTACTTTGACTACTGGGGCCAAGGAACCC	ADI-18597 LAD3453_P03_B03	Heavy chain variable region ("HC") nucleic acid sequence

		TGGTCACCGTCTCCTCA		
Ab 222	3538	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQGLEWIGWIDPENGNTIYDPKFQGRVTMTADTSTS TAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTV SS	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	TGGATCGACCCTGAAAATGGTAACACAATCTACGACCCG AAGTTCCAGGGC	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	GCGAGGGGACGGTTATGCTAGATATTACTTTGACTAC	ADI-18597 LAD3453_P03_B03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 222	3545	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAGAGTTACAATTTGAGAACTTT CGGCGGAGGGACCAAGGTGGAGATCAAA	ADI-18597 LAD3453_P03_B03	Light chain variable region("LC") nucleic acid sequence
Ab 222	3546	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYNLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTCCAGCTTGTACAGTCTGGGGCTGAGGTGAAGAA GCCTGGGGCCTCAGTGAAGATTTCCTGCAAGGCTTCGG GATACCCCTTCAGTTCCTATCCTATGCATTGGGTGCGCC AGGCCCCCGGACAAAGGCTTGAGTGGATGGGATGGATC AACGTTGACAATGAGAACACACAAATATTCATGGAAGTTC CGGGGCAGAGTCACCATTACCAGGGACACATCCGCGAG CACAGTTTACATGGAGCTGAGCAGTCTGATATCTGAAGA CACGGCTGTGTATTACTGTGGGAGAGACTGGGACGGG GCGATCCGTGTCTTGGACTACTGGGGCCAGGGAACCCT	ADI-18965 SAD4931_P05_F07	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 223	3554	QVQLVQSGAEVKKPGASVKISCKASGYPFSSYPMHWVRQ APGQRLEWMGWINVDNENTKYSWKFRGRVTITRDTSAS TVYMELSSLISEDTAVYYCGRDWDGAIRVLDYWGQGTLVT VSS	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	TGGATCAACGTTGACAATGAGAACACAAAATATTCATG GAAGTTCCGGGGC	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	GGGAGAGACTGGGACGGGGCGATCCGTGTCTTGGACT AC	ADI-18965 SAD4931_P05_F07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 223	3561	GATATTGTGATGACTCAGACTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCACCTGCAAGTCCAG CCAGAGTGTTTTATTCAGCTCCGACAATAAGAACTACTT AGCTTGGTACCAGCAGAAACCGGGACAGCCTCCTAAAT TGCTCATTTACTGGGCATCTATCCGGGAATCCGGGGTCC CTGACCGATTCGGTGGCAGCGGGTCTGGGACACATTTC ACTCTCACCATCACCAGCGTGCAGGCTGCAGATGTGGCA GTTTATTACTGTCAGCAATATTATGGTAATTTCCCCACCT TCGGCCAAGGGACACGACTGGAGATTAAA	ADI-18965 SAD4931_P05_F07	Light chain variable region("LC") nucleic acid sequence
Ab 223	3562	DIVMTQTPDSLAVSLGERATITCKSSQSVLFSSDNKNYLAW YQQKPGQPPKLLIYWASIRESGVPDRFGGSGSGTHFTLTIT SVQAADVAVYYCQQYYGNFPTFGQGTRLEIK	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	AAGTCCAGCCAGAGTGTTTTATTCAGCTCCGACAATAAG AACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG CTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTGG	ADI-20564 SAD5574_P03_C02	Heavy chain variable region ("HC") nucleic acid sequence

		TCACCGTCTCCTCA		
Ab 224	3570	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTTTCGGAGAGCTTTC GGCGGAGGGACCAAGGTTGAGATCAAA	ADI-20564 SAD5574_P03_C02	Light chain variable region("LC") nucleic acid sequence
Ab 224	3578	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYFRRAFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCCGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACACCAAGGACTACTATATGCACTGGGTGCG ACAGGCCCCCGGGCAAAGGCTTGAGTGGATGGGATGG ATCGGCCCTGAAAATGGTAACACAATCTATGACCCGAA GTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCG CCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGGTCT GAAGACACGGCGGTGTACTACTGCGCGAGGGATGGAT ACGCTAGATATTACTTTGACTACTGGGGCCAAGGAACCC	ADI-20565 SAD5574_P03_C06	Heavy chain variable region ("HC") nucleic acid sequence

		TGGTCACCGTCTCCTCA		
Ab 225	3586	QVQLVQSGAEVKKPGASVKVSCKASGFNTKDYYMHWVR QAPGQRLEWMGWIGPENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTV SS	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	TGGATCGGCCCTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GCGAGGGGATGGATACGCTAGATATTACTTTGACTAC	ADI-20565 SAD5574_P03_C06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 225	3593	GACATCGTAATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAGGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTC GGCGGAGGGACCAAGGTTGAGATCAAA	ADI-20565 SAD5574_P03_C06	Light chain variable region("LC") nucleic acid sequence
Ab 225	3594	DIVMTQSPDSLAVSLGERATINCRSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AGGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCCCCTGGACAAAGGCTTGAGTGGATGGGATGG ATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAA TTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGC CAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCCG AAGACACGGCGGTGTACTACTGCGCGAGAGATGGATAC GCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTG	ADI-20566 SAD5574_P03_G09	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 226	3602	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAATTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGACTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTC GGCGGAGGGACCAAGGTTGAGATCAAA	ADI-20566 SAD5574_P03_G09	Light chain variable region("LC") nucleic acid sequence
Ab 226	3610	DIVMTQSPDSLAVSLGERATINCKSSQSLLNGRTRKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGTGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAGGGCTTGAGTGGATGGGATGG ATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAG TTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGC CAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTG AAGACACGGCGGTGTACTACTGCGCGAGAGATGGATAC GCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTG	ADI-20567 SAD5574_P03_F09	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 227	3618	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQGLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTTTCGGAGAGCTTTC GGCGGAGGGACCAAGGTTGAGATCAAA	ADI-20567 SAD5574_P03_F09	Light chain variable region("LC") nucleic acid sequence
Ab 227	3626	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYFRRAFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCCCCTGGACAAAGGCTTGAGTGGATGGGATGG ATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAG TTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGC CAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTG AAGACACGGCGGTGTACTACTGCGCGAGAGATGGATAC GCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTG	ADI-20568 SAD5574_P03_A01	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 228	3634	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTC GGCGGAGGGACCAAGGTTGAGATCAAA	ADI-20568 SAD5574_P03_A01	Light chain variable region("LC") nucleic acid sequence
Ab 228	3642	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCCCCTGGACAAAGGCTTGAGTGGATGGGATGG ATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAA TTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGC CAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTG AAGACACGGCGGTGTACTACTGCGCGAGAGATGGATAC GCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTG	ADI-20569 SAD5574_P03_A05	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 229	3650	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAATTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-20569 SAD5574_P03_A05	Light chain variable region("LC") nucleic acid sequence
Ab 229	3658	DIVMTQSPDSLAVSLGGRATINCKSSQSLLNSRTRKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCCGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACACCAAGGACTACTATATGCACTGGGTGCG ACAGGCCCCCGGGCAAAGGCTTGAGTGGATGGGATGG ATCGGCCCTGAAAATGGTAACACAATCTATGACCCGAA GTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCG CCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGGTCT GAAGACACGGCGGTGTACTACTGCGCGAGGGATGGAT ACGCTAGATATTACTTTGACTACTGGGGCCAAGGAACCC	ADI-20570 SAD5574_P03_G06	Heavy chain variable region ("HC") nucleic acid sequence

		TGGTCACCGTCTCCTCA		
Ab 230	3666	QVQLVQSGAEVKKPGASVKVSCKASGFNTKDYYMHWVR QAPGQRLEWMGWIGPENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTV SS	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	TGGATCGGCCCTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GCGAGGGGATGGATACGCTAGATATTACTTTGACTAC	ADI-20570 SAD5574_P03_G06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 230	3673	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG CCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGCCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTC GGCGGAGGGACCAAGGTTGAGATCAAA	ADI-20570 SAD5574_P03_G06	Light chain variable region("LC") nucleic acid sequence
Ab 230	3674	DIVMTQSPDSLAVPLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGCCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCCCCTGGACAAAGGCTTGAGTGGATGGGATGG ATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAA TTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGC CAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTG AAGACACGGCGGTGTACTACTGCGCGAGAGATGGATAC GCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTG	ADI-20571 SAD5574_P03_B03	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 231	3682	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAATTTCAGGGC	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	GACATCGTAATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAGGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTATCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTC GGCGGAGGGACCAAGGTTGAGATCAAA	ADI-20571 SAD5574_P03_B03	Light chain variable region("LC") nucleic acid sequence
Ab 231	3690	DIVMTQSPDSLAVSLGERATINCRSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASIRESGVPDRFSGSGSGTDFTLTISS LQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AGGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG CTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTGG	ADI-20572 SAD5574_P03_H06	Heavy chain variable region ("HC") nucleic acid sequence

		TCACCGTCTCCTCA		
Ab 232	3698	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTTTCGGAGAGCTTTC GGCGGAGGGACCAAGGTTGAGATCAAA	ADI-20572 SAD5574_P03_H06	Light chain variable region("LC") nucleic acid sequence
Ab 232	3706	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYFRRAFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCCCCTGGACAAAGGCTTGAGTGGATGGGATGG ATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAA TTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGC CAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTG AAGACACGGCGGTGTACTACTGCGCGAGAGATGGATAC GCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTG	ADI-20573 SAD5574_P03_A02	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 233	3714	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAATTTCAGGGC	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	GACATCGTAATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAGGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTC GGCGGAGGGACCAAGGTTGAGATCAAA	ADI-20573 SAD5574_P03_A02	Light chain variable region("LC") nucleic acid sequence
Ab 233	3722	DIVMTQSPDSLAVSLGERATINCRSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AGGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG CTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTGG	ADI-20574 SAD5574_P03_A08	Heavy chain variable region ("HC") nucleic acid sequence

		TCACCGTCTCCTCA		
Ab 234	3730	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GGCATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTC GGCGGAGGGACCAAGGTCGAGATCAAA	ADI-20574 SAD5574_P03_A08	Light chain variable region("LC") nucleic acid sequence
Ab 234	3738	GIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCCCCTGGACAAAGGCTTGAGTGGATGGGATGG ATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAA TTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGC CAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTG AAGACACGGCGGTGTACTACTGCGCGAGAGATGGATAC GCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTG	ADI-20575 SAD5574_P03_H05	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 235	3746	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAATTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTC GGCGGAGGGACCAAGGTTGAGATCAAA	ADI-20575 SAD5574_P03_H05	Light chain variable region("LC") nucleic acid sequence
Ab 235	3754	DIVMTQSPDSLAVSLGERATINCKSSQSLLNGRTRKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCCCCTGGACAAAGGCTTGAGTGGATGGGATGG ATCGACCTTGACAATGGTAACACAATCTATGACCCGAAA TTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGC CAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTG AAGACACGGCGGTGTACTACTGCGCGAGAGATGGATAC GCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTG	ADI-20576 SAD5574_P03_A03	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 236	3762	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLDNGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTV SS	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	TGGATCGACCTTGACAATGGTAACACAATCTATGACCCG AAATTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG CCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGCCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTC GGCGGAGGGACCAAGGTTGAGATCAAA	ADI-20576 SAD5574_P03_A03	Light chain variable region("LC") nucleic acid sequence
Ab 236	3770	DIVMTQSPDSLAVPLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGCCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCCCCTGGACAAAGGCTTGAGTGGATGGGATGG ATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAA TTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGC CAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCCG AAGACACGGCGGTGTACTACTGCGCGAGAGATGGATAC GCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTG	ADI-20577 SAD5574_P03_F11	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 237	3778	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAATTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGACTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTC GGCGGAGGGACCAAGGTTGAGATCAAA	ADI-20577 SAD5574_P03_F11	Light chain variable region("LC") nucleic acid sequence
Ab 237	3786	DIVMTQSPDSLAVSLGERATINCKSSQSLLNGRTRKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGTGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCCCCTGGACAAAGGCTTGAGTGGATGGGATGG ATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAA TTTCAGGGCAGGGTCACCATAACCAGGAACACGTCCGC CAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTG AAGACACGGCGGTGTACTACTGCGCGAGAGATGGATAC GCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTG	ADI-20578 SAD5574_P03_B05	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTTTCCTCA		
Ab 238	3794	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRNTSAS TAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAATTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTC GGCGGAGGGACCAAGGTTGAGATCAAA	ADI-20578 SAD5574_P03_B05	Light chain variable region("LC") nucleic acid sequence
Ab 238	3802	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG CTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTGG	ADI-20579 SAD5574_P03_D04	Heavy chain variable region ("HC") nucleic acid sequence

		TCACCGTCTCCTCA		
Ab 239	3810	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG CCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGCCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTC GGCGGAGGGACCAAGGTTGAGATCAAA	ADI-20579 SAD5574_P03_D04	Light chain variable region("LC") nucleic acid sequence
Ab 239	3818	DIVMTQSPDSLAVPLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGCCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG CTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTGG	ADI-20580 SAD5574_P03_A04	Heavy chain variable region ("HC") nucleic acid sequence

		TCACCGTCTCCTCA		
Ab 240	3826	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTC GGCGGAGGGACCAAGGTGGAGATCAAA	ADI-20580 SAD5574_P03_A04	Light chain variable region("LC") nucleic acid sequence
Ab 240	3834	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGACTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCCCCTGGACAAAGGCTTGAGTGGATGGGATGG ATCGGCTCTGAAAATGGTAACACAATCTATGACCCGAAG TTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGC CAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTG AGGACACGGCGGTGTACTACTGCGCGAGAGATGGATAC GCTAGATATTACTTCGACTACTGGGGCCAAGGAACCCTG	ADI-20581 SAD5574_P03_B06	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 241	3842	QVQLVQSGAEVKKPGASVKVSCKASGLNIKDYYMHWVR QAPGQRLEWMGWIGSENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTV SS	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	TGGATCGGCTCTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG CCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGCCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTC GGCGGAGGGACCAAGGTTGAGATCAAA	ADI-20581 SAD5574_P03_B06	Light chain variable region("LC") nucleic acid sequence
Ab 241	3850	DIVMTQSPDSLAVPLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGCCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGACTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCCCCTGGACAAAGGCTTGAGTGGATGGGATGG ATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAA TTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGC CAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTG AAGACACGGCGGTGTACTACTGCGCGAGAGATGGATAC GCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTG	ADI-20582 SAD5574_P03_C08	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 242	3858	QVQLVQSGAEVKKPGASVKVSCKASGLNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAATTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-20582 SAD5574_P03_C08	Light chain variable region("LC") nucleic acid sequence
Ab 242	3866	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCCGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACACCAAGGACTACTATATGCACTGGGTGCG ACAGGCCCCCGGGCAAAGGCTTGAGTGGATGGGATGG ATCGGCCCTGAAAATGGTAACACAATCTATGACCCGAA GTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCG CCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGGTCT GAAGACACGGCGGTGTACTACTGCGCGAGGGATGGAT ACGCTAGATATTACTTTGACTACTGGGGCCAAGGAACCC	ADI-20583 SAD5574_P03_B11	Heavy chain variable region ("HC") nucleic acid sequence

		TGGTCACCGTCTCCTCA		
Ab 243	3874	QVQLVQSGAEVKKPGASVKVSCKASGFNTKDYYMHWVR QAPGQRLEWMGWIGPENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTV SS	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	TGGATCGGCCCTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GCGAGGGGATGGATACGCTAGATATTACTTTGACTAC	ADI-20583 SAD5574_P03_B11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 243	3881	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAACAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTC GGCGGAGGGACCAAGGTTGAGATCAAA	ADI-20583 SAD5574_P03_B11	Light chain variable region("LC") nucleic acid sequence
Ab 243	3882	DIVMTQSPDSLAVSLGERATINCKSSQSLLNNRTRKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAACAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCCCCTGGACAAAGGCTTGAGTGGATGGGATGG ATCGACCTTGAAAATGGTAACACAATCTATGACCCGAAA TTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGC CAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTG AAGACACGGCGGTGTACTACTGCGCGAGAGATGGATAC GCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTG	ADI-20584 SAD5574_P03_D10	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 244	3890	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAATTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTTTCGGAGAGCTTTC GGCGGAGGGACCAAGGTTGAGATCAAA	ADI-20584 SAD5574_P03_D10	Light chain variable region("LC") nucleic acid sequence
Ab 244	3898	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYFRRAFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCGCCTGCAAGGCTTCT GGATCCAATATCAAGGACTACTATGTGCACTGGGTGCG ACAGGCCCCTGGACAAAGGCTTGAGTGGATGGGATGG ATCGGCCCTGAAAATGGTAACACAGTCTATGACCCGAA GTTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCG CCAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCT GAAGACACGGCGGTGTACTACTGCGCGAGAGATGGATA CGCTAGATATTACTTTGACTACTGGGGCCAAGGAACCCT	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTC GGCGGAGGGACCAAGGTGGAGATCAAA	ADI-20585 SAD5402_P01_G02	Light chain variable region("LC") nucleic acid sequence
Ab 245	3914	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCT GGATACACCTTCACCAGCCACTATATACACTGGGTGCGA CAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGA TCTACCCTGGTGATGGTAGCACAAAGTACAACGAGAAG TTCAAGGGCAGAGTCACCATGACCGCGGACAAGTCCAC GAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTG AGGACACGGCGGTGTACTACTGCGCTAGAGATGGCTCA TATTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACC	ADI-20818 SAD5399_P01_C01	Heavy chain variable region ("HC") nucleic acid sequence

		GTCTCCTCA		
Ab 246	3922	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSHYIHWVRQ APGQGLEWMGWIYPGDGSTKYNEKFKGRVTMTADKSTS TAYMELSSLRSEDTAVYYCARDGSYYFDYWGQGTLVTVSS	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	TGGATCTACCCTGGTGATGGTAGCACAAAGTACAACGA GAAGTTCAAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTC GGCGGAGGGACCAAGGTGGAGATCAAA	ADI-20818 SAD5399_P01_C01	Light chain variable region("LC") nucleic acid sequence
Ab 246	3930	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCT GGATACACCTTCACCAGCTCCTATATACACTGGGTGCGA CAGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGGAT CTACCCTGGTAATGTTGACACAAGGTACAACGAGAAGTT CAAGGGCAGAGTCACCATAACCGCGGACAAGTCCGCGA GCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAG GACACGGCGGTGTACTACTGCGCGAGGGATTACGGATA CTACTTTGACTACTGGGGCCAAGGAACCCTGGTCACCGT	ADI-20820 SAD5400_P01_F07	Heavy chain variable region ("HC") nucleic acid sequence

		CTCCTCA		
Ab 247	3938	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSSYIHWVRQA PGQGLEWIGWIYPGNVDTRYNEKFKGRVTITADKSASTAY MELSSLRSEDTAVYYCARDYGYYFDYWGQGTLVTVSS	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	TGGATCTACCCTGGTAATGTTGACACAAGGTACAACGA GAAGTTCAAGGGC	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	GCGAGGGGATTACGGATACTACTTTGACTAC	ADI-20820 SAD5400_P01_F07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 247	3945	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTC GGCGGAGGGACCAAGGTGGAGATCAAA	ADI-20820 SAD5400_P01_F07	Light chain variable region("LC") nucleic acid sequence
Ab 247	3946	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCCCCTGGACAAAGGCTTGAGTGGATAGGATGGA TCGACCCTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGTCACCATAACCGCGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCTAGAGACGGTTACG CCAGATATTACTTTGACTACTGGGGCCAAGGAACCCTGG	ADI-21097 SAD5574_P03_D07	Heavy chain variable region ("HC") nucleic acid sequence

		TCACCGTCTCCTCA		
Ab 248	3954	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWIGWIDPENGNTIYDPKFQGRVTITADTSAST AYMELSSLRSEDTAVYYCARDGYARYYFDYWGQGTLVTVS S	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	TGGATCGACCCTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTC GGCGGAGGGACCAAGGTGGAGATCAAA	ADI-21097 SAD5574_P03_D07	Light chain variable region("LC") nucleic acid sequence
Ab 248	3962	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTACTTTGACTACTGGGGCCAAGGAACCCTG	ADI-21959 SAD5837_P01_E02	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 249	3970	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYYFDYWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-21959 SAD5837_P01_E02	Light chain variable region("LC") nucleic acid sequence
Ab 249	3978	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG CTAGATATTACTTTGACATTTGGGGCCAAGGAACCCTGG	ADI-21963 SAD5837_P01_F07	Heavy chain variable region ("HC") nucleic acid sequence

		TCACCGTCTCCTCA		
Ab 250	3986	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYARYYFDIWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-21963 SAD5837_P01_F07	Light chain variable region("LC") nucleic acid sequence
Ab 250	3994	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTACTTTGACGCTTGGGGCCAAGGAACCCTG	ADI-21965 SAD5837_P01_D09	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 251	4002	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYYFDAWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-21965 SAD5837_P01_D09	Light chain variable region("LC") nucleic acid sequence
Ab 251	4010	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG CTAGATATTTTTTTGACTACTGGGGCCAAGGAACCCTGG	ADI-21967 SAD5837_P01_C11	Heavy chain variable region ("HC") nucleic acid sequence

		TCACCGTCTCCTCA		
Ab 252	4018	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYARYFFDYWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-21967 SAD5837_P01_C11	Light chain variable region("LC") nucleic acid sequence
Ab 252	4026	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTTTGACTACTGGGGCCAAGGAACCCTG	ADI-21970 SAD5837_P02_B02	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 253	4034	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFFDYWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT GGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-21970 SAD5837_P02_B02	Light chain variable region("LC") nucleic acid sequence
Ab 253	4042	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTGGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTACTACGACTACTGGGGCCAAGGAACCCTG	ADI-21971 SAD5837_P02_C03	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 254	4050	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYYYDYWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-21971 SAD5837_P02_C03	Light chain variable region("LC") nucleic acid sequence
Ab 254	4058	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTACTACGACGTGTGGGGCCAAGGAACCCTG	ADI-21972 SAD5837_P02_A04	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 255	4066	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYYYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-21972 SAD5837_P02_A04	Light chain variable region("LC") nucleic acid sequence
Ab 255	4074	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACTACTGGGGCCAAGGAACCCTG	ADI-21973 SAD5837_P02_B05	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 256	4082	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDYWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-21973 SAD5837_P02_B05	Light chain variable region("LC") nucleic acid sequence
Ab 256	4090	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTTTGACGTGTGGGGCCAAGGAACCCTG	ADI-21974 SAD5837_P02_A06	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 257	4098	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFFDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GCGAGAGATGGATACGGGAGATATTTTTTTTGACGTG	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 CTAGATATTTTTTTTGACATATGGGGCCAAGGAACCCTGG	ADI-21975 SAD5837_P02_F08	Heavy chain variable region ("HC") nucleic acid sequence

		TCACCGTCTCCTCA		
Ab 258	4114	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYARYFFDIWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GCGAGAGATGGATACGCTAGATATTTTTTTTGACATA	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	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYARYFFDVWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-21976 SAD5837_P02_B09	Light chain variable region("LC") nucleic acid sequence
Ab 259	4138	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG CTAGATATTTTTACGACGTCTGGGGCCAAGGAACCCTGG	ADI-21977 SAD5837_P02_B11	Heavy chain variable region ("HC") nucleic acid sequence

		TCACCGTCTCCTCA		
Ab 260	4146	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYARYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-21977 SAD5837_P02_B11	Light chain variable region("LC") nucleic acid sequence
Ab 260	4154	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-21978 SAD5837_P04_A01	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 261	4162	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-21978 SAD5837_P04_A01	Light chain variable region("LC") nucleic acid sequence
Ab 261	4170	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG CTAGATATTTTTACGACTACTGGGGCCAAGGAACCCTGG	ADI-21979 SAD5837_P04_A03	Heavy chain variable region ("HC") nucleic acid sequence

		TCACCGTCTCCTCA		
Ab 262	4178	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYARYFYDYWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-21979 SAD5837_P04_A03	Light chain variable region("LC") nucleic acid sequence
Ab 262	4186	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-22523 LAD4606_P01_H12	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 263	4194	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-22523 LAD4606_P01_H12	Light chain variable region("LC") nucleic acid sequence
Ab 263	4202	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCCTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23639 LAD4707_P01_D01	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 264	4210	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDPENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCCTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-23639 LAD4707_P01_D01	Light chain variable region("LC") nucleic acid sequence
Ab 264	4218	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCCCCTGGACAAAGGCTTGAGTGGATAGGATGGA TCGACCCTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCGCGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCTAGAGACGGTTACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23640 LAD4708_P01_H02	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 265	4226	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWIGWIDPENGNTIYDPKFQGRVTITADTSAST AYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTV SS	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	TGGATCGACCCTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GCTAGAGACGGTTACGGGGAGATATTTTTACGACGTG	ADI-23640 LAD4708_P01_H02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 265	4233	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-23640 LAD4708_P01_H02	Light chain variable region("LC") nucleic acid sequence
Ab 265	4234	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23641 LAD4709_P01_E03	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 266	4242	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-23641 LAD4709_P01_E03	Light chain variable region("LC") nucleic acid sequence
Ab 266	4250	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCCTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23642 LAD4710_P01_C04	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 267	4258	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDPENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCCTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-23642 LAD4710_P01_C04	Light chain variable region("LC") nucleic acid sequence
Ab 267	4266	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCCCCTGGACAAAGGCTTGAGTGGATAGGATGGA TCGACCCTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCGCGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCTAGAGACGGTTACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23643 LAD4711_P01_C05	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 268	4274	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWIGWIDPENGNTIYDPKFQGRVTITADTSAST AYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVTV SS	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	TGGATCGACCCTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GCTAGAGACGGTTACGGGGAGATATTTTTACGACGTG	ADI-23643 LAD4711_P01_C05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 268	4281	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-23643 LAD4711_P01_C05	Light chain variable region("LC") nucleic acid sequence
Ab 268	4282	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAGAAGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23644 LAD4758_P02_H01	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 269	4290	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLEEGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAGAAGGTAACACAATCTATGACCC GAAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAGAAAGCAGAACCGGAAAGAACTACT TAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAG CTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTC CCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTT CACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTC GGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23644 LAD4758_P02_H01	Light chain variable region("LC") nucleic acid sequence
Ab 269	4298	DIVMTQSPDSLAVSLGERATINCKSSQSLLESRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAGAAAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATCAACCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23645 LAD4759_P02_A02	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 270	4306	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYQPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATCAACCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAGAAAGCAGAACCGGAAAGAACTACT TAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAG CTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTC CCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTT CACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTC GGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23645 LAD4759_P02_A02	Light chain variable region("LC") nucleic acid sequence
Ab 270	4314	DIVMTQSPDSLAVSLGERATINCKSSQSLLESRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAGAAAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGAAGGATAC GGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-23646 LAD4760_P02_A03	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 271	4322	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCAREGYGRYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GCGAGAGAAGGATACGGGAGATATTTTTTACGACGTG	ADI-23646 LAD4760_P02_A03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 271	4329	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAGAAAGCAGAACCGGAAAGAACTACT TAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAG CTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTC CCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTT CACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTC GGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23646 LAD4760_P02_A03	Light chain variable region("LC") nucleic acid sequence
Ab 271	4330	DIVMTQSPDSLAVSLGERATINCKSSQSLLESRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAGAAAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAGAAGGTAACACAATCTATCAACCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23647 LAD4761_P02_A04	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 272	4338	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLEEGNTIYQPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAGAAGGTAACACAATCTATCAACCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAGAAAGCAGAACCGGAAAGAACTACT TAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAG CTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTC CCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTT CACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTC GGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23647 LAD4761_P02_A04	Light chain variable region("LC") nucleic acid sequence
Ab 272	4346	DIVMTQSPDSLAVSLGERATINCKSSQSLLESRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAGAAAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATCAACCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGAAGGATAC GGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-23648 LAD4762_P02_A05	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 273	4354	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYQPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCAREGYGRYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATCAACCG AAGTTTCAGGGC	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	GCGAGAGAAGGATACGGGAGATATTTTTTACGACGTG	ADI-23648 LAD4762_P02_A05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 273	4361	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAGAAAGCAGAACCGGAAAGAACTACT TAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAG CTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTC CCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTT CACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTC GGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23648 LAD4762_P02_A05	Light chain variable region("LC") nucleic acid sequence
Ab 273	4362	DIVMTQSPDSLAVSLGERATINCKSSQSLLESRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAGAAAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAGAAGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGAAGGATAC GGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-23649 LAD4763_P02_A06	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 274	4370	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLEEGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCAREGYGRYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAGAAGGTAACACAATCTATGACCC GAAGTTTCAGGGC	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	GCGAGAGAAGGATACGGGAGATATTTTTTACGACGTG	ADI-23649 LAD4763_P02_A06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 274	4377	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAGAAAGCAGAACCGGAAAGAACTACT TAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAG CTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTC CCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTT CACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTC GGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23649 LAD4763_P02_A06	Light chain variable region("LC") nucleic acid sequence
Ab 274	4378	DIVMTQSPDSLAVSLGERATINCKSSQSLLESRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAGAAAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAGAAGGTAACACAATCTATCAACCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGAAGGATAC GGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-23650 LAD4764_P02_A07	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 275	4386	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLEEGNTIYQPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCAREGYGRYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAGAAGGTAACACAATCTATCAACCG AAGTTTCAGGGC	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	GCGAGAGAAGGATACGGGAGATATTTTTTACGACGTG	ADI-23650 LAD4764_P02_A07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 275	4393	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAGAAAGCAGAACCGGAAAGAACTACT TAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAG CTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTC CCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTT CACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTC GGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23650 LAD4764_P02_A07	Light chain variable region("LC") nucleic acid sequence
Ab 275	4394	DIVMTQSPDSLAVSLGERATINCKSSQSLLESRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAGAAAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23651 LAD4765_P02_A08	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 276	4402	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAGAAAGCAGAACCGGAAAGAACTACT TAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAG CTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTC CCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTT CACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTC GGCGGAGGGACCAAGGTCGAGATCAAA	ADI-23651 LAD4765_P02_A08	Light chain variable region("LC") nucleic acid sequence
Ab 276	4410	DIVMTQSPDSLAVSLGERATINCKSSQSLLESRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAGAAAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAGAAGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23652 LAD4766_P02_A09	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 277	4418	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLEEGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAGAAGGTAACACAATCTATGACCC GAAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-23652 LAD4766_P02_A09	Light chain variable region("LC") nucleic acid sequence
Ab 277	4426	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATCAACCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23653 LAD4767_P02_A10	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 278	4434	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYQPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATCAACCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-23653 LAD4767_P02_A10	Light chain variable region("LC") nucleic acid sequence
Ab 278	4442	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGAAGGATAC GGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-23654 LAD4768_P02_F11	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 279	4450	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCAREGYGRYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GCGAGAGAAGGATACGGGAGATATTTTTTACGACGTG	ADI-23654 LAD4768_P02_F11	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 279	4457	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-23654 LAD4768_P02_F11	Light chain variable region("LC") nucleic acid sequence
Ab 279	4458	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAGAAGGTAACACAATCTATCAACCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23655 LAD4769_P02_H01	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 280	4466	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLEEGNTIYQPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAGAAGGTAACACAATCTATCAACCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-23655 LAD4769_P02_H01	Light chain variable region("LC") nucleic acid sequence
Ab 280	4474	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATCAACCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGAAGGATAC GGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-23656 LAD4770_P02_A02	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 281	4482	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYQPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCAREGYGRYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATCAACCG AAGTTTCAGGGC	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	GCGAGAGAAGGATACGGGAGATATTTTTTACGACGTG	ADI-23656 LAD4770_P02_A02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 281	4489	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-23656 LAD4770_P02_A02	Light chain variable region("LC") nucleic acid sequence
Ab 281	4490	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAGAAGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGAAGGATAC GGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-23657 LAD4771_P02_H03	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 282	4498	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLEEGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCAREGYGRYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAGAAGGTAACACAATCTATGACCC GAAGTTTCAGGGC	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	GCGAGAGAAGGATACGGGAGATATTTTTTACGACGTG	ADI-23657 LAD4771_P02_H03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 282	4505	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-23657 LAD4771_P02_H03	Light chain variable region("LC") nucleic acid sequence
Ab 282	4506	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAGAAGGTAACACAATCTATCAACCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGAAGGATAC GGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-23658 LAD4772_P02_A04	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 283	4514	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLEEGNTIYQPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCAREGYGRYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAGAAGGTAACACAATCTATCAACCG AAGTTTCAGGGC	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	GCGAGAGAAGGATACGGGAGATATTTTTTACGACGTG	ADI-23658 LAD4772_P02_A04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 283	4521	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-23658 LAD4772_P02_A04	Light chain variable region("LC") nucleic acid sequence
Ab 283	4522	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23659 LAD4779_P01_A04	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 284	4530	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-23659 LAD4779_P01_A04	Light chain variable region("LC") nucleic acid sequence
Ab 284	4538	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23660 LAD4780_P01_B05	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 285	4546	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-23660 LAD4780_P01_B05	Light chain variable region("LC") nucleic acid sequence
Ab 285	4554	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGCTTACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23661 LAD4781_P01_A06	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 286	4562	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GCGAGAGATGCTTACGGGGAGATATTTTTACGACGTG	ADI-23661 LAD4781_P01_A06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 286	4569	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-23661 LAD4781_P01_A06	Light chain variable region("LC") nucleic acid sequence
Ab 286	4570	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGCTTACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23663 LAD4783_P01_C08	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 287	4578	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GCGAGAGATGCTTACGGGGAGATATTTTTACGACGTG	ADI-23663 LAD4783_P01_C08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 287	4585	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-23663 LAD4783_P01_C08	Light chain variable region("LC") nucleic acid sequence
Ab 287	4586	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGCTTACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23664 LAD4784_P01_A09	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 288	4594	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GCGAGAGATGCTTACGGGGAGATATTTTTACGACGTG	ADI-23664 LAD4784_P01_A09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 288	4601	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-23664 LAD4784_P01_A09	Light chain variable region("LC") nucleic acid sequence
Ab 288	4602	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCCTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23667 LAD4787_P01_A12	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 289	4610	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-23667 LAD4787_P01_A12	Light chain variable region("LC") nucleic acid sequence
Ab 289	4618	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23668 LAD4788_P01_C01	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 290	4626	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-23668 LAD4788_P01_C01	Light chain variable region("LC") nucleic acid sequence
Ab 290	4634	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGCTTACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23669 LAD4789_P01_A02	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 291	4642	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GCGAGAGATGCTTACGGGGAGATATTTTTACGACGTG	ADI-23669 LAD4789_P01_A02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 291	4649	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-23669 LAD4789_P01_A02	Light chain variable region("LC") nucleic acid sequence
Ab 291	4650	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23670 LAD4790_P01_H03	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 292	4658	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-23670 LAD4790_P01_H03	Light chain variable region("LC") nucleic acid sequence
Ab 292	4666	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGCTTACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23671 LAD4791_P01_A04	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 293	4674	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAAATCTATGACGCT AAGTTTCAGGGC	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	GCGAGAGATGCTTACGGGGAGATATTTTTACGACGTG	ADI-23671 LAD4791_P01_A04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 293	4681	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-23671 LAD4791_P01_A04	Light chain variable region("LC") nucleic acid sequence
Ab 293	4682	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGCTTACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23672 LAD4792_P01_A05	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 294	4690	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GCGAGAGATGCTTACGGGGAGATATTTTTACGACGTG	ADI-23672 LAD4792_P01_A05	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 294	4697	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-23672 LAD4792_P01_A05	Light chain variable region("LC") nucleic acid sequence
Ab 294	4698	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGCTTACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-23673 LAD4793_P01_D06	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 295	4706	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GCGAGAGATGCTTACGGGGAGATATTTTTACGACGTG	ADI-23673 LAD4793_P01_D06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 295	4713	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-23673 LAD4793_P01_D06	Light chain variable region("LC") nucleic acid sequence
Ab 295	4714	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24403 BAD24629_D09	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 296	4722	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-24403 BAD24629_D09	Light chain variable region("LC") nucleic acid sequence
Ab 296	4730	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24404 BAD24629_H09	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 297	4738	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-24404 BAD24629_H09	Light chain variable region("LC") nucleic acid sequence
Ab 297	4746	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24405 BAD24629_C10	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 298	4754	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-24405 BAD24629_C10	Light chain variable region("LC") nucleic acid sequence
Ab 298	4762	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24407 BAD24629_C11	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 299	4770	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-24407 BAD24629_C11	Light chain variable region("LC") nucleic acid sequence
Ab 299	4778	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24408 BAD24629_F11	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 300	4786	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-24408 BAD24629_F11	Light chain variable region("LC") nucleic acid sequence
Ab 300	4794	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24409 BAD24629_A12	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 301	4802	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-24409 BAD24629_A12	Light chain variable region("LC") nucleic acid sequence
Ab 301	4810	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24410 BAD24629_F12	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 302	4818	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-24410 BAD24629_F12	Light chain variable region("LC") nucleic acid sequence
Ab 302	4826	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24411 BAD24630_C01	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 303	4834	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-24411 BAD24630_C01	Light chain variable region("LC") nucleic acid sequence
Ab 303	4842	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24412 BAD24630_G01	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 304	4850	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-24412 BAD24630_G01	Light chain variable region("LC") nucleic acid sequence
Ab 304	4858	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24413 BAD24630_D02	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 305	4866	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-24413 BAD24630_D02	Light chain variable region("LC") nucleic acid sequence
Ab 305	4874	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24414 BAD24734_G01	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 306	4882	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-24414 BAD24734_G01	Light chain variable region("LC") nucleic acid sequence
Ab 306	4890	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24415 BAD24702_D04	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 307	4898	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-24415 BAD24702_D04	Light chain variable region("LC") nucleic acid sequence
Ab 307	4906	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24416 BAD24702_C05	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 308	4914	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-24416 BAD24702_C05	Light chain variable region("LC") nucleic acid sequence
Ab 308	4922	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24417 BAD24702_E05	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 309	4930	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-24417 BAD24702_E05	Light chain variable region("LC") nucleic acid sequence
Ab 309	4938	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCAGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24418 BAD24734_B02	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 310	4946	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-24418 BAD24734_B02	Light chain variable region("LC") nucleic acid sequence
Ab 310	4954	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAATGTCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24434 BAD24631_D01	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 311	4962	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQCLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCTGTGGGACCAAGGTCGAGATCAAA	ADI-24434 BAD24631_D01	Light chain variable region("LC") nucleic acid sequence
Ab 311	4970	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAATGTCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24435 BAD24631_G01	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 312	4978	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQCLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCTGTGGGACCAAGGTCGAGATCAAA	ADI-24435 BAD24631_G01	Light chain variable region("LC") nucleic acid sequence
Ab 312	4986	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAATGTCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24436 BAD24631_A02	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 313	4994	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQCLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCTGTGGGACCAAGGTCGAGATCAAA	ADI-24436 BAD24631_A02	Light chain variable region("LC") nucleic acid sequence
Ab 313	5002	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAATGTCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24437 BAD24631_E02	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 314	5010	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQCLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCTGTGGGACCAAGGTCGAGATCAAA	ADI-24437 BAD24631_E02	Light chain variable region("LC") nucleic acid sequence
Ab 314	5018	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAATGTCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24438 BAD24734_A06	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 315	5026	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQCLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCTGTGGGACCAAGGTCGAGATCAAA	ADI-24438 BAD24734_A06	Light chain variable region("LC") nucleic acid sequence
Ab 315	5034	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAATGTCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGATGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24439 BAD24631_G04	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 316	5042	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQCLEWMGWIDLENGNTIYDPMFQGRVTITRDTSA STAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG ATGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCTGTGGGACCAAGGTCGAGATCAAA	ADI-24439 BAD24631_G04	Light chain variable region("LC") nucleic acid sequence
Ab 316	5050	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAATGTCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24440 BAD24631_D05	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 317	5058	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQCLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCTGTGGGACCAAGGTCGAGATCAAA	ADI-24440 BAD24631_D05	Light chain variable region("LC") nucleic acid sequence
Ab 317	5066	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAATGTCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24441 BAD24631_E05	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 318	5074	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQCLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCTGTGGGACCAAGGTCGAGATCAAA	ADI-24441 BAD24631_E05	Light chain variable region("LC") nucleic acid sequence
Ab 318	5082	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAATGTCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24442 BAD24734_C07	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 319	5090	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQCLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCTGTGGGACCAAGGTCGAGATCAAA	ADI-24442 BAD24734_C07	Light chain variable region("LC") nucleic acid sequence
Ab 319	5098	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAATGTCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24443 BAD24631_F06	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 320	5106	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQCLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCTGTGGGACCAAGGTCGAGATCAAA	ADI-24443 BAD24631_F06	Light chain variable region("LC") nucleic acid sequence
Ab 320	5114	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAATGTCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24444 BAD24631_B07	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 321	5122	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQCLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCTGTGGGACCAAGGTCGAGATCAAA	ADI-24444 BAD24631_B07	Light chain variable region("LC") nucleic acid sequence
Ab 321	5130	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAATGTCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24445 BAD24631_H07	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 322	5138	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQCLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCTGTGGGACCAAGGTCGAGATCAAA	ADI-24445 BAD24631_H07	Light chain variable region("LC") nucleic acid sequence
Ab 322	5146	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAATGTCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24446 BAD24631_H08	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 323	5154	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQCLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCTGTGGGACCAAGGTCGAGATCAAA	ADI-24446 BAD24631_H08	Light chain variable region("LC") nucleic acid sequence
Ab 323	5162	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGAGGATGTCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-24449 BAD24631_H12	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 324	5170	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGGCLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCTGTGGGACCAAGGTCGAGATCAAA	ADI-24449 BAD24631_H12	Light chain variable region("LC") nucleic acid sequence
Ab 324	5178	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGCTTACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26906 LAD5224_P03_A01	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 325	5186	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GCGAGAGATGCTTACGGGGAGATATTTTTTACGACGTG	ADI-26906 LAD5224_P03_A01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 325	5193	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-26906 LAD5224_P03_A01	Light chain variable region("LC") nucleic acid sequence
Ab 325	5194	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGGTAGAGATGCGTACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26907 LAD5224_P03_D02	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 326	5202	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCGRDAYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-26907 LAD5224_P03_D02	Light chain variable region("LC") nucleic acid sequence
Ab 326	5210	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAGAGGGCAACACAATCTATGACGCTAAG TTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGC CAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTG AAGACACGGCGGTGTACTACTGCGCGAGAGATGCTTAC GGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-26908 LAD5224_P03_A03	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 327	5218	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLEEGNTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAGAGGGCAACACAATCTATGACGC TAAGTTTCAGGGC	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	GCGAGAGATGCTTACGGGGAGATATTTTTACGACGTG	ADI-26908 LAD5224_P03_A03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 327	5225	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-26908 LAD5224_P03_A03	Light chain variable region("LC") nucleic acid sequence
Ab 327	5226	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAGAGGGCAACACAATCTATGACGCTAAG TTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGC CAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTG AAGACACGGCGGTGTACTACTGCGGTAGAGATGCGTAC GGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-26909 LAD5224_P03_E03	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 328	5234	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLEEGNTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCGRDAYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAGAGGGCAACACAATCTATGACGC TAAGTTTCAGGGC	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	GGTAGAGATGCGTACGGGGAGATATTTTTACGACGTG	ADI-26909 LAD5224_P03_E03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 328	5241	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-26909 LAD5224_P03_E03	Light chain variable region("LC") nucleic acid sequence
Ab 328	5242	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATCGTTACG GGGCTTATTTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26910 LAD5224_P03_G04	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 329	5250	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDRYGAYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GCGAGAGATCGTTACGGGGGCTTATTTTTTACGACGTG	ADI-26910 LAD5224_P03_G04	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 329	5257	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-26910 LAD5224_P03_G04	Light chain variable region("LC") nucleic acid sequence
Ab 329	5258	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGTGTTGG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26912 LAD5224_P03_E05	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 330	5266	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDVLGRYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-26912 LAD5224_P03_E05	Light chain variable region("LC") nucleic acid sequence
Ab 330	5274	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATCAGTACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26913 LAD5224_P03_A06	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 331	5282	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDQYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-26913 LAD5224_P03_A06	Light chain variable region("LC") nucleic acid sequence
Ab 331	5290	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAGAGGGCAACACAATCTATGACGCTAAG TTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGC CAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTG AAGACACGGCGGTGTACTACTGCGCGAGAGATGTGTTG GGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-26915 LAD5224_P03_G07	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 332	5298	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLEEGNTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDVLGRYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAGAGGGCAACACAATCTATGACGC TAAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-26915 LAD5224_P03_G07	Light chain variable region("LC") nucleic acid sequence
Ab 332	5306	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGTGTACG GGAGATATTTTTACGACCTTTGGGGCCAAGGAACCCTG	ADI-26916 LAD5224_P03_F08	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 333	5314	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDVYGRYFYDLWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-26916 LAD5224_P03_F08	Light chain variable region("LC") nucleic acid sequence
Ab 333	5322	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGCGTACG GGGGGTATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26917 LAD5224_P03_B09	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 334	5330	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDAYGGYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GCGAGAGATGCGTACGGGGGGGTATTTTTTACGACGTG	ADI-26917 LAD5224_P03_B09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 334	5337	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-26917 LAD5224_P03_B09	Light chain variable region("LC") nucleic acid sequence
Ab 334	5338	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATAATTACG GGGGGTATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26918 LAD5224_P03_E09	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 335	5346	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDNYGGYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GCGAGAGATAATTACGGGGGGGTATTTTTACGACGTG	ADI-26918 LAD5224_P03_E09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 335	5353	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-26918 LAD5224_P03_E09	Light chain variable region("LC") nucleic acid sequence
Ab 335	5354	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGCTTACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26919 LAD5225_P03_D10	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 336	5362	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GCGAGAGATGCTTACGGGGAGATATTTTTACGACGTG	ADI-26919 LAD5225_P03_D10	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 336	5369	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-26919 LAD5225_P03_D10	Light chain variable region("LC") nucleic acid sequence
Ab 336	5370	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGGTAGAGATGCGTACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26920 LAD5225_P03_A11	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 337	5378	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCGRDAYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-26920 LAD5225_P03_A11	Light chain variable region("LC") nucleic acid sequence
Ab 337	5386	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAGAGGGCAACACAATCTATGACGCTAAG TTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGC CAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTG AAGACACGGCGGTGTACTACTGCGCGAGAGATGCTTAC GGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-26921 LAD5225_P03_B12	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 338	5394	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLEEGNTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAGAGGGCAACACAATCTATGACGC TAAGTTTCAGGGC	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	GCGAGAGATGCTTACGGGGAGATATTTTTACGACGTG	ADI-26921 LAD5225_P03_B12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 338	5401	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-26921 LAD5225_P03_B12	Light chain variable region("LC") nucleic acid sequence
Ab 338	5402	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGGTAGAGATGCGTACG GGCTGTATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26924 LAD5225_P04_A02	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 339	5410	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCGRDAYGLYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-26924 LAD5225_P04_A02	Light chain variable region("LC") nucleic acid sequence
Ab 339	5418	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGTGTTGG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26925 LAD5225_P04_E02	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 340	5426	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDVLGRYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-26925 LAD5225_P04_E02	Light chain variable region("LC") nucleic acid sequence
Ab 340	5434	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAGAGGGCAACACAATCTATGACGCTAAG TTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGC CAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTG AAGACACGGCGGTGTACTACTGCGCGAGAGATCGTTAC GGGGCTTATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-26927 LAD5225_P04_G03	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 341	5442	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLEEGNTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDRYGAYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAGAGGGCAACACAATCTATGACGC TAAGTTTCAGGGC	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	GCGAGAGATCGTTACGGGGGCTTATTTTTTACGACGTG	ADI-26927 LAD5225_P04_G03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 341	5449	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-26927 LAD5225_P04_G03	Light chain variable region("LC") nucleic acid sequence
Ab 341	5450	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAGAGGGCAACACAATCTATGACGCTAAG TTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGC CAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTG AAGACACGGCGGTGTACTACTGCGGTAGAGATGCGTAC GGGCTGTATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-26928 LAD5225_P04_A04	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 342	5458	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLEEGNTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCGRDAYGLYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAGAGGGCAACACAATCTATGACGC TAAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-26928 LAD5225_P04_A04	Light chain variable region("LC") nucleic acid sequence
Ab 342	5466	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAGAGGGCAACACAATCTATGACGCTAAG TTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGC CAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTG AAGACACGGCGGTGTACTACTGCGCGAGAGATGTGTTG GGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-26929 LAD5225_P04_E04	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 343	5474	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLEEGNTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDVLGRYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAGAGGGCAACACAATCTATGACGC TAAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-26929 LAD5225_P04_E04	Light chain variable region("LC") nucleic acid sequence
Ab 343	5482	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGTGTACG GGAGATATTTTTACGACCTTTGGGGCCAAGGAACCCTG	ADI-26930 LAD5225_P04_F05	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 344	5490	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDVYGRYFYDLWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-26930 LAD5225_P04_F05	Light chain variable region("LC") nucleic acid sequence
Ab 344	5498	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATAATTACG GGGGGTATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26932 LAD5225_P04_E06	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 345	5506	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDNYGGYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GCGAGAGATAATTACGGGGGGGTATTTTTACGACGTG	ADI-26932 LAD5225_P04_E06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 345	5513	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-26932 LAD5225_P04_E06	Light chain variable region("LC") nucleic acid sequence
Ab 345	5514	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGCTTACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26933 LAD5226_P04_A07	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 346	5522	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GCGAGAGATGCTTACGGGGAGATATTTTTACGACGTG	ADI-26933 LAD5226_P04_A07	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 346	5529	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTATCAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-26933 LAD5226_P04_A07	Light chain variable region("LC") nucleic acid sequence
Ab 346	5530	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSIRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGTGTTGG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26938 LAD5226_P04_E11	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 347	5538	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDVLGRYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTATCAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-26938 LAD5226_P04_E11	Light chain variable region("LC") nucleic acid sequence
Ab 347	5546	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSIRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATCAGTACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26939 LAD5226_P04_B12	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 348	5554	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDQYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTATCAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-26939 LAD5226_P04_B12	Light chain variable region("LC") nucleic acid sequence
Ab 348	5562	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSIRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAGAGGGCAACACAATCTATGACGCTAAG TTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGC CAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTG AAGACACGGCGGTGTACTACTGCGCGAGAGATCGTTAC GGGGCTTATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-26940 LAD5226_P04_E12	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 349	5570	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLEEGNTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDRYGAYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAGAGGGCAACACAATCTATGACGC TAAGTTTCAGGGC	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	GCGAGAGATCGTTACGGGGGCTTATTTTTTACGACGTG	ADI-26940 LAD5226_P04_E12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 349	5577	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTATCAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-26940 LAD5226_P04_E12	Light chain variable region("LC") nucleic acid sequence
Ab 349	5578	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSIRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAGAGGGCAACACAATCTATGACGCTAAG TTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGC CAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTG AAGACACGGCGGTGTACTACTGCGCGAGAGATCAGTAC GGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-26941 LAD5226_P05_A02	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 350	5586	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLEEGNTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDQYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAGAGGGCAACACAATCTATGACGC TAAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTATCAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-26941 LAD5226_P05_A02	Light chain variable region("LC") nucleic acid sequence
Ab 350	5594	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSIRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGTGTACG GGAGATATTTTTACGACCTTTGGGGCCAAGGAACCCTG	ADI-26942 LAD5226_P05_F02	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 351	5602	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDVYGRYFYDLWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTATCAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-26942 LAD5226_P05_F02	Light chain variable region("LC") nucleic acid sequence
Ab 351	5610	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSIRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGCGTACG GGGGGTATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26943 LAD5226_P05_A03	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 352	5618	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDAYGGYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GCGAGAGATGCGTACGGGGGGGTATTTTTTACGACGTG	ADI-26943 LAD5226_P05_A03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 352	5625	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTATCAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-26943 LAD5226_P05_A03	Light chain variable region("LC") nucleic acid sequence
Ab 352	5626	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSIRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATAATTACG GGGGGTATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26944 LAD5226_P05_G03	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 353	5634	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDNYGGYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GCGAGAGATAATTACGGGGGGGTATTTTTACGACGTG	ADI-26944 LAD5226_P05_G03	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 353	5641	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTATCAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-26944 LAD5226_P05_G03	Light chain variable region("LC") nucleic acid sequence
Ab 353	5642	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSIRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAGAGGGCAACACAATCTATGACGCTAAG TTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGC CAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTG AAGACACGGCGGTGTACTACTGCGGTAGAGATGCGTAC GGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-26945 LAD5227_P03_E06	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 354	5650	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLEEGNTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCGRDAYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAGAGGGCAACACAATCTATGACGC TAAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAGAAAGCAGAACCGGAAAGAACTACT TAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAG CTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTC CCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTT CACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTC GGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26945 LAD5227_P03_E06	Light chain variable region("LC") nucleic acid sequence
Ab 354	5658	DIVMTQSPDSLAVSLGERATINCKSSQSLLESRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAGAAAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAGAGGGCAACACAATCTATGACGCTAAG TTTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGC CAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTG AAGACACGGCGGTGTACTACTGCGCGAGAGATGTGTTG GGGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCT	ADI-26950 LAD5227_P03_E10	Heavy chain variable region ("HC") nucleic acid sequence

		GGTCACCGTCTCCTCA		
Ab 355	5666	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLEEGNTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDVLGRYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAGAGGGCAACACAATCTATGACGC TAAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAGAAAGCAGAACCGGAAAGAACTACT TAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAG CTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTC CCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTT CACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTC GGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26950 LAD5227_P03_E10	Light chain variable region("LC") nucleic acid sequence
Ab 355	5674	DIVMTQSPDSLAVSLGERATINCKSSQSLLESRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAGAAAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATAATTACG GGGGGTATTTTTACGACGTGTGGGGCCAAGGAACCCTG	ADI-26954 LAD5227_P03_G12	Heavy chain variable region ("HC") nucleic acid sequence

		GTCACCGTCTCCTCA		
Ab 356	5682	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDNYGGYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GCGAGAGATAATTACGGGGGGGTATTTTTACGACGTG	ADI-26954 LAD5227_P03_G12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 356	5689	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAGAAAGCAGAACCGGAAAGAACTACT TAGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAG CTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTC CCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTT CACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAATCTTATTCTCTGAGAACTTTC GGCGGAGGGACCAAGGTCGAGATCAAA	ADI-26954 LAD5227_P03_G12	Light chain variable region("LC") nucleic acid sequence
Ab 356	5690	DIVMTQSPDSLAVSLGERATINCKSSQSLLESRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSLRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAGAAAGCAGAACCGGAAA GAACTACTTAGCT	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	GAAGTGAAGCTGCAGCAGTCTGGGGCTGAGCTTGTGAG GCCAGGGGCCTTAGTCAAGTTGTCCTGCAAAGCTTCTGA CTTCAACATTAAAGACTACTATATGCACTGGGTGAAGCA GAGGCCTGAACAGGGCCTGGAGTGGATTGGATGGATT GATCCTGAGAATGGTAATACTATATATGACCCGAAGTTC CAGGGCAAGGCCAGTATAACAGCAGACACATCCTCCAA CACAGCCTACCTGCAGCTCAGCAGCCTGACATCTGAGGA CACTGCCGTCTATTACTGTGGTAGGGATGGTAACTACTT TTTTGACTACTGGGGCCAAGGCACCACGGTCACCGTCTC	ADI-29534 SAD4961_P03_C10	Heavy chain variable region ("HC") nucleic acid sequence

		CTCA		
Ab 357	5698	EVKLQQSGAELVRPGALVKLSCKASDFNIKDYYMHWVKQ RPEQGLEWIGWIDPENGNTIYDPKFQGKASITADTSSNTA YLQLSSLTSEDTAVYYCGRDGNYFFDYWGQGTTVTVSS	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	TGGATTGATCCTGAGAATGGTAATACTATATATGACCCG AAGTTCCAGGGC	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	GACATCCAGCTGACTCAGTCTCCATCCTCCCTGGCTGTG TCAGCAGGAGAGAAGGTCACTATGAGCTGCAAATCCAG TCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTT GGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAAC TGCTGATCTACTGGGCATCCACTAGGGAATCTGGAGTCC CTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCA CTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCA GTTTATTACTGCAAGCAATCTTATAATCTTCGGACGTTCG GTGGAGGGACCAAGCTGGAGCTGAAA	ADI-29534 SAD4961_P03_C10	Light chain variable region("LC") nucleic acid sequence
Ab 357	5706	DIQLTQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAW YQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTIS SVQAEDLAVYYCKQSYNLRTFGGGTKLELK	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	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAA GAACTACTTGGCT	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	GAAGTGCAGCTGCAGCAGTCAGGACCTGAGCTGGTGAA GCCTGGGGCTTCAGTGAGGATCTCCTGCAAGGCTTCTG ACTACACCTTCACAAGCTACTATATTCACTGGGTGAAGC AGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGATT TATCCTGGAAATGTTAATACTAAGTACAATGAGAATTTC AAGGACAAGGCCACACTGACTGCAGACAAATCCTCCAG CACAGCCTACATGCACCTCAGCAGCCTGACCTCTGAGGA CTCTGCGGTCTATTTCTGTGCAAGAGATGATGGTTACTA CTTTGACTACTGGGGCCAAGGCACCACGGTCACCGTCTC	ADI-29535 SAD4961_P03_B08	Heavy chain variable region ("HC") nucleic acid sequence

		CTCA		
Ab 358	5714	EVQLQQSGPELVKPGASVRISCKASDYTFTSYYIHWVKQRP GQGLEWIGWIYPGNVNTKYNENFKDKATLTADKSSSTAY MHLSSLTSEDSAVYFCARDDGYYFDYWGQGTTVTVSS	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	TGGATTTATCCTGGAAATGTTAATACTAAGTACAATGAG AATTTCAAGGAC	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	GACATCCAGCTGACCCAGTCTCCATCCTCCCTGGCTGTG TCAGCAGGAGAGAAGGTCACTATGAGCTGCAAATCCAG TCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTT GGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAAC TGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCC CTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCA CTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCA GTTTATTACTGCAAGCAATCTTATAATCTTCGGACGTTCG GTGGAGGCACAAAGCTGGAAATCAAA	ADI-29535 SAD4961_P03_B08	Light chain variable region("LC") nucleic acid sequence
Ab 358	5722	DIQLTQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAW YQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTIS SVQAEDLAVYYCKQSYNLRTFGGGTKLEIK	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	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAA GAACTACTTGGCT	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	CAAGTCAAGCTGGAGCAGTCTGGACCTGAGCTGGTGAA GCCTGGGGCTTCAGTGAAGATGTCCTGCAAGGCTTCTG GCTACACCTTCACAAACTACTATATACACTGGGTGAAGC AGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGATT TATCCTGAAGATGGTAATACTAAATACAATGAGAAATTC AAGGGCAAGACCACACTGACTGCAGACAAATCCTCCAG CACAGCCTACATGTTGCTCAGCAGCCTGACCTCTGAGGA CTCTGCGATCTATTTCTGTGCAAGGAATAACGGTAGTAG CTATGCTATGGACTACTGGGGCCAAGGCACCACGGTCA	ADI-29536 SAD4961_P03_G07	Heavy chain variable region ("HC") nucleic acid sequence

		CCGTCTCCTCA		
Ab 359	5730	QVKLEQSGPELVKPGASVKMSCKASGYTFTNYYIHWVKQR PGQGLEWIGWIYPEDGNTKYNEKFKGKTTLTADKSSSTAY MLLSSLTSEDSAIYFCARNNGSSYAMDYWGQGTTVTVSS	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	TGGATTTATCCTGAAGATGGTAAATACTAAATACAATGAG AAATTCAAGGGC	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	GGCATCCAGCTGACTCAGTCTCCATCCTCCCTGGCTGTG TCAGCAGGAGAGAAGGTCACTATGAGCTGCAAATCCAG TCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTT GGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAAC TGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCC CTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCA CTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCA GTTTATTACTGCAAGCAGTCTTATAATCTTCGGACGTTCG GTGGAGGGACCAAGCTGGAGCTGAAA	ADI-29536 SAD4961_P03_G07	Light chain variable region("LC") nucleic acid sequence
Ab 359	5738	GIQLTQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAW YQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTIS SVQAEDLAVYYCKQSYNLRTFGGGTKLELK	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	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAA GAACTACTTGGCT	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	CAAGTACAGCTGGAGCAGTCAGGACCTGAGCTGGTGAA GCCTGGGGCTTCAGTGAGGATATCCTGCAAGGCTTCTG GCTACACCTTCACAAGCTACTATATACACTGGGTGAGGC AGAGGCCTGGTCAGGGACTTGAGTGGATTGGATGGATT TTTCCTGGAAATGTTAATACTAAGTACAATGAGAAGTTC AAGGGCAAGGCCACACTGACTGCAGACAAATCCTCCAG CACAGCCTACATGCAGCTCAGCAGCCTGACCTCTGAGGA CTCTGCGGTCTATTTCTGTGCAAGAGATGGTAACTACTC CTTTGCTTACTGGGGCCAAGGCACCACGGTCACCGTCTC	ADI-29537 SAD4961_P03_A06	Heavy chain variable region ("HC") nucleic acid sequence

		CTCA		
Ab 360	5746	QVQLEQSGPELVKPGASVRISCKASGYTFTSYYIHWVRQRP GQGLEWIGWIFPGNVNTKYNEKFKGKATLTADKSSSTAY MQLSSLTSEDSAVYFCARDGNYSFAYWGQGTTVTVSS	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	TGGATTTTTCCTGGAAATGTTAATACTAAGTACAATGAG AAGTTCAAGGGC	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	GACATTCAGCTCACTCAGTCTCCATCCTCCCTGGCTGTGT CAGCAGGAGAGAAGGTCACTATGAGCTGCAAATCCAGT CAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTT GGCTTGGTACCAGCAAAAACCAGGGCAGTCTCCTAAAC TGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCC CTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCA CTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCA GTTTATTACTGCAAGCAATCTTATAATCTTCGGACGTTCG GTGGAGGGACAAAGCTGGAAATAAAA	ADI-29537 SAD4961_P03_A06	Light chain variable region("LC") nucleic acid sequence
Ab 360	5754	DIQLTQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAW YQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTIS SVQAEDLAVYYCKQSYNLRTFGGGTKLEIK	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	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAA GAACTACTTGGCT	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	CAGGTGAAGCTGGAGCAGTCTGGACCTGAGCTGGTGAA GCCTGGGGCTTCAGTGAGGATATCCTGCAAGGCTTCTG GCTACACCTTCACAACCTACTATATACACTGGGTGAAGC AGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGATT TATCCTGGAAATGTTAATGCTAAGTACAATGAGAAGTTC AAGGGCAAGGCCACACTGACTGCAGACAAATCCTCCAG CACAGCCTACATGCAGCTCAGCAGCCTGACCTCTGAGGA CTCTGCGGTCTATTTCTGTGCAAGAGATGATGGGTACTA CTTTGACTACTGGGGCCAAGGCACCACGGTCACCGTCTC	ADI-29538 SAD4961_P03_A05	Heavy chain variable region ("HC") nucleic acid sequence

		CTCA		
Ab 361	5762	QVKLEQSGPELVKPGASVRISCKASGYTFTTYYIHWVKQRP GQGLEWIGWIYPGNVNAKYNEKFKGKATLTADKSSSTAY MQLSSLTSEDSAVYFCARDDGYYFDYWGQGTTVTVSS	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	TGGATTTATCCTGGAAATGTTAATGCTAAGTACAATGAG AAGTTCAAGGGC	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	GACATCCAGCTGACTCAGTCTCCATCCTCCCTGGCTGTG TCAGCAGGAGAGAAGGTCACTATGAGCTGCAAATCCAG TCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTT GGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAAC TGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCC CTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCA CTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCA GTTTATTACTGCAAGCAATCTTATAATCTTCGGACGTTCG GTGGAGGCACAAAGCTGGAAAATAAA	ADI-29538 SAD4961_P03_A05	Light chain variable region("LC") nucleic acid sequence
Ab 361	5770	DIQLTQSPSSLAVSAGEKVTMSCKSSQSLLNSRTRKNYLAW YQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTIS SVQAEDLAVYYCKQSYNLRTFGGGTKLENK	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	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAA GAACTACTTGGCT	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	GAGGTCCAGCTGCAACAATCAGGACCTGAGCTGGTGAA GCCTGGGGCCTCAGTGAGGGTATCCTGCAAGGCTTCTG GCTACACCTTCACAAGCTACTATATACACTGGGTGAAGC AGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGATT TATCCTGGAAATGTTAATACTCAGTACAATGAGAAGTTC AAGGGCAAGGCCACACTGACTGCAGACAAATCCTCCAG CACAACCTACATGCAGCTCAGCAGCCTGACCTCTGAGGA CTCTGCGGTCTATTTCTGTGCAAGAGATGGTGATTACTA CTTTGACTACTGGGGCCAAGGCACCACGGTCACCGTCTC	ADI-29539 SAD4961_P03_B04	Heavy chain variable region ("HC") nucleic acid sequence

		CTCA		
Ab 362	5778	EVQLQQSGPELVKPGASVRVSCKASGYTFTSYYIHWVKQR PGQGLEWIGWIYPGNVNTQYNEKFKGKATLTADKSSSTTY MQLSSLTSEDSAVYFCARDGDYYFDYWGQGTTVTVSS	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	TGGATTTATCCTGGAAATGTTAATACTCAGTACAATGAG AAGTTCAAGGGC	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	GGCATTCAGCTGACCCAGTCTCCATCCTCCCTGGCTGTG TCAGCAGGAGAGAAGGTCACTATGACCTGCAAATCCAG TCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTT GGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAAC TGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCC CTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCA CTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCA GTTTATTACTGCAAGCAATCTTATAATCTTCGGACGTTCG GTGGAGGCACAAAGTTGGAAATAAAA	ADI-29539 SAD4961_P03_B04	Light chain variable region("LC") nucleic acid sequence
Ab 362	5786	GIQLTQSPSSLAVSAGEKVTMTCKSSQSLLNSRTRKNYLAW YQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTIS SVQAEDLAVYYCKQSYNLRTFGGGTKLEIK	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	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAA GAACTACTTGGCT	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	GAGGTCAAGCTGCAGGAGTCTGGACCTGAGCTGGTGAA GCCTGGGGCTTCAGTGAGGATATCCTGCAAGGCTTCTG GCTACACCTTCACAAGCTACTATATACACTGGGTGAAGC AGAGGCCTGGACAGGGACTTGAGTGGATTGGATGGATT TATCCTGGAAATGTTAATACTAAGTACAATGAGAAGTTC AAGGGCAAGGCCACACTGACTGCAGACAAATCCTCCAG CACAGCCTACATGCAGCTCAGCAGCCTGACCTCTGAGGA CTCTGCGGTCTATTTCTGTGCAAGAGATGGTGATTACTT CTTTGACTACTGGGGCCAAGGCACCACGGTCACCGTCTC	ADI-29540 SAD4961_P03_E01	Heavy chain variable region ("HC") nucleic acid sequence

		CTCA		
Ab 363	5794	EVKLQESGPELVKPGASVRISCKASGYTFTSYYIHWVKQRP GQGLEWIGWIYPGNVNTKYNEKFKGKATLTADKSSSTAY MQLSSLTSEDSAVYFCARDGDYFFDYWGQGTTVTVSS	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	TGGATTTATCCTGGAAATGTTAATACTAAGTACAATGAG AAGTTCAAGGGC	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	GACATCCAGCTCACCCAGTCTCCATCCTCCCTGGCTGTGT CAGCAGGAGAGAAGGTCACTATGAGCTGCAAATCCAGT CAGAGTCTGCTCAACAGTAGAACCCAAAAGAACTACTTG GCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACT GCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCC CTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCA CTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCA GTTTATTACTGCAAGCAATCTTATAATCTTCGGACGTTCG GTGGAGGCACCAAGCTGAAAATCAAA	ADI-29540 SAD4961_P03_E01	Light chain variable region("LC") nucleic acid sequence
Ab 363	5802	DIQLTQSPSSLAVSAGEKVTMSCKSSQSLLNSRTQKNYLA WYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLT ISSVQAEDLAVYYCKQSYNLRTFGGGTKLKIK	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	AAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCAAAA GAACTACTTGGCT	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	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCC AGCCTGGAGGGTCCCTGAAACTCTCCTGTGCAGCCTCTG GATTCACCTTCAATAAATACGCCATGAACTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTTGCCCGTATT AGAAGCAAATATAACAATTACGCCACATACTACGCCGAC TCTGTGAAAGACAGATTCACCATCTCAAGAGATGATTCA AAGAACACAGCGTATCTGCAAATGAACAACCTGAAAAC CGAGGACACGGCGGTGTACTACTGCGTGAGGCACGGCA ACTTCGGGAATTCCTATATTTCATACTGGGCCTACTGGG	CTL-19613 LAD3583_P02_A09	Heavy chain variable region ("HC") nucleic acid sequence

		GCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 364	5810	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVR QAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSK NTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS	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	CGTATTAGAAGCAAATATAACAATTACGCCACATACTAC GCCGACTCTGTGAAAGAC	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	GTGAGGCACGGCAACTTCGGGAATTCCTATATTTCATAC TGGGCCTAC	CTL-19613 LAD3583_P02_A09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 364	5817	CAGACTGTGGTGACTCAGGAGCCCTCACTGACTGTGTCC CCAGGAGGGACAGTCACTCTCACCTGTGGCTCCAGCACT GGAGCTGTCACCAGTGGTAATTATCCCAACTGGGTCCA GCAGAAGCCTGGCCAAGCCCCCAGGGGACTGATTGGTG GTACAAAATTCCTGGCCCCCGGGACACCTGCCCGGTTCT CAGGCTCCCTCCTTGGGGGCAAAGCTGCCCTGACCCTTT CGGGTGTGCAGCCTGAGGATGAGGCTGAGTATTACTGC GTGCTCTGGTATAGTAATCGGTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	CTL-19613 LAD3583_P02_A09	Light chain variable region("LC") nucleic acid sequence
Ab 364	5818	QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQ QKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCVLWYSNRWVFGGGTKLTVL	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	GGCTCCAGCACTGGAGCTGTCACCAGTGGTAATTATCCC AAC	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	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCC AGCCTGGAGGGTCCCTGAAACTCTCCTGTGCAGCCTCTG GATTCACCTTCAATAAATACGCCATGAACTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTTGCCCGTATT AGAAGCAAATATAACAATTACGCCACATACTACGCCGAC TCTGTGAAAGACAGATTCACCATCTCAAGAGATGATTCA AAGAACACAGCGTATCTGCAAATGAACAACCTGAAAAC CGAGGACACGGCGGTGTACTACTGCGTGAGGCACGGCA ACTTCGGGAATTCCTATATTTCATACTGGGCCTACTGGG	CTL-19669 LAD3584_P02_H12	Heavy chain variable region ("HC") nucleic acid sequence

		GCCAAGGAACCCTGGTCACCGTCTCCTCA		
Ab 365	5826	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVR QAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSK NTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSS	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	CGTATTAGAAGCAAATATAACAATTACGCCACATACTAC GCCGACTCTGTGAAAGAC	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	GTGAGGCACGGCAACTTCGGGAATTCCTATATTTCATAC TGGGCCTAC	CTL-19669 LAD3584_P02_H12	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 365	5833	CAGACTGTGGTGACTCAGGAGCCCTCACTGACTGTGTCC CCAGGAGGGACAGTCACTCTCACCTGTGGCTCCAGCACT GGAGCTGTCACCAGTGGTAATTATCCCAACTGGGTCCA GCAGAAGCCTGGCCAAGCCCCCAGGGGACTGATTGGTG GTACAAAATTCCTGGCCCCCGGGACACCTGCCCGGTTCT CAGGCTCCCTCCTTGGGGGCAAAGCTGCCCTGACCCTTT CGGGTGTGCAGCCTGAGGATGAGGCTGAGTATTACTGC GTGCTCTGGTATAGTAATCGGTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	CTL-19669 LAD3584_P02_H12	Light chain variable region("LC") nucleic acid sequence
Ab 365	5834	QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQ QKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCVLWYSNRWVFGGGTKLTVL	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	GGCTCCAGCACTGGAGCTGTCACCAGTGGTAATTATCCC AAC	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	GAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCT GGATTCACCTTCACCAGCTACTATATACACTGGGTGCGA CAGGCCCCTGGACAAGGGCTTGAGTGGATAGGATGGAT CTACCCTGAAAATGATAACACAAAGTACAACGAGAAGT TCAAGGACAGAGTCACCATAACCGCGGACACGTCCACG AGCACAGCCTACCTGGAGCTGAGCAGCCTGAGATCTGA GGACACGGCGGTGTACTACTGCGCCAGGGACGGATATT CTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTGG	CTL-19672 SAD5477_P02_H03	Heavy chain variable region ("HC") nucleic acid sequence

		TCACCGTCTCCTCA		
Ab 366	5842	EVQLVQSGAEVKKPGASVKVSCKASGFTFSYYIHWVRQA PGQGLEWIGWIYPENDNTKYNEKFKDRVTITADTSTSTAYL ELSSLRSEDTAVYYCARDGYSRYYFDYWGQGTLVTVSS	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	TGGATCTACCCTGAAAATGATAACACAAAGTACAACGA GAAGTTCAAGGAC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCAGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGTCTCCTAAGC TGCTCATTTACTGGACATCTACCCGGAAGTCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTC ACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTGGC AGTTTATTACTGTAAGCAAAGCTTCATCCTTAGGACGTT CGGCCAAGGGACCAAGGTGGAAATCAAA	CTL-19672 SAD5477_P02_H03	Light chain variable region("LC") nucleic acid sequence
Ab 366	5850	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAW YQQKPGQSPKLLIYWTSTRKSGVPDRFSGSGSGTDFTLTISS LQAEDVAVYYCKQSFILRTFGQGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCAGAAA GAACTACTTAGCT	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	GAAGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGCAGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGATGATTATACCATGCACTGGGTCCGGC AAGCTCCAGGGAAGGGCCTGGAGTGGGTCTCAGGTATT AGTTGGAATAGTGGTAGCATAGGCTATGCGGACTCTGT GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGA AGTCCCTGTATCTGCAAATGAACAGTCTGAGAGCTGAG GACACGGCGTTGTACTACTGCGCCAAGGACAATTCCGG ATACGGCCACTACTACGGTATGGACGTCTGGGGGC	CAB21609_A01	Heavy chain variable region ("HC") nucleic acid sequence

		AAGGGACCACGGTCACCGTCGCCTCA		
Ab 367	5858	EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYTMHWVRQ APGKGLEWVSGISWNSGSIGYADSVKGRFTISRDNAKKSLY LQMNSLRAEDTALYYCAKDNSGYGHYYYGMDVWGQGTT VTVAS	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	GGTATTAGTTGGAATAGTGGTAGCATAGGCTATGCGGA CTCTGTGAAGGGC	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	GCCAAGGACAATTCCGGATACGGCCACTACTACTACGGT ATGGACGTC	CAB21609_A01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence
Ab 367	5865	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTG TCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAG TCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGA AACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCAT CCACCAGGCCACTGGTATCCCAGCCAGGTTCAGTGGC AGTGGGTCTGGGACAGAGTTTCACTCTCACCATCAGCAG CCTGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAACAT TACATCAATTGGCCTCTCACTTTCGGCGGAGGGACCAAG	CAB21609_A01	Light chain variable region("LC") nucleic acid sequence

		GTGGAGATCAAA		
Ab 367	5866	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKP GQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQSEDF AVYYCQHYINWPLTFGGGTKVEIK	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	GAAGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGCGGGATCCCTGAGACTCTCCTGTGCAGCCACTG GATTCACCTTTGATGATTTCACCATGCACTGGGTCCGGC AAGCTCCAGGGAAGGGCCTGGAGTGGGTCTCAGGTATT AGTTGGAATAGTGGTAGCATAGGCTATGTGGACTCTGT GAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGA ACTCCCTGTATCTGCAAATGAACAGTCTGAGAGCTGAGG ACACGGCGTTGTACTACTGCGCCAAGGACAACAGCGGA TACGGCTACTACTACTACGGTATGGACGTCTGGGGGCA AGGGACCACGGTCACCGTCTCCTCA	CAB21609_B01	Heavy chain variable region ("HC") nucleic acid sequence

Ab 368	5874	EVQLVESGGGLVQPGGSLRLSCAATGFTFDDFTMHWVRQ APGKGLEWVSGISWNSGSIGYVDSVKGRFTISRDNAKNSL YLQMNSLRAEDTALYYCAKDNSGYGYYYYGMDVWGQGT TVTVSS	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	GGTATTAGTTGGAATAGTGGTAGCATAGGCTATGTGGA CTCTGTGAAGGGC	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	GCCAAGGACAACAGCGGATACGGCTACTACTACTACGG TATGGACGTC	CAB21609_B01	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence
Ab 368	5881	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTG TCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAG TCACAGTGTTAGCAGAAACTCAGCCTGGTACCAGCAGA AACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCAT CCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGTGGC AGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAG CCTGCAGTCTGAAGATTTTGCAATTTATTACTGTCAACA GTATAATAATTGGCCGCTCACTTTCGGCGGAGGGACCA AGGTGGAGATCAAA	CAB21609_B01	Light chain variable region("LC") nucleic acid sequence
Ab 368	5882	EIVMTQSPATLSVSPGERATLSCRASHSVSRNSAWYQQKP GQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQSEDF AIYYCQQYNNWPLTFGGGTKVEIK	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	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCC AGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCT GGATTCACCTTCAGAAGCTATGCCATGCACTGGGTCCGC CAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAATGG TATACTATGATGGAAATAATCAATACTATGCAGACTCCG TGAGGGGCCGATTCACCATCTCCAGAGACAATTCCAAG AACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGA CGACACGGCGGTGTACTTCTGCGCTAGAGGTCCTGGCT ATAACTGGTTGGACCCCTGGGGCCAGGGAACCCTGGTC ACCGTCTCCTCA	CAB21609_C01	Heavy chain variable region ("HC") nucleic acid sequence
Ab 369	5890	QVQLVESGGGVVQPGRSLRLSCAASGFTFRSYAMHWVR QAPGKGLEWVAMVYYDGNNQYYADSVRGRFTISRDNSK NTLYLQMNSLRADDTAVYFCARGPGYNWLDPWGQGTLV TVSS	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	ATGGTATACTATGATGGAAATAATCAATACTATGCAGAC TCCGTGAGGGGC	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	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTG TCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAG TCAGAGTGTTAGCAGAAACTTAGCCTGGTACCAGCAGA AACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCAT CCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGTGGC AGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGC CTGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAACAG TACAACAATTGGCCTCTCACTTTCGGCGGAGGGACCAAG GTGGTGATCAAA	CAB21609_C01	Light chain variable region("LC") nucleic acid sequence
Ab 369	5898	EIVMTQSPATLSVSPGERATLSCRASQSVSRNLAWYQQKP GQAPRLLIYGASTRATGIPARFSGSGSGTDFTLTISSLQSEDF AVYYCQQYNNWPLTFGGGTKVVIK	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	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCC AGCCTGGGAGGTCCCTGAGACTCGCCTGTGTAGCGTCT GGATTCACCTTCAGAAGCTATGGCATGCACTGGGTCCGC CAGGCTCCAGGCAAGGGGCTGCAGTGGGTGGCAATGA TATACTATGATGGAAAGAATAAATACTATGCAGACTCCG TGAGGGGCCGATTCACCATCTCCAGAGACAATTCCAAG AACACGCTGTATCTGCAAATGAACAACCTGAGAGTCGA GGACACGGCGATGTACTTCTGCGCCAGAGGTCCAGGCT ATAACTGGTTGGACCCCTGGGGCCAGGGAACCCTGGTC	CAB21609_D01	Heavy chain variable region ("HC") nucleic acid sequence

		ACCGTCTCCTCA		
Ab 370	5906	QVQLVESGGGVVQPGRSLRLACVASGFTFRSYGMHWVR QAPGKGLQWVAMIYYDGKNKYYADSVRGRFTISRDNSKN TLYLQMNNLRVEDTAMYFCARGPGYNWLDPWGQGTLV TVSS	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	ATGATATACTATGATGGAAAGAATAAATACTATGCAGAC TCCGTGAGGGGGC	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	GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTG TCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAG TCAGAGAATTAGCAGCAACTTAGCCTGGTACCAGCAGA AACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCAT CCACCAGGGCCACTGGTAGCCCAGCCAGGTTCAGTGGC AGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGC CTGCAGTCTGAAGATGTTGCAGTTTATTACTGTCAGCAG CATCATAACTGGCCTCTCACTTTCGGCGGAGGGACCAAG	CAB21609_D01	Light chain variable region("LC") nucleic acid sequence

		GTGGAGATCAAA		
Ab 370	5914	EIVMTQSPATLSVSPGERATLSCRASQRISSNLAWYQQKP GQAPRLLIYGASTRATGSPARFSGSGSGTDFTLTISSLQSED VAVYYCQQHHNWPLTFGGGTKVEIK	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTAACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCCGTGTACTACTGCGTCAGGCACGGT AACTTCGGGAACAGTTATGTATCCTGGTTTGCTTATTGG GGCCAAGGAACCCTGGTCACCGTCTCCTCA	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG CTAGATATTACTTTGATGTGTGGGGCCAAGGAACCCTG GTCACCGTCTCCTCA	ADI-21960 SAD5837_P01_A04	Heavy chain variable region ("HC") nucleic acid sequence
Ab 372	5938	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYARYYFDVWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-21960 SAD5837_P01_A04	Light chain variable region("LC") nucleic acid sequence
Ab 372	5946	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCCGTGTACTACTGCGCGAGAGATGGATACG CTAGATATTACTATGACTACTGGGGCCAAGGAACCCTGG TCACCGTCTCCTCA	ADI-21961 SAD5837_P01_C05	Heavy chain variable region ("HC") nucleic acid sequence

Ab 373	5954	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYARYYYDYWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-21961 SAD5837_P01_C05	Light chain variable region("LC") nucleic acid sequence
Ab 373	5962	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCAGTAGAGATGGATACG CTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTGG TCACCGTCTCCTCA	ADI-21962 SAD5837_P01_B06	Heavy chain variable region ("HC") nucleic acid sequence
Ab 374	5970	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCSRDGYARYYFDYWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-21962 SAD5837_P01_B06	Light chain variable region("LC") nucleic acid sequence
Ab 374	5978	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCCGTGTACTACTGCAATAGAGATGGATACG CTAGATATTACTATGACTACTGGGGCCAAGGAACCCTGG TCACCGTCTCCTCA	ADI-21964 SAD5837_P01_B08	Heavy chain variable region ("HC") nucleic acid sequence

Ab 375	5986	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCNRDGYARYYYDYWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-21964 SAD5837_P01_B08	Light chain variable region("LC") nucleic acid sequence
Ab 375	5994	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGGATACG CTAGATATTTTTTTGACAATTGGGGCCAAGGAACCCTGG TCACCGTCTCCTCA	ADI-21966 SAD5837_P01_G10	Heavy chain variable region ("HC") nucleic acid sequence
Ab 376	6002	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYARYFFDNWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-21966 SAD5837_P01_G10	Light chain variable region("LC") nucleic acid sequence
Ab 376	6010	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCCGTGTACTACTGCGCGAGAGATGGGTACG GGAGATATTACTTTGACCGTTGGGGCCAAGGAACCCTG GTCACCGTCTCCTCA	ADI-21968 SAD5837_P01_A12	Heavy chain variable region ("HC") nucleic acid sequence

Ab 377	6018	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDGYGRYYFDRWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCCCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-21968 SAD5837_P01_A12	Light chain variable region("LC") nucleic acid sequence
Ab 377	6026	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGGTAACACAATCTATGACCCGAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGGGTCGGATGGATACG CTAGATATTACTTTGACTACTGGGGCCAAGGAACCCTGG TCACCGTCTCCTCA	ADI-21969 SAD5837_P02_C01	Heavy chain variable region ("HC") nucleic acid sequence
Ab 378	6034	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENGNTIYDPKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCGSDGYARYYFDYWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGGTAACACAATCTATGACCCG AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACAGCAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-21969 SAD5837_P02_C01	Light chain variable region("LC") nucleic acid sequence
Ab 378	6042	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACAGCAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCCGTGTACTACTGCGGTAGAGATGCGTACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG GTCACCGTCTCCTCA	ADI-26907 LAD5224_P03_D02	Heavy chain variable region ("HC") nucleic acid sequence

Ab 379	6050	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCGRDAYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-26907 LAD5224_P03_D02	Light chain variable region("LC") nucleic acid sequence
Ab 379	6058	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGTGTTGG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG GTCACCGTCTCCTCA	ADI-26912 LAD5224_P03_E05	Heavy chain variable region ("HC") nucleic acid sequence
Ab 380	6066	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDVLGRYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-26912 LAD5224_P03_E05	Light chain variable region("LC") nucleic acid sequence
Ab 380	6074	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATCAGTACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG GTCACCGTCTCCTCA	ADI-26913 LAD5224_P03_A06	Heavy chain variable region ("HC") nucleic acid sequence

Ab 381	6082	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDQYGRYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-26913 LAD5224_P03_A06	Light chain variable region("LC") nucleic acid sequence
Ab 381	6090	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGTGTACG GGAGATATTTTTACGACCTTTGGGGCCAAGGAACCCTG GTCACCGTCTCCTCA	ADI-26916 LAD5224_P03_F08	Heavy chain variable region ("HC") nucleic acid sequence
Ab 382	6098	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDVYGRYFYDLWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-26916 LAD5224_P03_F08	Light chain variable region("LC") nucleic acid sequence
Ab 382	6106	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCCGTGTACTACTGCGCGAGAGATGCGTACG GGGGGTATTTTTACGACGTGTGGGGCCAAGGAACCCTG GTCACCGTCTCCTCA	ADI-26917 LAD5224_P03_B09	Heavy chain variable region ("HC") nucleic acid sequence

Ab 383	6114	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDAYGGYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-26917 LAD5224_P03_B09	Light chain variable region("LC") nucleic acid sequence
Ab 383	6122	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATAATTACG GGGGGTATTTTTACGACGTGTGGGGCCAAGGAACCCTG GTCACCGTCTCCTCA	ADI-26918 LAD5224_P03_E09	Heavy chain variable region ("HC") nucleic acid sequence
Ab 384	6130	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDNYGGYFYDVWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-26918 LAD5224_P03_E09	Light chain variable region("LC") nucleic acid sequence
Ab 384	6138	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTAACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCCGTGTACTACTGCGTCAGGCACGGT AACTTCGGGAACAGTTATGTATCCTGGTTTGCTTATTGG GGCCAAGGAACCCTGGTCACCGTCTCCTCA	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTAACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGAACAGTTATGTATCCTGGTTTGCTTATTGG GGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-29602 SAD5269_P02_G06	Heavy chain variable region ("HC") nucleic acid sequence
Ab 386	6162	EVQLLESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACAGTTATGTATCCTG GTTTGCTTAT	ADI-29602 SAD5269_P02_G06	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 386	6169	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTAGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAAACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGATGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCTTTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-29602 SAD5269_P02_G06	Light chain variable region("LC") nucleic acid sequence
Ab 386	6170	QTVVTQEPSLSVSPGGTVTLTCRSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTNKRAPGVPDRFSGSLLGDKAALTITG AQADDEADYYCALWYSNLWVFGGGTKLTVL	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	AGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAG CCGAGGACACGGCCGTGTACTACTGCGTCAGGCACGGT AACTTCGGGAACAGTTACGTATCCTGGTTTGCTCATTGG GGCCAAGGAACCCTGGTCACCGTCTCCTCA	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGCGTACG GGAGATATTTTTACAGGGTGTGGGGCCAAGGAACCCTG GTCACCGTCTCCTCA	ADI-29607 SAD6444_P02_F05	Heavy chain variable region ("HC") nucleic acid sequence
Ab 388	6194	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDAYGRYFYRVWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-29607 SAD6444_P02_F05	Light chain variable region("LC") nucleic acid sequence
Ab 388	6202	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCCGTGTACTACTGCCCGAGAGATGCTTACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG GTCACCGTCTCCTCA	ADI-29608 SAD6444_P01_G02	Heavy chain variable region ("HC") nucleic acid sequence

Ab 389	6210	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCPRDAYGRYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-29608 SAD6444_P01_G02	Light chain variable region("LC") nucleic acid sequence
Ab 389	6218	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGCGTACG GGAGATATTTTTACGACGGGTGGGGCCAAGGAACCCTG GTCACCGTCTCCTCA	ADI-29609 SAD6444_P02_C05	Heavy chain variable region ("HC") nucleic acid sequence
Ab 390	6226	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDAYGRYFYDGWGQGTLVT VSS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-29609 SAD6444_P02_C05	Light chain variable region("LC") nucleic acid sequence
Ab 390	6234	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCCGTGTACTACTGCGCGAGAGATCGTTACG GGGCTTATTTTTACGACGTGTGGGGCCAAGGAACCCTG GTCACCGTCTCCTCA	ADI-29610 SAD6444_P02_D06	Heavy chain variable region ("HC") nucleic acid sequence

Ab 391	6242	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDRYGAYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-29610 SAD6444_P02_D06	Light chain variable region("LC") nucleic acid sequence
Ab 391	6250	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATCGGTACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG GTCACCGTCTCCTCA	ADI-29611 SAD6444_P02_D04	Heavy chain variable region ("HC") nucleic acid sequence
Ab 392	6258	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDRYGRYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-29611 SAD6444_P02_D04	Light chain variable region("LC") nucleic acid sequence
Ab 392	6266	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCCGTGTACTACTGCGCGAGAGATTCGTACG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG GTCACCGTCTCCTCA	ADI-29613 SAD6444_P01_C03	Heavy chain variable region ("HC") nucleic acid sequence

Ab 393	6274	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDSYGRYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-29613 SAD6444_P01_C03	Light chain variable region("LC") nucleic acid sequence
Ab 393	6282	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGCGAGAGATGTGTACG GGAGATATCTTTACGACGTGTGGGGCCAAGGAACCCTG GTCACCGTCTCCTCA	ADI-29614 SAD6444_P01_G03	Heavy chain variable region ("HC") nucleic acid sequence
Ab 394	6290	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDVYGRYLYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-29614 SAD6444_P01_G03	Light chain variable region("LC") nucleic acid sequence
Ab 394	6298	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCCGTGTACTACTGCGCGAGAGATGTGTACA GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG GTCACCGTCTCCTCA	ADI-29617 SAD6444_P01_E01	Heavy chain variable region ("HC") nucleic acid sequence

Ab 395	6306	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDVYRRYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-29617 SAD6444_P01_E01	Light chain variable region("LC") nucleic acid sequence
Ab 395	6314	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGA AGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCT GGATTCAACATCAAGGACTACTATATGCACTGGGTGCG ACAGGCTCCTGGACAAAGGCTTGAGTGGATGGGATGGA TCGACCTTGAAAATGCTAACACAATCTATGACGCTAAGT TTCAGGGCAGGGTCACCATAACCAGGGACACGTCCGCC AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGA AGACACGGCGGTGTACTACTGCGTGAGAGATCTTCGGG GGAGATATTTTTACGACGTGTGGGGCCAAGGAACCCTG GTCACCGTCTCCTCA	ADI-29618 SAD6444_P01_A03	Heavy chain variable region ("HC") nucleic acid sequence
Ab 396	6322	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCVRDLRGRYFYDVWGQGTLVTV SS	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	TGGATCGACCTTGAAAATGCTAACACAATCTATGACGCT AAGTTTCAGGGC	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	GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTG TCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAG CCAGAGTCTTTTAAACGCTAGAACCGGAAAGAACTACTT AGCTTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGC TGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAGTGGCAGCGGGTCTGGGACAGACTTC ACTCTCACTATCAGTAGCCTGCAGGCTGAAGATGTGGCA GTTTATTACTGTAAGCAATCTTATTCTCGGAGAACTTTCG GCGGAGGGACCAAGGTCGAGATCAAA	ADI-29618 SAD6444_P01_A03	Light chain variable region("LC") nucleic acid sequence
Ab 396	6330	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	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	AAGTCCAGCCAGAGTCTTTTAAACGCTAGAACCGGAAA GAACTACTTAGCT	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCAAGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCCGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGGTGGTTACGTATCCTGGTTTGCTCATTGG GGCCAAGGAACCCTGGTCACCGTCTCCTCA	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	GAGGTGCAGCTGTTGGGGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGAACTCGTACGTTTCCTGGTTTGCTCATTGG GGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-29717 SAD6619_P01_B02	Heavy chain variable region ("HC") nucleic acid sequence
Ab 398	6354	EVQLLGSGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHGNFGNSYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACTCGTACGTTTCCTGG TTTGCTCAT	ADI-29717 SAD6619_P01_B02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 398	6361	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-29717 SAD6619_P01_B02	Light chain variable region("LC") nucleic acid sequence
Ab 398	6362	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCCGTGTACTACTGCGTCAGGCACGGT AACTTCGGTGGGGGTTACGTAGCCTGGTTTGCTCATTGG GGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-29718 SAD6619_P04_G09	Heavy chain variable region ("HC") nucleic acid sequence

Ab 399	6370	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHGNFGGGYVAWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGTGGGGGTTACGTAGCCTG GTTTGCTCAT	ADI-29718 SAD6619_P04_G09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence
Ab 399	6377	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-29718 SAD6619_P04_G09	Light chain variable region("LC") nucleic acid sequence
Ab 399	6378	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTTTAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCCAGGGTGGTTACGTATCCTGGTTTGCTCATTGG GGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-29719 SAD6619_P04_A09	Heavy chain variable region ("HC") nucleic acid sequence
Ab 400	6386	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKFNNYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHGNFQGGYVSWFAHWGQ GTLVTVSS	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	AGGATTAGATCCAAGTTTAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCCAGGGTGGTTACGTATCCTG GTTTGCTCAT	ADI-29719 SAD6619_P04_A09	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 400	6393	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-29719 SAD6619_P04_A09	Light chain variable region("LC") nucleic acid sequence
Ab 400	6394	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCCGTGTACTACTGCGTCAGGCACGGT AACGTGGGGGGGTGGTTACGTATCCTGGTTTGCTCATTG GGGCCAAGGAACCCTGGTCACCGTCTCCTCA	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGAT AACTTCGGGGCTGGTTACGTATCCTGGTTTGCTCATTGG GGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-29721 SAD6619_P01_A02	Heavy chain variable region ("HC") nucleic acid sequence
Ab 402	6418	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHDNFGAGYVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGATAACTTCGGGGCTGGTTACGTATCCTG GTTTGCTCAT	ADI-29721 SAD6619_P01_A02	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 402	6425	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-29721 SAD6619_P01_A02	Light chain variable region("LC") nucleic acid sequence
Ab 402	6426	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCCGTGTACTACTGCGTCAGGCACGGT AACTTCGGGGTTGGTTACGTATCCTGGTTTGCTTCTTGG GGCCAAGGAACCCTGGTCACCGTCTCCTCA	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGTTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCGGTGTACTACTGCGTCAGGCACGGT AACTTCGGGAACTATGCTGTATCCTGGTTTGCTCATTGG GGCCAAGGAACCCTGGTCACCGTCTCCTCA	ADI-29723 SAD6619_P04_G08	Heavy chain variable region ("HC") nucleic acid sequence
Ab 404	6450	EVQLLESGGGLVQPGGSLRLSCAASGFTFDTYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKST LYLQMESLRAEDTAVYYCVRHGNFGNYAVSWFAHWGQG TLVTVSS	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	AGGATTAGATCCAAGTATAACAATTACGCTACATACTAC GCAGACTCCGTGAAGGAT	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	GTCAGGCACGGTAACTTCGGGAACTATGCTGTATCCTG GTTTGCTCAT	ADI-29723 SAD6619_P04_G08	Heavy chain variable region CDR H3 ("H3") nucleic acid sequence

Ab 404	6457	CAGACTGTGGTGACCCAGGAGCCATCGCTCTCAGTGTCC CCTGGAGGGGACAGTCACACTCACTTGTGGATCAAGCACT GGCGCAGTCACTACTAGTAACTACGCCAACTGGGTCCA GCAGACCCCAGGCCAGGCTCCGCGCGGACTCATCGGCG GCACAGACAAGCGCGCTCCTGGGGTCCCTGATCGCTTCT CTGGCTCCCTGCTTGGGGACAAAGCTGCCCTCACCATCA CGGGGGCCCAGGCAGAGGATGAAGCTGATTATTACTGT GCGCTGTGGTACAGTAACCATTGGGTGTTCGGCGGAGG GACCAAGCTGACCGTCCTA	ADI-29723 SAD6619_P04_G08	Light chain variable region("LC") nucleic acid sequence
Ab 404	6458	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITG AQAEDEADYYCALWYSNHWVFGGGTKLTVL	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	GGATCAAGCACTGGCGCAGTCACTACTAGTAACTACGCC AAC	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	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGACACATATGCCATGAATTGGGTTCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCAAGGAT TAGATCCAAGTATAACAATTACGCTACATACTACGCAGA CTCCGTGAAGGATCGGTTCACCATCTCCAGAGACGATTC CAAGAGCACGCTGTATCTGCAAATGGAAAGCCTGAGAG CCGAGGACACGGCCGTGTACTACTGCGTCAGGCACGGT AGCTTCGGGAACCATATTGTATCCTGGTTTGCTCATTGG GGCCAAGGAACCCTGGTCACCGTCTCCTCA	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**YY**MH	ADI-32238	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 406	6483	WI**DLE**N**A**NTI**YDA**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**LL**N**ARTG**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	**KQ**S**S**YS**RR**T	ADI-32238	Light chain variable region CDR L3 ("L3") amino acid sequence

Ab 407	6489	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTV SS	ADI-32241	Heavy chain variable region ("HC") amino acid sequence
Ab 407	6490	**FNIKDYY**MH	ADI-32241	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 407	6491	WI**DLENA**NTIY**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	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-32241	Light chain variable region ("LC") amino acid sequence
Ab 407	6494	KSSQS**LLNARTG**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	**KQSYSRRT**	ADI-32241	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 408	6497	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTV SS	ADI-32244	Heavy chain variable region ("HC") amino acid sequence
Ab 408	6498	**FNIKDYY**MH	ADI-32244	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 408	6499	WI**DLENANTVYDA**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	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-32244	Light chain variable region ("LC") amino acid sequence
Ab 408	6502	KSSQS**LL**N**ARTG**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	**KQ**Y**S**S**RR**T	ADI-32244	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 409	6505	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTV SS	ADI-32247	Heavy chain variable region ("HC") amino acid sequence
Ab 409	6506	**FNIKD**Y**YM**H	ADI-32247	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 409	6507	WI**DLE**N**A**NTI**YDA**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	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYFRRTFGGGTKVEIK	ADI-32247	Light chain variable region ("LC") amino acid sequence
Ab 409	6510	KSSQS**LL**N**ARTG**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	**KQ**Y**S**F**RR**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

		QAPGQRLEWMGWIDLENANTVYDAKFQGRVTITRDTSA STAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVT VSS		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	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYFRRTFGGGTKVEIK	ADI-32250	Light chain variable region ("LC") amino acid sequence
Ab 410	6518	KSSQS**LL**N**ARTG**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	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTVYDAKFQGRVTITRDTSA STAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVT VSS	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	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT	ADI-32253	Light chain variable region ("LC") amino acid sequence

		ISSLQAEDVAVYYCKQSYFRRTFGGGTKVEIK		
Ab 411	6526	KSSQSLL**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	**KQS**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	**KQS**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**YY**M**H	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	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-32259	Light chain variable region ("LC") amino acid sequence
Ab 413	6542	KSSQS**LL**N**ARTG**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	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWIGWIDLENANTVYDAKFQGRVTITRDTSAST AYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVS S	ADI-32239	Heavy chain variable region ("HC") amino acid sequence
Ab 414	6546	**FNIKD**YY**M**H	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	DIVMTQSPDSLAVSLGERATINCRSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGGGTKVEIK	ADI-32239	Light chain variable region ("LC") amino acid sequence
Ab 414	6550	**R**SSQS**LL**N**ARTG**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	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWIGWIDLENANTVYDAKFQGRVTITRDTSAST AYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVS S	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	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYFRRTFGGGTKVEIK	ADI-32242	Light chain variable region ("LC") amino acid sequence
Ab 415	6558	KSSQS**LLNARTG**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	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTV SS	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**NTI**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	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCTQSYSRRTFGGGTKVEIK	ADI-32245	Light chain variable region ("LC") amino acid sequence
Ab 416	6566	KSSQS**LL**N**ART**GKNYLA	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	**TQ**Y**S**Y**SRR**T	ADI-32245	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 417	6569	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQRLEWMGWIDLENANTVYDAKFQGRVTITRDTSA STAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVT VSS	ADI-32248	Heavy chain variable region ("HC") amino acid sequence
Ab 417	6570	**FNIKD**Y**YM**H	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	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCTQSYSRRTFGGGTKVEIK	ADI-32248	Light chain variable region ("LC") amino acid sequence
Ab 417	6574	KSSQS**LL**N**ART**GKNYLA	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	**TQ**Y**S**Y**SRR**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

		QAPGQRLEWMGWIDLENANTVYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSS		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	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCTQSYFRRTFGGGTKVEIK	ADI-32251	Light chain variable region ("LC") amino acid sequence
Ab 418	6582	KSSQS**LL****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	**TQ****S**Y**FRR**T	ADI-32251	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 419	6585	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVRQAPGQCLEWMGWIDLENANTIYDAKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTVSS	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**NTI**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	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT	ADI-32254	Light chain variable region ("LC") amino acid sequence

		ISSLQAEDVAVYYCKQSYSRRTFGCGTKVEIK		
Ab 419	6590	KSSQSLL**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	**KQ**S**YS**R**R**T	ADI-32254	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 420	6593	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQCLEWMGWIDLENANTIYDAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTV SS	ADI-32257	Heavy chain variable region ("HC") amino acid sequence
Ab 420	6594	WI**DLE**N**A**NTI**YDA**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	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	ADI-32257	Light chain variable region ("LC") amino acid sequence
Ab 420	6597	KSSQSLL**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	**KQ**S**YS**R**R**T	ADI-32257	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 421	6600	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQCLEWMGWIDLENANTVYDAKFQGRVTITRDTSA STAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVT VSS	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	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCTQSYSRRTFGCGTKVEIK	ADI-32260	Light chain variable region ("LC") amino acid sequence
Ab 421	6605	KSSQS**LL**N**ARTG**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	**TQ**S**R**S**RR**T	ADI-32260	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 422	6608	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQCLEWMGWIDLENANTVYDAKFQGRVTITRDTSA STAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVT VSS	ADI-32240	Heavy chain variable region ("HC") amino acid sequence
Ab 422	6609	**FNIKD**Y**YY**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	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYFRRTFGCGTKVEIK	ADI-32240	Light chain variable region ("LC") amino acid sequence
Ab 422	6613	KSSQS**LL**N**ARTG**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	**KQ**S**F**S**RR**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**YY**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**LL**N**ARTG**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	**KQ**S**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**YY**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**LL**N**ARTG**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**LL**N**ARTG**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**YY**M**H	ADI-32252	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 426	6642	WI**DLE**N**A**NTI**YNA**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	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	ADI-32252	Light chain variable region ("LC") amino acid sequence
Ab 426	6645	KSSQS**LLNARTG**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	**KQ**YS**RR**T	ADI-32252	Light chain variable region CDR L3 ("L3") amino acid sequence
Ab 427	6648	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQCLEWMGWIDLENANTIYNAKFQGRVTITRDTSAS TAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVTV SS	ADI-32255	Heavy chain variable region ("HC") amino acid sequence
Ab 427	6649	**FNIKD**YY**M**H	ADI-32255	Heavy chain variable region CDR H1 ("H1") amino acid sequence
Ab 427	6650	WI**DLE**N**A**NTI**YNA**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	DIVMTQSPDSLAVSLGERVTINCKSSQSLLNARTGKSYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	ADI-32255	Light chain variable region ("LC") amino acid sequence
Ab 427	6653	KSSQS**LLNARTG**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	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQCLEWMGWIDLENANTVYNAKFQGRVTITRDTSA STAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVT VSS	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	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYLA WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ISSLQAEDVAVYYCKQSYSRRTFGCGTKVEIK	ADI-32258	Light chain variable region ("LC") amino acid sequence
Ab 428	6661	KSSQS**LL****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	QVQLVQSGAEVKKPGASVKVSCKASGFNIKDYYMHWVR QAPGQCLEWMGWIDLENANTVYNAKFQGRVTITRDTSA STAYMELSSLRSEDTAVYYCARDAYGRYFYDVWGQGTLVT VSS	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**LLNARTG**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	**KQS**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)

		KTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHE ALHNRFTQKSLSLSPG		
Ab 430	6674	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQK PGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSL QPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC	ADI-29291	Light chain LC
Ab 431	6675	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQ APGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNT AYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV CTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPG	ADI-29292	Heavy chain HC1
Ab 431	6676	QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQ QKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLS GVQPEDEAEYYCVLWYSNRWVFGCGTKLTVLGGGGSGGG GSGGGGSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGF TFNKYAMNWVRQAPGKCLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFG NSYISYWAYWGQGTLVTVSSGSEPKSSDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPCREEMTKNQVSLWCLVKGFYPSDIAVEWESSGQPE NNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSV MHEALHNRFTQKSLSLSPG	ADI-29292	Heavy chain HC2 (CD3 binder as scFv)
Ab 431	6677	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQK PGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSL QPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC	ADI-29292	Light chain LC

Ab 432	6678	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQ APGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNT AYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV CTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPG	ADI-29293	Heavy chain HC1
Ab 432	6679	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQK PGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQADLPAFAFGCGTKVEIKGGGGSGGGGS GGGGSGGGGSEVRLLESGGGLVQPGGSLRLSCAASGFTF SNYAMGWVRQAPGKCLEWVSAISGSGGSTYYADSVKGRF TTSRDDSKNALYLQMNSLRAEDTAVYYCARGGPGWYAAD VWGQGTTVTVSSGSEPKSSDKTHTCPPCPAPEAAGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCREE MTKNQVSLWCLVKGFYPSDIAVEWESSGQPENNYKTTPP MLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNR FTQKSLSLSPG	ADI-29293	Heavy chain HC2 (CD3 binder as scFv)
Ab 432	6680	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQK PGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSL QPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC	ADI-29293	Light chain LC
Ab 433	6681	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQ APGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNT AYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV CTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCS	ADI-29294	Heavy chain HC1

		VMHEALHNHYTQKSLSLSPG		
Ab 433	6682	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYL AWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFT LTISSLQAEDVAVYYCKQSYSYRRTFGCGTKVEIKGGGGS GGGGSGGGGSGGGGSQVQLVQSGAEVKKPGASVKVSCKA SGFNIKDYYMHWVRQAPGQCLEWMGWIDLENGNTIYDPK FQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYG RYFYDVWGQGTLVTVSSGSEPKSSDKTHTCPPCPAPEAA GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP PCREEMTKNQVSLWCLVKGFYPSDIAVEWESSGQPENNY KTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHE ALHNRFTQKSLSLSPG	ADI-29294	Heavy chain HC2 (CD3 binder as scFv)
Ab 433	6683	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQK PGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSL QPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC	ADI-29294	Light chain LC
Ab 434	6684	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQ APGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNT AYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV CTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPG	ADI-29295	Heavy chain HC1
Ab 434	6685	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYL AWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFT LTISSLQAEDVAVYYCKQSYSYRRTFGCGTKVEIKGGGGS GGGGSGGGGSGGGGSQVQLVQSGAEVKKPGASVKVSCKA SGFNIKDYYMHWVRQAPGQCLEWMGWIDLENANTIYDAK FQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYG RYFYDVWGQGTLVTVSSGSEPKSSDKTHTCPPCPAPEAA GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW	ADI-29295	Heavy chain HC2 (CD3 binder as scFv)

		LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP PCREEMTKNQVSLWCLVKGFYPSDIAVEWESSGQPENNY KTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHE ALHNRFTQKSLSLSPG		
Ab 434	6686	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQK PGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSL QPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC	ADI-29295	Light chain LC
Ab 435	6687	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQ APGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNT AYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV CTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPG	ADI-29297	Heavy chain HC1
Ab 435	6688	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYL AWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFT LTISSLQAEDVAVYYCKQSYSRRTFGCGTKVEIKGGGGS GGGGSGGGGSGGGGSQVQLVQSGAEVKKPGASVKVSCKA SGFNIKDYYMHWVRQAPGQCLEWMGWIDLENANTIYDAK FQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDQYG RYFYDVWGQGTLVTVSSGSEPKSSDKTHTCPPCPAPEAA GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP PCREEMTKNQVSLWCLVKGFYPSDIAVEWESSGQPENNY KTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHE ALHNRFTQKSLSLSPG	ADI-29297	Heavy chain HC2 (CD3 binder as scFv)
Ab 435	6689	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQK PGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSL QPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE	ADI-29297	Light chain LC

		VTHQGLSSPVTKSFNRGEC		
Ab 436	6690	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQ APGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNT AYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV CTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPG	ADI-29298	Heavy chain HC1
Ab 436	6691	DIVMTQSPDSLAVSLGERATINCKSSQSLLNARTGKNYL AWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFT LTISSLQAEDVAVYYCKQSYSLRTFGCGTKVEIKGGGGS GGGGSGGGGSGGGGSQVQLVQSGAEVKKPGASVKVSCKA SGFNIKDYYMHWVRQAPGQCLEWMGWIDLEEGNTIYDAK FQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDAYG RYFYDVWGQGTLVTVSSGSEPKSSDKTHTCPPCPAPEAA GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP PCREEMTKNQVSLWCLVKGFYPSDIAVEWESSGQPENNY KTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHE ALHNRFTQKSLSLSPG	ADI-29298	Heavy chain HC2 (CD3 binder as scFv)
Ab 436	6692	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQK PGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSL QPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC	ADI-29298	Light chain LC
Ab 437	6693	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQ APGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNT AYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV	ADI-29300	Heavy chain HC1

		CTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPG		
Ab 437	6694	DIVMTQSPDSLAVSLGERATINCKSSQSLLESRTGKNYL AWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFT LTISSLQAEDVAVYYCKQSYSLRTFGCGTKVEIKGGGGS GGGGSGGGGSGGGGSQVQLVQSGAEVKKPGASVKVSCKA SGFNIKDYYMHWVRQAPGQCLEWMGWIDLENANTIYDAK FQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDNYG GYFYDVWGQGTLVTVSSGSEPKSSDKTHTCPPCPAPEAA GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP PCREEMTKNQVSLWCLVKGFYPSDIAVEWESSGQPENNY KTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHE ALHNRFTQKSLSLSPG	ADI-29300	Heavy chain HC2 (CD3 binder as scFv)
Ab 437	6695	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQK PGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSL QPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC	ADI-29300	Light chain LC
Ab 438	6696	EVRLLESGGGLVQPGGSLRLSCAASGFTFSNYAMGWVRQ APGKGLEWVSAISGSGGSTYYADSVKGRFTTSRDDSKNA LYLQMNSLRAEDTAVYYCARGGPGWYAADVWGQGTTVTV SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVC TLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPG	ADI-29301	Heavy chain HC1
Ab 438	6697	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTGKNYL AWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFT LTISSLQAEDVAVYYCKQSYSRRTFGCGTKVEIKGGGGS GGGGSGGGGSGGGGSQVQLVQSGAEVKKPGASVKVSCKA SGFNIKDYYMHWVRQAPGQCLEWMGWIDLENGNTIYDPK FQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDGYG RYFYDVWGQGTLVTVSSGSEPKSSDKTHTCPPCPAPEAA	ADI-29301	Heavy chain HC2 (CD3 binder as scFv)

		GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP PCREEMTKNQVSLWCLVKGFYPSDIAVEWESSGQPENNY KTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHE ALHNRFTQKSLSLSPG		
Ab 438	6698	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQK PGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQADLPAFAFGGGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC	Light chain LC	
			ADI-29301	
AB 439	6699	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQ APGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNT AYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV CTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPG	Heavy chain HC1	
			ADI-29302	
Ab 439	6700	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTIT GAQAEDEADYYCALWYSNHWVFGCGTKLTVLGGGGSGGG GSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGF TFDTYAMNWVRQAPGKCLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFQ GGYVSWFAHWGQGTLVTVSSGSEPKSSDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPCREEMTKNQVSLWCLVKGFYPSDIAVEWESSGQPE NNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSV MHEALHNRFTQKSLSLSPG	Heavy chain HC2 (CD3 binder as scFv)	
			ADI-29302	
Ab 439	6701	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQK PGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSL QPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS	Light chain LC	
			ADI-29302	

		GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC		
Ab 440	6702	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQ APGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNT AYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV CTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPG	ADI-29303	Heavy chain HC1
Ab 440	6703	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTIT GAQAEDEADYYCALWYSNHWVFGCGTKLTVLGGGGSGGG GSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGF TFDTYAMNWVRQAPGKCLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFG GGYVSWFAWWGQGTLVTVSSGSEPKSSDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPCREEMTKNQVSLWCLVKGFYPSDIAVEWESSGQPE NNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSV MHEALHNRFTQKSLSLSPG	ADI-29303	Heavy chain HC2 (CD3 binder as scFv)
Ab 440	6704	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQK PGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSL QPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC	ADI-29303	Light chain LC
Ab 441	6705	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQ APGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNT AYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL	ADI-29304	Heavy chain HC1

		HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV CTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPG		Heavy chain HC2 (CD3 binder as scFv)
Ab 441	6706	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTIT GAQAEDEADYYCALWYSNLWVFGCGTKLTVLGGGGSGGG GSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGF TFDTYAMNWVRQAPGKCLEWVARIRSKYNDYATYYADSV KDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFG GAYVSWFAHWGQGTLVTVSSGSEPKSSDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPCREEMTKNQVSLWCLVKGFYPSDIAVEWESSGQPE NNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSV MHEALHNRFTQKSLSLSPG	ADI-29304	
Ab 441	6707	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQK PGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSL QPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC	ADI-29304	Light chain LC
Ab 442	6708	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQ APGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNT AYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVT VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV CTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPG	ADI-29305	Heavy chain HC1
Ab 442	6709	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTIT GAQAEDEADYYCALWYSDLWVFGCGTKLTVLGGGGSGGG GSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGF TFDAYAMNWVRQAPGKCLEWVARIRSKYNDYATYYADSV KDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNVG	ADI-29305	Heavy chain HC2 (CD3 binder as scFv)

		GGYVSWFAHWGQGTLVTVSSGSEPKSSDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPCREEMTKNQVSLWCLVKGFYPSDIAVEWESSGQPE NNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSV MHEALHNRFTQKSLSLSPG		
Ab 442	6710	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQK PGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSL QPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC	ADI-29305	Light chain LC
Ab 443	6711	EVRLLESGGGLVQPGGSLRLSCAASGFTFSNYAMGWVRQ APGKGLEWVSAISGSGGSTYYADSVKGRFTTSRDDSKNA LYLQMNSLRAEDTAVYYCARGGPGWYAADVWGQGTTVTV SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVC TLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPG	ADI-29306	Heavy chain HC1
Ab 443	6712	QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQ QTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTIT GAQAEDEADYYCALWYSNHWVFGCGTKLTVLGGGGSGGG GSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGF TFDTYAMNWVRQAPGKCLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKSTLYLQMESLRAEDTAVYYCVRHGNFG GGYVSWFAWWGQGTLVTVSSGSEPKSSDKTHTCPPCPAP EAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPCREEMTKNQVSLWCLVKGFYPSDIAVEWESSGQPE NNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSV MHEALHNRFTQKSLSLSPG	ADI-29306	Heavy chain HC2 (CD3 binder as scFv)
Ab 443	6713	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQK PGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQADLPAFAFGGGTKVEIKRTVAAPSVFI	ADI-29306	Light chain LC

		FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC		

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, FcγRIIIa (CD16), FcγRIIa (CD32a), FcγRIIb (CD32b), FcγRI (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:

QDGNEEMGGITQTPYKVSISGTTVILTCPQYPGSEILWQHNDKNIGGDEDDKNIGSDEDHLSLKEFSELEQSGYYVCYP
RGSKPEDANFYLYLRARVCENCMEMDGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF
SCSVMHEALHNHYTQKSLSLSPGK;

and the second polypeptide chain comprises the following amino acid sequence:

FKIPIEELEDRVFVNCNTSITWVEGTVGTLLSDITRLDLGKRILDPRGIYRCNGTDIYKDKESTVQVHYRMCQSCVELDG
GSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
ASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK.

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:
QDGNEEMGSITQTPYQVSISGTTVILTCSQHLGSEAQWQHNGKNKEDSGDRLFLPEFSEMEQSGYYVCYPRGSNPEDA
SHHLYLKARVCENCMEMDGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN
WYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH
EALHNHYTQKSLSLSPGK;

and the second polypeptide chain comprises the following amino acid sequence:
FKIPVEELEDRVFVKCNTSVTWVEGTVGTLLTNNTRLDLGKRILDPRGIYRCNGTDIYKDKESAVQVHYRMCQNCVE
LDPGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE
EQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK.

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.

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The claims defining the invention are as follows:

1. An anti-cluster of differentiation three (CD3) antibody or antigen-binding polypeptide thereof, which comprises:

(A) a heavy chain variable region (VH) comprising a CDRH1, a CDRH2, and a CDRH3; and

(B) a light chain variable region (VL) comprising a CDRL1, a CDRL2, and a CDRL3,

wherein:

(i) the amino acid sequences of the CDRH1, the CDRH2, and the CDRH3 comprise the heavy chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5186, and the amino acid sequences of the CDRL1, the CDRL2, and the CDRL3 comprise the light chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5194; or
the amino acid sequences of the CDRH1, the CDRH2, the CDRH3, the CDRL1, the CDRL2, and the CDRL3 comprise SEQ ID NOS: 5187, 5189, 5191, 5195, 5197, and 5199, respectively;

(ii) the amino acid sequences of the CDRH1, the CDRH2, and the CDRH3 comprise the heavy chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5202, and the amino acid sequences of the CDRL1, the CDRL2, and the CDRL3 comprise the light chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5210; or
the amino acid sequences of the CDRH1, the CDRH2, the CDRH3, the CDRL1, the CDRL2, and the CDRL3 comprise SEQ ID NOS: 5203, 5205, 5207, 5211, 5213, and 5215, respectively;

(iii) the amino acid sequences of the CDRH1, the CDRH2, and the CDRH3 comprise the heavy chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5218, and the amino acid sequences of the CDRL1, the CDRL2, and the CDRL3 comprise the light chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5226; or
the amino acid sequences of the CDRH1, the CDRH2, the CDRH3, the CDRL1, the CDRL2, and the CDRL3 comprise SEQ ID NOS: 5219, 5221, 5223, 5227, 5229, and 5231, respectively;

(iv) the amino acid sequences of the CDRH1, the CDRH2, and the CDRH3 comprise the heavy chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5234, and the

amino acid sequences of the CDRL1, the CDRL2, and the CDRL3 comprise the light chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5242; or
the amino acid sequences of the CDRH1, the CDRH2, the CDRH3, the CDRL1, the CDRL2, and the CDRL3 comprise SEQ ID NOS: 5235, 5237, 5239, 5243, 5245, and 5247, respectively;

(v) the amino acid sequences of the CDRH1, the CDRH2, and the CDRH3 comprise the heavy chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5266, and the amino acid sequences of the CDRL1, the CDRL2, and the CDRL3 comprise the light chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5274; or
the amino acid sequences of the CDRH1, the CDRH2, the CDRH3, the CDRL1, the CDRL2, and the CDRL3 comprise SEQ ID NOS: 5267, 5269, 5271, 5275, 5277, and 5279, respectively;

(vi) the amino acid sequences of the CDRH1, the CDRH2, and the CDRH3 comprise the heavy chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5282, and the amino acid sequences of the CDRL1, CDRL2, and the CDRL3 comprise the light chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5290; or
the amino acid sequences of the CDRH1, the CDRH2, the CDRH3, the CDRL1, the CDRL2, and the CDRL3 comprise SEQ ID NOS: 5283, 5285, 5287, 5291, 5293, and 5295, respectively;

(vii) the amino acid sequences of the CDRH1, the CDRH2, and the CDRH3 comprise the heavy chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5298, and the amino acid sequences of the CDRL1, the CDRL2, and the CDRL3 comprise the light chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5306; or
the amino acid sequences of the CDRH1, the CDRH2, the CDRH3, the CDRL1, the CDRL2, and the CDRL3 comprise SEQ ID NOS: 5299, 5301, 5303, 5307, 5309, and 5311, respectively;

(viii) the amino acid sequences of the CDRH1, the CDRH2, and the CDRH3 comprise the heavy chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5314, and the amino acid sequences of the CDRL1, the CDRL2, and the CDRL3 comprise the light chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5322; or

the amino acid sequences of the CDRH1, the CDRH2, the CDRH3, the CDRL1, the CDRL2, and the CDRL3 comprise SEQ ID NOS: 5315, 5317, 5319, 5323, 5325, and 5327, respectively;

(ix) the amino acid sequences of the CDRH1, the CDRH2, and the CDRH3 comprise the heavy chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5330, and the amino acid sequences of the CDRL1, the CDRL2, and the CDRL3 comprise the light chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5338; or
the amino acid sequences of the CDRH1, the CDRH2, the CDRH3, the CDRL1, the CDRL2, and the CDRL3 comprise SEQ ID NOS: 5331, 5333, 5335, 5339, 5341, and 5343, respectively;

(x) the amino acid sequences of the CDRH1, the CDRH2, and the CDRH3 comprise the heavy chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5362, and the amino acid sequences of the CDRL1, the CDRL2, and the CDRL3 comprise the light chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5370; or
the amino acid sequences of the CDRH1, the CDRH2, the CDRH3, the CDRL1, the CDRL2, and the CDRL3 comprise SEQ ID NOS: 5363, 5365, 5367, 5371, 5373, and 5375, respectively;

(xi) the amino acid sequences of the CDRH1, the CDRH2, and the CDRH3 comprise the heavy chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5378, and the amino acid sequences of the CDRL1, the CDRL2, and the CDRL3 comprise the light chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5386; or
the amino acid sequences of the CDRH1, the CDRH2, the CDRH3, the CDRL1, the CDRL2, and the CDRL3 comprise SEQ ID NOS: 5379, 5381, 5383, 5387, 5389, and 5391, respectively;

(xii) the amino acid sequences of the CDRH1, the CDRH2, and the CDRH3 comprise the heavy chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5394, and the amino acid sequences of the CDRL1, the CDRL2, and the CDRL3 comprise the light chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5402; or

the amino acid sequences of the CDRH1, the CDRH2, the CDRH3, the CDRL1, the CDRL2, and the CDRL3 comprise SEQ ID NOS: 5395, 5397, 5399, 5403, 5405, and 5407, respectively;

(xiii) the amino acid sequences of the CDRH1, the CDRH2, and the CDRH3 comprise the heavy chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5410, and the amino acid sequences of the CDRL1, the CDRL2, and the CDRL3 comprise the light chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5418; or
the amino acid sequences of the CDRH1, the CDRH2, the CDRH3, the CDRL1, the CDRL2, and the CDRL3 comprise SEQ ID NOS: 5411, 5413, 5415, 5419, 5421, and 5423, respectively;

(xiv) the amino acid sequences of the CDRH1, the CDRH2, and the CDRH3 comprise the heavy chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5426, and the amino acid sequences of the CDRL1, the CDRL2, and the CDRL3, respectively comprise the light chain CDR1, 2, and 3 sequences, contained in SEQ ID NO: 5434; or
the amino acid sequences of the CDRH1, the CDRH2, the CDRH3, the CDRL1, the CDRL2, and the CDRL3 comprise SEQ ID NOS: 5427, 5429, 5431, 5435, 5437, and 5439, respectively;

(xv) the amino acid sequences of the CDRH1, the CDRH2, and the CDRH3 comprise the heavy chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5458, and the amino acid sequences of the CDRL1, the CDRL2, and the CDRL3 comprise the light chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5466; or
the amino acid sequences of the CDRH1, the CDRH2, the CDRH3, the CDRL1, the CDRL2, and the CDRL3 comprise SEQ ID NOS: 5459, 5461, 5463, 5467, 5469, and 5471, respectively;

(xvi) the amino acid sequences of the CDRH1, the CDRH2, and the CDRH3 comprise the heavy chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5474, and the amino acid sequences of the CDRL1, the CDRL2, and the CDRL3 comprise the light chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5482; or

the amino acid sequences of the CDRH1, the CDRH2, the CDRH3, the CDRL1, the CDRL2, and the CDRL3 comprise SEQ ID NOS: 5475, 5477, 5479, 5483, 5485, and 5487, respectively;

(xvii) the amino acid sequences of the CDRH1, the CDRH2, and the CDRH3 comprise the heavy chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5490, and the amino acid sequences of the CDRL1, the CDRL2, and the CDRL3 comprise the light chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5498; or the amino acid sequences of the CDRH1, the CDRH2, the CDRH3, the CDRL1, the CDRL2, and the CDRL3 comprise SEQ ID NOS: 5491, 5493, 5495, 5499, 5501, and 5503, respectively;

(xviii) the amino acid sequences of the CDRH1, the CDRH2, and the CDRH3 comprise the heavy chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5538, and the amino acid sequences of the CDRL1, the CDRL2, and the CDRL3 comprise the light chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5546; or the amino acid sequences of the CDRH1, the CDRH2, the CDRH3, the CDRL1, the CDRL2, and the CDRL3 comprise SEQ ID NOS: 5539, 5541, 5543, 5547, 5549, and 5551, respectively;

(xix) the amino acid sequences of the CDRH1, the CDRH2, and the CDRH3 comprise the heavy chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5554, and the amino acid sequences of the CDRL1, the CDRL2, and the CDRL3 comprise the light chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5562; or the amino acid sequences of the CDRH1, the CDRH2, the CDRH3, the CDRL1, the CDRL2, and the CDRL3 comprise SEQ ID NOS: 5555, 5557, 5559, 5563, 5565, and 5567, respectively;

(xx) the amino acid sequences of the CDRH1, the CDRH2, and the CDRH3 comprise the heavy chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5586, and the amino acid sequences of the CDRL1, the CDRL2, and the CDRL3 comprise the light chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5594; or

the amino acid sequences of the CDRH1, the CDRH2, the CDRH3, the CDRL1, the CDRL2, and the CDRL3 comprise SEQ ID NOS: 5587, 5589, 5591, 5595, 5597, and 5599, respectively;

(xxi) the amino acid sequences of the CDRH1, the CDRH2, and the CDRH3 comprise the heavy chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5602, and the amino acid sequences of the CDRL1, the CDRL2, and the CDRL3 comprise the light chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5610; or the amino acid sequences of the CDRH1, the CDRH2, the CDRH3, the CDRL1, the CDRL2, and the CDRL3 comprise SEQ ID NOS: 5603, 5605, 5607, 5611, 5613, and 5615, respectively;

(xxii) the amino acid sequences of the CDRH1, the CDRH2, and the CDRH3 comprise the heavy chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5618, and the amino acid sequences of the CDRL1, the CDRL2, and the CDRL3 comprise the light chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5626; or the amino acid sequences of the CDRH1, the CDRH2, the CDRH3, the CDRL1, the CDRL2, and the CDRL3 comprise SEQ ID NOS: 5619, 5621, 5623, 5627, 5629, and 5631, respectively; or

(xxiii) the amino acid sequences of the CDRH1, the CDRH2, and the CDRH3 comprise the heavy chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5650, and the amino acid sequences of the CDRL1, the CDRL2, and the CDRL3 comprise the light chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5658; or the amino acid sequences of the CDRH1, the CDRH2, the CDRH3, the CDRL1, the CDRL2, and the CDRL3 comprise SEQ ID NOS: 5651, 5653, 5655, 5659, 5661, and 5663, respectively.

2. The anti-CD3 antibody or antigen-binding polypeptide thereof of claim 1, wherein:

in (i), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 90% sequence identity to SEQ ID NO: 5186; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5194;

in (ii), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 90% sequence identity to SEQ ID NO: 5202; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5210;

in (iii), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 90% sequence identity to SEQ ID NO: 5218; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5226;

in (iv), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 90% sequence identity to SEQ ID NO: 5234; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5242;

in (v), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 90% sequence identity to SEQ ID NO: 5266; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5274;

in (vi), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 90% sequence identity to SEQ ID NO: 5282; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5290;

in (vii), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 90% sequence identity to of SEQ ID NO: 5298; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5306;

in (viii), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 90% sequence identity to SEQ ID NO: 5314; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5322;

in (ix), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 90% sequence identity to SEQ ID NO: 5330; and

the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5338;

in (x), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 90% sequence identity to SEQ ID NO: 5362; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5370;

in (xi), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 90% sequence identity to SEQ ID NO: 5378; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5386;

in (xii), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 90% sequence identity to SEQ ID NO: 5394; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5402;

in (xiii), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 90% sequence identity to SEQ ID NO: 5410; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5418;

in (xiv), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 90% sequence identity to SEQ ID NO: 5426; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5434;

in (xv), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 90% sequence identity to SEQ ID NO: 5458; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5466;

in (xvi), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 90% sequence identity to SEQ ID NO: 5474; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5482;

in (xvii), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 90% sequence identity to SEQ ID NO: 5490; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5498;

in (xviii), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 90% sequence identity to SEQ ID NO: 5538; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5546;

in (xix), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 90% sequence identity to SEQ ID NO: 5554; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5562;

in (xx), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 90% sequence identity to SEQ ID NO: 5586; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5594;

in (xxi), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 90% sequence identity to SEQ ID NO: 5602; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5610;

in (xxii), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 90% sequence identity to SEQ ID NO: 5618; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5626; or

in (xxiii), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 90% sequence identity to SEQ ID NO: 5650; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5658.

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3. The anti-CD3 antibody or antigen-binding polypeptide thereof of claim 1, wherein said VH and VL comprise:

in (i), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 95% sequence identity to SEQ ID NO: 5186; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5194;

in (ii), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 95% sequence identity to SEQ ID NO: 5202; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5210;

in (iii), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 95% sequence identity to SEQ ID NO: 5218; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5226;

in (iv), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 95% sequence identity to SEQ ID NO: 5234; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5242;

in (v), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 95% sequence identity to SEQ ID NO: 5266; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5274;

in (vi), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 95% sequence identity to SEQ ID NO: 5282; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5290;

in (vii), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 95% sequence identity to SEQ ID NO: 5298; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5306;

in (viii), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 95% sequence identity to SEQ ID NO: 5314; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5322;

in (ix), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 95% sequence identity to SEQ ID NO: 5330; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5338;

in (x), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 95% sequence identity to SEQ ID NO: 5362; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5370;

in (xi), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 95% sequence identity to SEQ ID NO: 5378; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5386;

in (xii), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 95% sequence identity to SEQ ID NO: 5394; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5402;

in (xiii), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 95% sequence identity to SEQ ID NO: 5410; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5418;

in (xiv), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 95% sequence identity to SEQ ID NO: 5426; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5434;

in (xv), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 95% sequence identity to SEQ ID NO: 5458; and

the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5466;

in (xvi), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 95% sequence identity to SEQ ID NO: 5474; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5482;

in (xvii), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 95% sequence identity to SEQ ID NO: 5490; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5498;

in (xviii), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 95% sequence identity to SEQ ID NO: 5538; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5546;

in (xix), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 95% sequence identity to SEQ ID NO: 5554; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5562;

in (xx), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 95% sequence identity to SEQ ID NO: 5586; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5594;

in (xxi), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 95% sequence identity to SEQ ID NO: 5602; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5610;

in (xxii), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 95% sequence identity to SEQ ID NO: 5618; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5626; or

in (xxiii), the VH comprises the CDRH1, the CDRH2, and the CDRH3, and the amino acid sequence of the VH has at least 95% sequence identity to SEQ ID NO: 5650; and the VL comprises the CDRL1, the CDRL2, and the CDRL3, and the amino acid sequence of the VL has at least 90% sequence identity to SEQ ID NO: 5658.

4. The anti-CD3 antibody or antigen-binding polypeptide thereof of claim 1, wherein said VH and VL comprise:

in (i), the amino acid sequences of SEQ ID NOS: 5186 and 5194, respectively, or SEQ ID NOS: 6585 and 6589, respectively;

in (ii), the amino acid sequences of SEQ ID NOS: 5202 and 5210, respectively;

in (iii), the amino acid sequences of SEQ ID NOS: 5218 and 5226, respectively;

in (iv), the amino acid sequences of SEQ ID NOS: 5234 and 5242, respectively;

in (v), the amino acid sequences of SEQ ID NOS: 5266 and 5274, respectively;

in (vi), the amino acid sequences of SEQ ID NOS: 5282 and 5290, respectively, or the VH and VL sequences, respectively, contained in SEQ ID NO: 6688;

in (vii), the amino acid sequences of SEQ ID NOS: 5298 and 5306, respectively;

in (viii), the amino acid sequences of SEQ ID NOS: 5314 and 5322, respectively;

in (ix), the amino acid sequences of SEQ ID NOS: 5330 and 5338, respectively;

in (x), the amino acid sequences of SEQ ID NOS: 5362 and 5370, respectively;

in (xi), the amino acid sequences of SEQ ID NOS: 5378 and 5386, respectively;

in (xii), the amino acid sequences of SEQ ID NOS: 5394 and 5402, respectively;

in (xiii), the amino acid sequences of SEQ ID NOS: 5410 and 5418, respectively;

in (xiv), the amino acid sequences of SEQ ID NOS: 5426 and 5434, respectively;

in (xv), the amino acid sequences of SEQ ID NOS: 5458 and 5466, respectively;

in (xvi), the amino acid sequences of SEQ ID NOS: 5474 and 5482, respectively;

in (xvii), the amino acid sequences of SEQ ID NOS: 5490 and 5498, respectively;

in (xviii), the amino acid sequences of SEQ ID NOS: 5538 and 5546, respectively;

in (xix), the amino acid sequence of SEQ ID NOS: 5554 and 5562, respectively;

in (xx), the amino acid sequences of SEQ ID NOS: 5586 and 5594, respectively;

in (xxi), the amino acid sequences of SEQ ID NOS: 5602 and 5610, respectively;

in (xxii), the amino acid sequences of SEQ ID NOS: 5618 and 5626, respectively;

or

in (xxiii), the amino acid sequences of SEQ ID NOS: 5650 and 5658, respectively.

5. The anti-CD3 antibody or antigen-binding polypeptide thereof of any one of claims 1 to 4, wherein: the amino acid sequences of the CDRH1, the CDRH2, and the CDRH3 comprise the heavy chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5186, and the amino acid sequences of the CDRL1, the CDRL2, and the CDRL3 comprise the light chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5194; or the amino acid sequences of the CDRH1, the CDRH2, the CDRH3, the CDRL1, the CDRL2, and the CDRL3 comprise SEQ ID NOS: 5187, 5189, 5191, 5195, 5197, and 5199, respectively.

6. The anti-CD3 antibody or antigen-binding polypeptide thereof of claim 5, wherein said VH and VL comprise the amino acid sequences of SEQ ID NOS: 5186 and 5194, respectively, or SEQ ID NOS: 6585 and 6589, respectively.

7. The anti-CD3 antibody or antigen-binding polypeptide thereof of any one of claims 1 to 4, wherein: the amino acid sequences of the CDRH1, the CDRH2, and the CDRH3 comprise the heavy chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5234, and the amino acid sequences of the CDRL1, the CDRL2, and the CDRL3 comprise the light chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5242; or the amino acid sequences of the CDRH1, the CDRH2, the CDRH3, the CDRL1, the CDRL2, and the CDRL3 comprise SEQ ID NOS: 5235, 5237, 5239, 5243, 5245, and 5247, respectively.

8. The anti-CD3 antibody or antigen-binding polypeptide thereof of claim 7, wherein said VH and VL comprise the amino acid sequences of SEQ ID NOS: 5234 and 5242, respectively.

9. The anti-CD3 antibody or antigen-binding polypeptide thereof of any one of claims 1 to 4, wherein: the amino acid sequences of the CDRH1, the CDRH2, and the CDRH3 comprise the heavy chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5282, and the amino acid sequences

of the CDRL1, the CDRL2, and the CDRL3 comprise the light chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5290; or the amino acid sequences of the CDRH1, the CDRH2, the CDRH3, the CDRL1, the CDRL2, and the CDRL3 comprise SEQ ID NOS: 5283, 5285, 5287, 5291, 5293, and 5295, respectively.

10. The anti-CD3 antibody or antigen-binding polypeptide thereof of claim 9, wherein said VH and VL comprise the amino acid sequences of SEQ ID NOS: 5282 and 5290, respectively, or the VH and VL sequences, respectively, contained in SEQ ID NO: 6688.

11. The anti-CD3 antibody or antigen-binding polypeptide thereof of any one of claims 1 to 4, wherein: the amino acid sequences of the CDRH1, the CDRH2, and the CDRH3 comprise the heavy chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5362, and the amino acid sequences of the CDRL1, the CDRL2, and the CDRL3 comprise the light chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5370; or the amino acid sequences of the CDRH1, the CDRH2, the CDRH3, the CDRL1, the CDRL2, and the CDRL3 comprise SEQ ID NOS: 5363, 5365, 5367, 5371, 5373, and 5375, respectively.

12. The anti-CD3 antibody or antigen-binding polypeptide thereof of claim 11, wherein said VH and VL comprise the amino acid sequences of SEQ ID NOS: 5362 and 5370, respectively.

13. The anti-CD3 antibody or antigen-binding polypeptide thereof of any one of claims 1 to 4, wherein: the amino acid sequences of the CDRH1, the CDRH2, and the CDRH3 comprise the heavy chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5394, and the amino acid sequences of the CDRL1, the CDRL2, and the CDRL3 comprise the light chain CDR1, 2, and 3 sequences, respectively, contained in SEQ ID NO: 5402; or the amino acid sequences of the CDRH1, the CDRH2, the CDRH3, the CDRL1, the CDRL2, and the CDRL3 comprise SEQ ID NOS: 5395, 5397, 5399, 5403, 5405, and 5407, respectively.

14. The anti-CD3 antibody or antigen-binding polypeptide thereof of claim 13, wherein said VH and VL comprise the amino acid sequences of SEQ ID NOS: 5394 and 5402, respectively.

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15. The anti-CD3 antibody or antigen-binding polypeptide thereof according to any one of claims 1 to 14, which comprises:

(I) a scFv fragment, a diabody, a minibody, a scFv-Fc, a Fab fragment, a Fab' fragment, a Fab'-SH fragment, a $F(ab')_2$ fragment, a small modular immunopharmaceutical (SMIP), or a Fv fragment; or

(II) (A) a heavy chain comprising the VH and a heavy chain constant region, and

(B) a light chain comprising the VL and a light chain constant region,

optionally comprising: an immunoglobulin molecule comprised of two said heavy chains and two said light chains interconnected by disulfide bonds, or a multimer of said immunoglobulin molecule, optionally an IgG, IgA, IgD, IgE, or IgM antibody, further optionally an IgG1, IgG2, IgG3, IgG4, IgA1, or IgA2 antibody.

16. The anti-CD3 antibody or antigen-binding polypeptide thereof according to any one of claims 1 to 15, which does not form a succinimide intermediate as determined by size exclusion chromatography (SEC) peak breadth.

17. The anti-CD3 antibody or antigen-binding polypeptide thereof according to any one of claims 1 to 16, which comprises a polyspecific reactivity (PSR) score of between about 0.0 and about 0.33 or between about 0.0 and about 0.10 as determined by a PSR assay.

18. The anti-CD3 antibody or antigen-binding polypeptide thereof according to any one of claims 1 to 17, which comprises:

(i) a multispecific antibody or antibody fragment;

(ii) a bispecific antibody or antibody fragment;

(iii) 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, ADAM 15, ADAM 17/T ACE, ADAM8, ADAM9, ADAMTS,

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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, BFM, 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, CCL1, CCL11, CCL12, CCL13, CCL 14, CCL15, CCL16, CCL1 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, CD11a, CD11b, CD11c, 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, CXCL1, 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,

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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 IIb/IIIa (GP IIb/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, a metalloprotease, 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,

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MPIF, Mpo, MSK, MSP, mucin (Mucl), MUC18, Muellerian- inhibiting substance, Mug, MuSK, NAIP, NAP, NCAD, N-Cadherin, NCA 90, 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), PIGF, 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, 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), TNFRSF 18 (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), TNFRSF 5 (CD40 p50), TNFRSF6 (Fas Apo-1, APT1, CD95), TNFRSF6B (DcR3 M68, TR6), TNFRSF7 (CD27), TNFRSF8 (CD30), TNFRSF9 (4-1BB 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),

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TNFSF12 (TWEAK Apo-3 Ligand, DR3 Ligand), TNFSF13 (APRIL TALL2), TNFSF13B (BAFF BLYS, TALL1, THANK, TNFSF20), TNFSF14 (LIGHT HVEM Ligand, LTg), TNFSF15 (TLIA/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 (4-1BB 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, VFM, 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), hormone receptors and growth factors;

(iv) 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, FcγRIIIa (CD16), FcγRIIa (CD32a), FcγRIIb (CD32b), FcγRI (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; and/or

(v) at least a second antigen binding domain that specifically binds to an antigen, wherein said anti-CD3 antibody or antigen-binding polypeptide thereof 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,

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DART, BiTE, common light chain-IgG, TandAb, Cross-Mab, SEED, BEAT, TrioMab, and DuetMab.

19. An isolated or recombinant nucleic acid encoding an anti-CD3 antibody or antigen-binding polypeptide thereof according to any one of claims 1 to 18.

20. The isolated or recombinant nucleic acid of claim 19, which encodes an anti-CD3 antibody or antigen-binding polypeptide thereof according to any one of claims 1 to 4 and comprises a nucleic acid encoding the VH and a nucleic acid encoding the VL, which comprise:

in (i), the nucleic acid sequences of SEQ ID NOS: 5185 and 5193, respectively;
in (ii), the nucleic acid sequences of SEQ ID NOS: 5201 and 5209, respectively;
in (iii), the nucleic acid sequences of SEQ ID NOS: 5217 and 5225, respectively;
in (iv), the nucleic acid sequences of SEQ ID NOS: 5233 and 5241, respectively;
in (v), the nucleic acid sequences of SEQ ID NOS: 5265 and 5273, respectively;
in (vi), the nucleic acid sequences of SEQ ID NOS: 5281 and 5289, respectively;
in (vii), the nucleic acid sequences of SEQ ID NOS: 5297 and 5305, respectively;
in (viii), the nucleic acid sequences of SEQ ID NOS: 5313 and 5321, respectively;
in (ix), the nucleic acid sequences of SEQ ID NOS: 5329 and 5337, respectively;
in (x), the nucleic acid sequences of SEQ ID NOS: 5361 and 5369, respectively;
in (xi), the nucleic acid sequences of SEQ ID NOS: 5377 and 5385, respectively;
in (xii), the nucleic acid sequences of SEQ ID NOS: 5393 and 5401, respectively;
in (xiii), the nucleic acid sequences of SEQ ID NOS: 5409 and 5417, respectively;
in (xiv), the nucleic acid sequences of SEQ ID NOS: 5425 and 5433, respectively;
in (xv), the nucleic acid sequences of SEQ ID NOS: 5457 and 5465, respectively;
in (xvi), the nucleic acid sequences of SEQ ID NOS: 5473 and 5481, respectively;
in (xvii), the nucleic acid sequences of SEQ ID NOS: 5489 and 5497, respectively;
in (xviii), the nucleic acid sequences of SEQ ID NOS: 5537 and 5545, respectively;
in (xix), the nucleic acid sequence of SEQ ID NOS: 5553 and 5561, respectively;
in (xx), the nucleic acid sequences of SEQ ID NOS: 5585 and 5593, respectively;
in (xxi), the nucleic acid sequences of SEQ ID NOS: 5601 and 5609, respectively;

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in (xxii), the nucleic acid sequences of SEQ ID NOS: 5617 and 5625, respectively; or
in (xxiii), the nucleic acid sequences of SEQ ID NOS: 5649 and 5657, respectively.

21. An expression vector comprising an isolated or recombinant nucleic acid according to claim 19 or 20.

22. A host cell transfected, transformed, or transduced with a nucleic acid according to claim 19 or 20, or a vector according to claim 21.

23. A pharmaceutical composition comprising:
(a) an anti-CD3 antibody or antigen-binding polypeptide thereof according to any one of claims 1-18, one or more nucleic acids encoding an anti-CD3 antibody or antigen-binding polypeptide thereof according to any one of claims 1 to 18, and/or one or more vectors comprising one or more nucleic acids encoding an anti-CD3 antibody or antigen-binding polypeptide thereof according to any one of claims 1 to 18; and
(b) a pharmaceutically acceptable carrier and/or excipient.

24. Use of an anti-CD3 antibody or antigen-binding polypeptide thereof according to any one of claims 1 to 18 for the manufacture of a medicament for treating or preventing a disorder in a mammal, wherein the disorder comprises an oncological disorder, an immuno-oncological disorder, a neurological disorder, a hematological cancer, a neurodegenerative disorder, or an autoimmune disorder.

25. A method of treating or preventing a disorder in a mammal, the method comprising administering to the mammal an anti-CD3 antibody or antigen-binding polypeptide thereof according to any one of claims 1 to 18, wherein the disorder comprises an oncological disorder, an immuno-oncological disorder, a neurological disorder, a hematological cancer, a neurodegenerative disorder, or an autoimmune disorder.

26. The use according to claim 24 or the method according to claim 25, wherein the hematological cancer is selected from the group consisting of germinal-center B-cell-like (GCB) diffuse large B-cell

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lymphoma (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), and Burkitt's lymphoma (BL).

27. The use according to claim 24 or the method according to claim 25, wherein the disorder comprises an autoimmune disease selected from the group consisting of arthritis, rheumatoid arthritis, colitis, inflammatory bowel disease, and autoimmune type I diabetes.

28. The use according to claim 24, wherein the medicament further comprises an additional therapeutic agent.

29. The method according to claim 25, further comprising administering to the mammal an additional therapeutic agent.

30. The use according to claim 24 or the method according to claim 25 wherein the mammal is a human.

31. A method of making an anti-CD3 antibody or antigen-binding polypeptide thereof according to any one of claims 1 to 18, wherein the method comprises:

(a) culturing a host cell comprising a nucleic acid encoding the antibody or antigen-binding polypeptide thereof according to any one of claims 1 to 18 under a condition suitable for expression of the antibody or antigen-binding polypeptide thereof; and

(b) optionally recovering the antibody or antigen-binding polypeptide thereof from the host cell or the culture medium of (a).

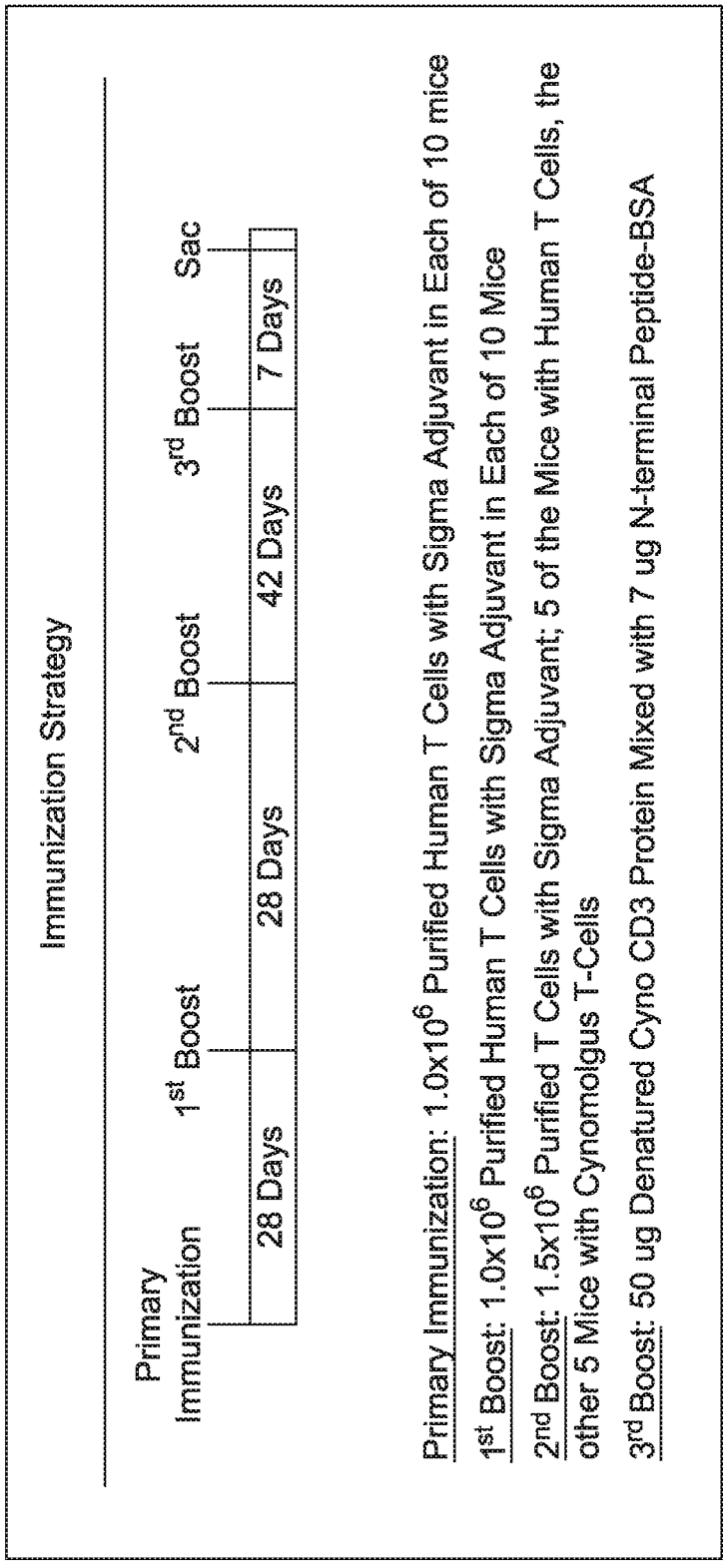

Immunization Strategy
Primary Immunization
1st Boost
2nd Boost
3rd Boost
Sac
28 Days
28 Days
42 Days
7 Days
Primary Immunization: 1.0x10^6 Purified Human T Cells with Sigma Adjuvant in Each of 10 mice
1st Boost: 1.0x10^6 Purified Human T Cells with Sigma Adjuvant in Each of 10 Mice
2nd Boost: 1.5x10^6 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

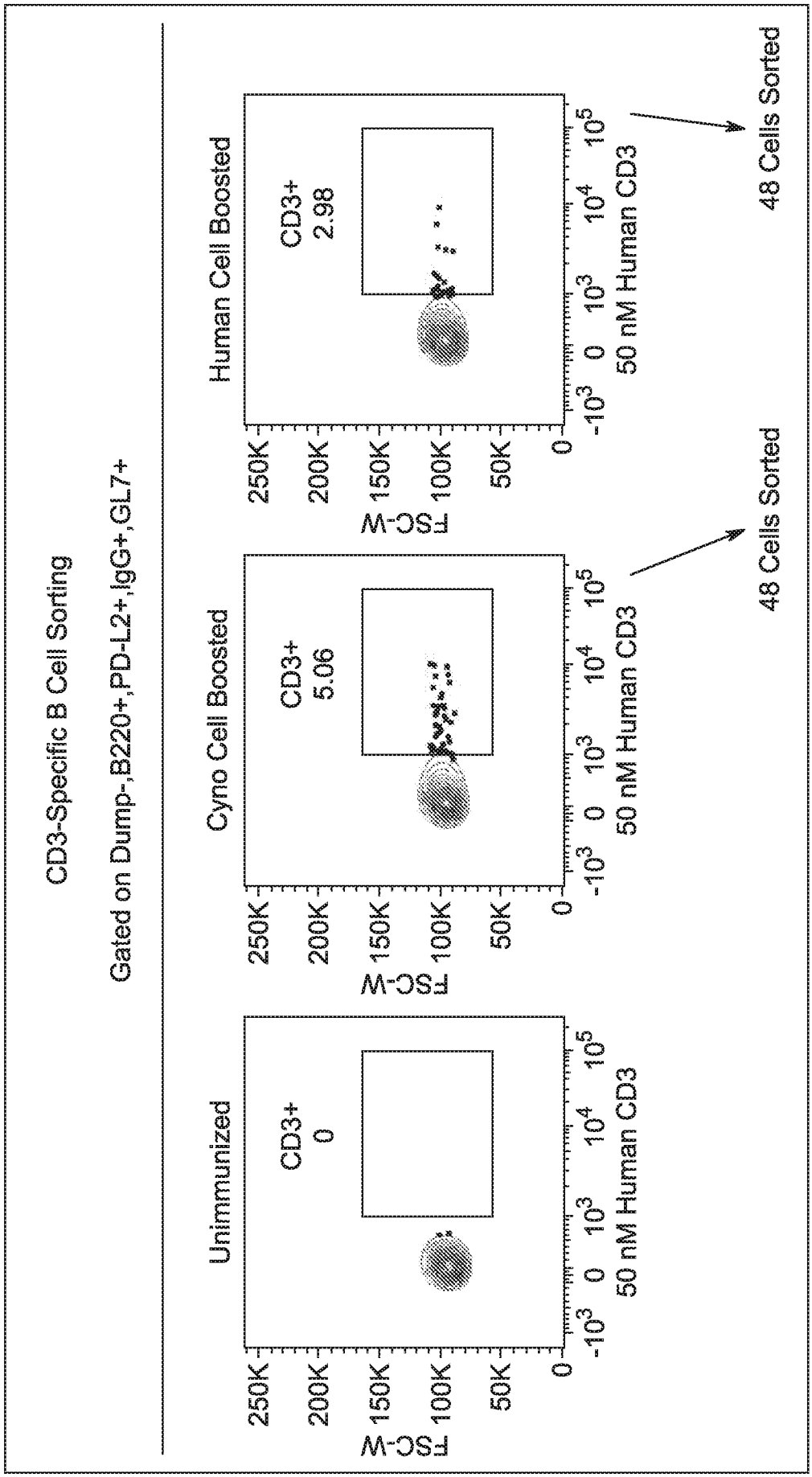

CD3-Specific B Cell Sorting
Gated on Dump-,B220+,PD-L2+,IgG+,GL7+
Unimmunized
CD3+
0
Cyno Cell Boosted
CD3+
5.06
Human Cell Boosted
CD3+
2.98
FSC-W
250K
200K
150K
100K
50K
0
-10^3 0 10^3 10^4 10^5
50 nM Human CD3
48 Cells Sorted
48 Cells Sorted

Figure 2

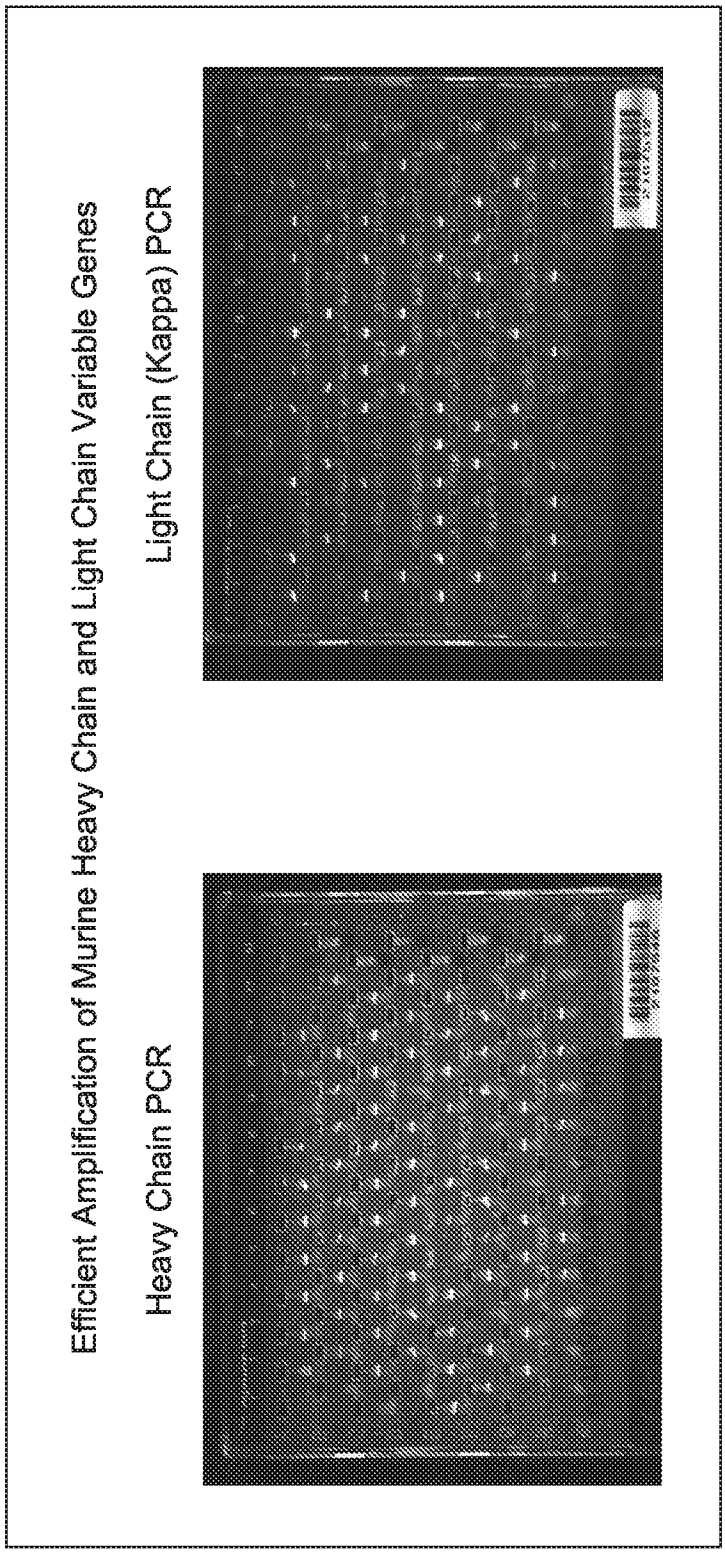

Efficient Amplification of Murine Heavy Chain and Light Chain Variable Genes
Heavy Chain PCR
Light Chain (Kappa) PCR

Figure 3

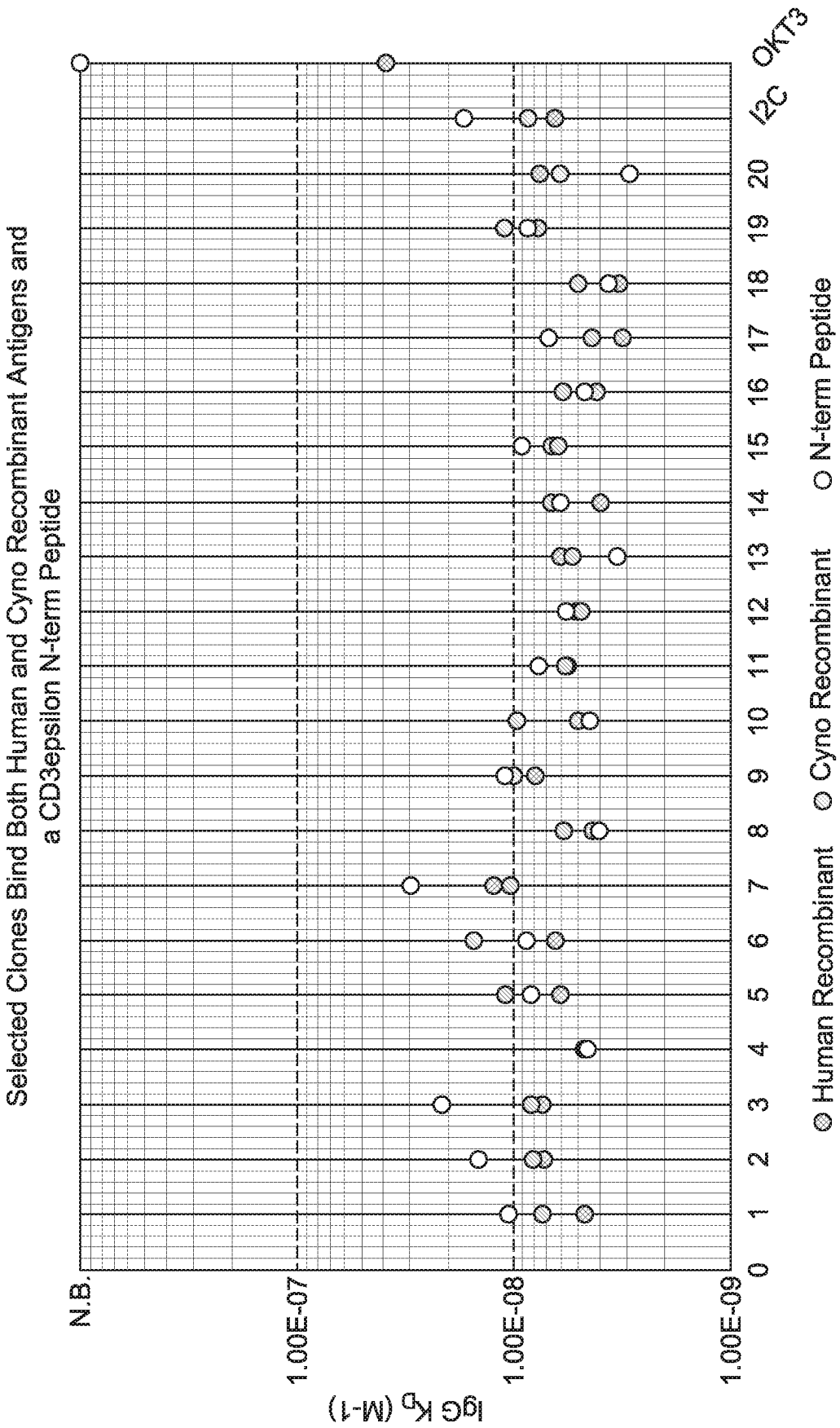

Selected Clones Bind Both Human and Cyno Recombinant Antigens and a CD3epsilon N-term Peptide
N.B.
1.00E-07
1.00E-08
1.00E-09
IgG K_D (M-1)
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
$I2C$ OKT_3
Human Recombinant
Cyno Recombinant
N-term Peptide

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

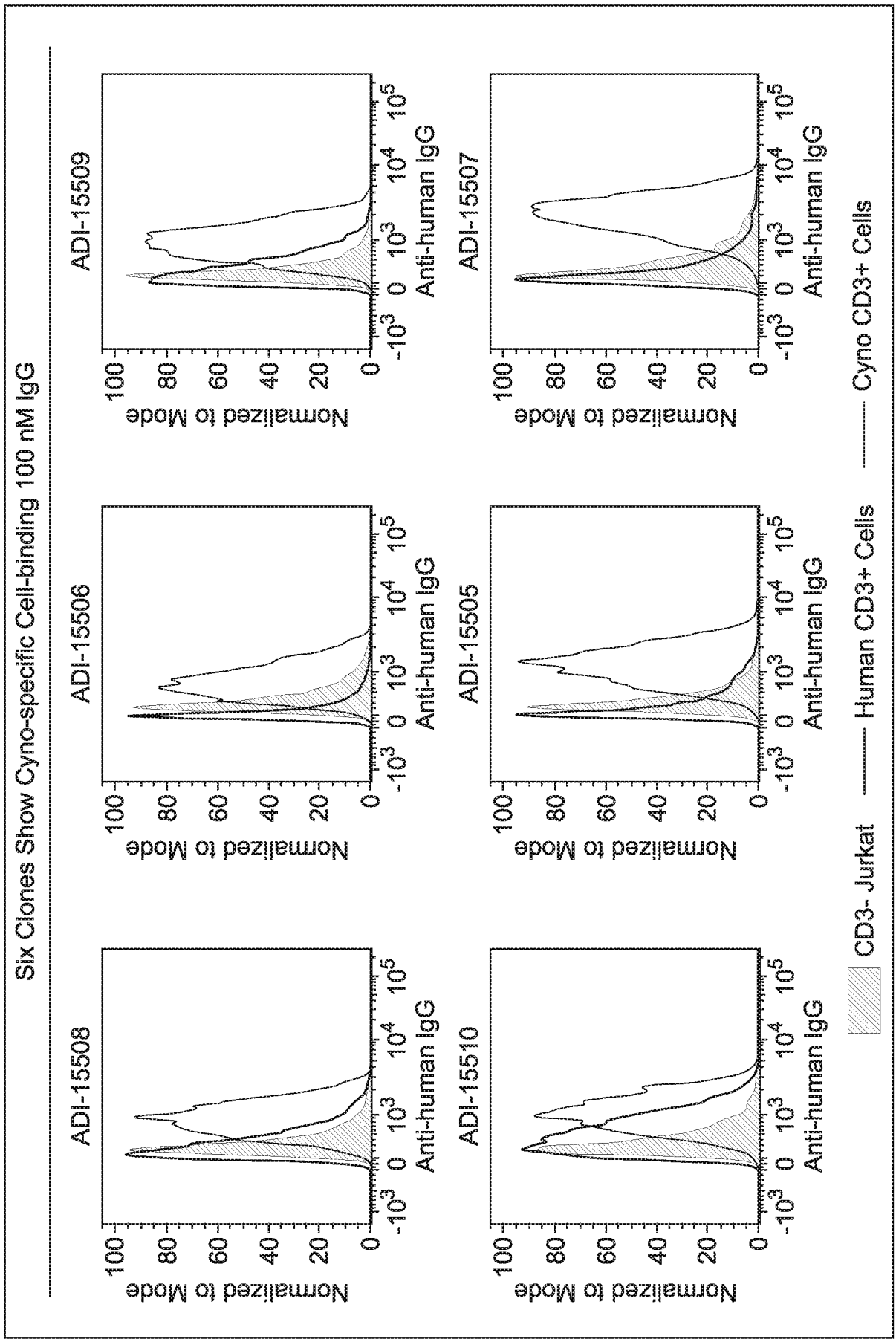

Six Clones Show Cyno-specific Cell-binding 100 nM IgG
ADI-15508
ADI-15506
ADI-15509
ADI-15505
ADI-15507
ADI-15510
Normalized to Mode
Anti-human IgG
CD3- Jurkat
Human CD3+ Cells
Cyno CD3+ Cells

Figure 5

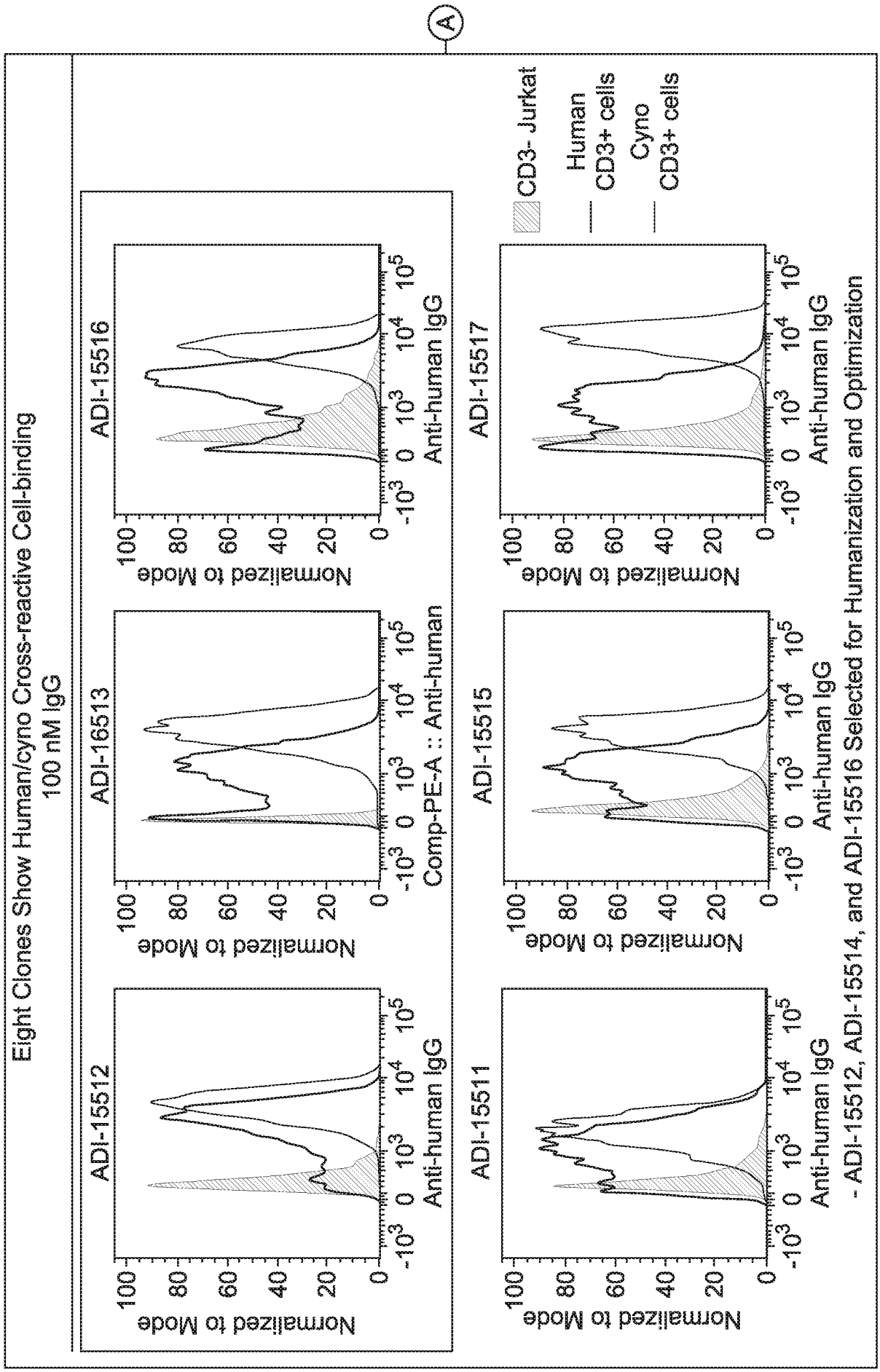

A
Eight Clones Show Human/cyno Cross-reactive Cell-binding
100 nM IgG
ADI-15512
ADI-16513
ADI-15516
ADI-15511
ADI-15515
ADI-15517
Normalized to Mode
Anti-human IgG
Comp-PE-A :: Anti-human
CD3- Jurkat
Human
CD3+ cells
Cyno
CD3+ cells
- ADI-15512, ADI-15514, and ADI-15516 Selected for Humanization and Optimization

Figure 6

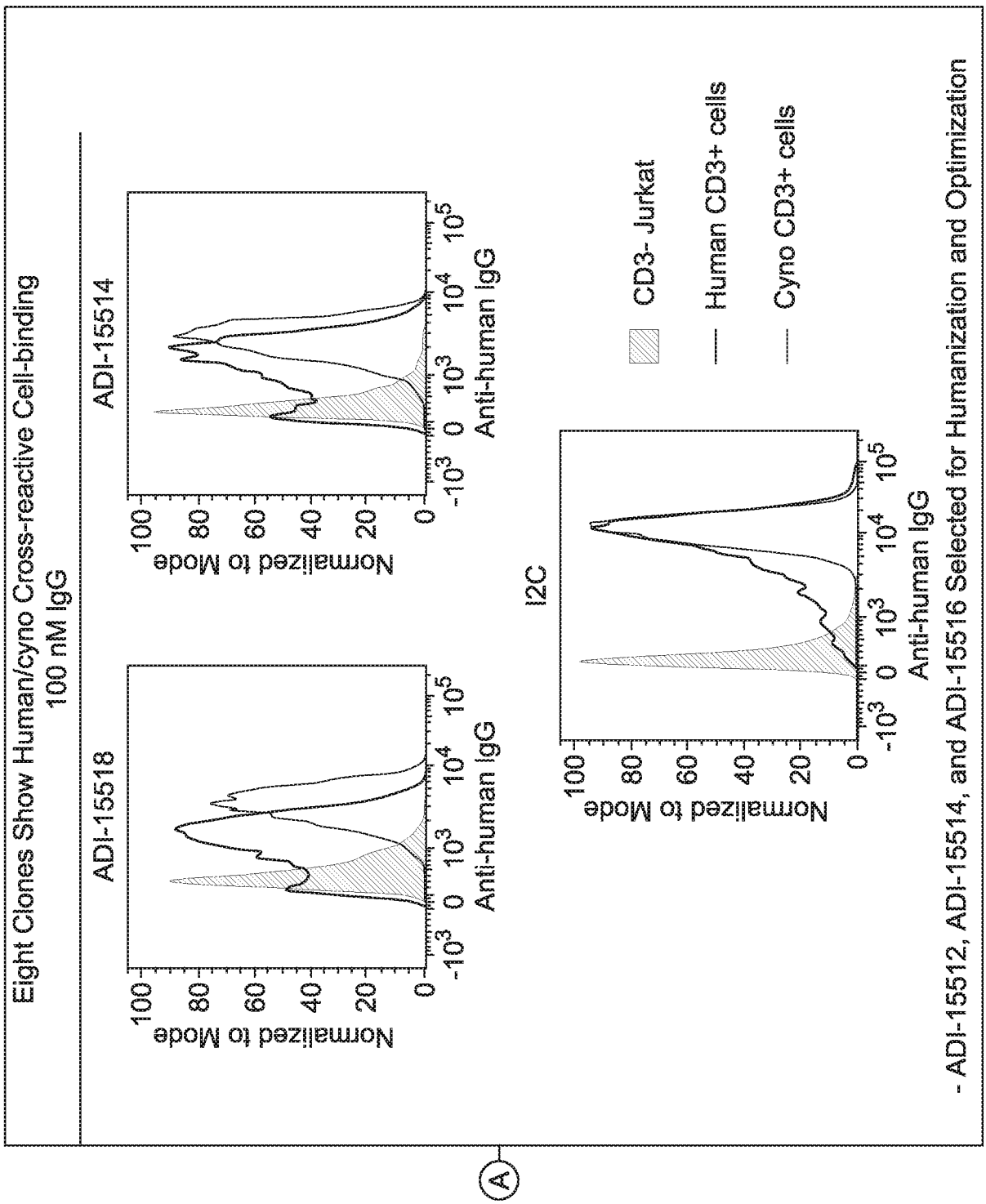


Figure 6 (Continued)

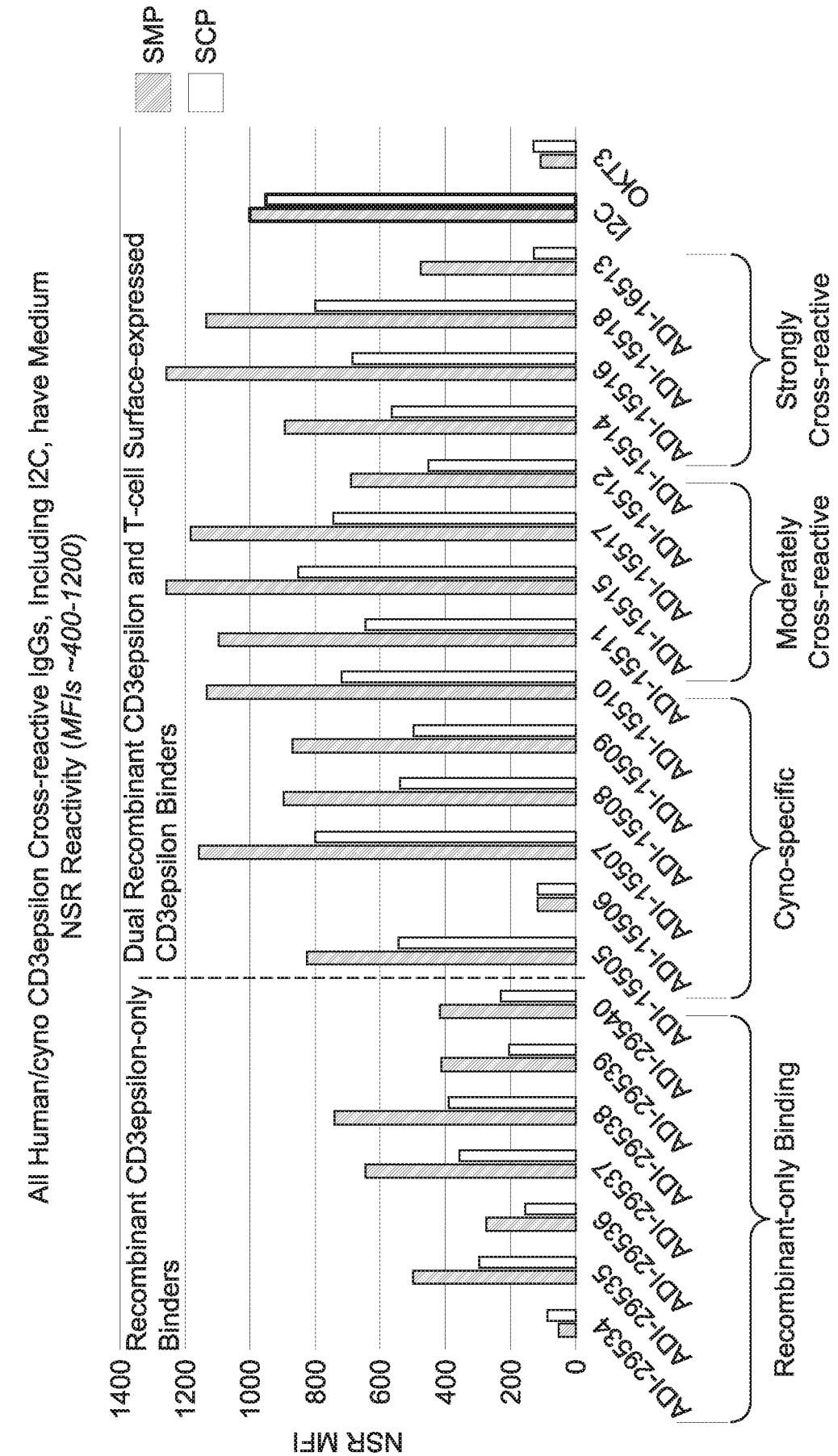

All Human/cyno CD3epsilon Cross-reactive IgGs, Including I2C, have Medium NSR Reactivity (MFIs ~400-1200)
SMP
SCP
NSR MFI
1400
1200
1000
800
600
400
200
0
Recombinant CD3epsilon-only Binders
Dual Recombinant CD3epsilon and T-cell Surface-expressed CD3epsilon Binders
OKT3
I2C
ADI-16513
ADI-15518
ADI-15516
ADI-15514
ADI-15512
ADI-15517
ADI-15515
ADI-15511
ADI-15510
ADI-15509
ADI-15508
ADI-15507
ADI-15506
ADI-15505
ADI-29540
ADI-29539
ADI-29538
ADI-29537
ADI-29536
ADI-29535
ADI-29534
Strongly Cross-reactive
Moderately Cross-reactive
Cyno-specific
Recombinant-only Binding

Figure 7

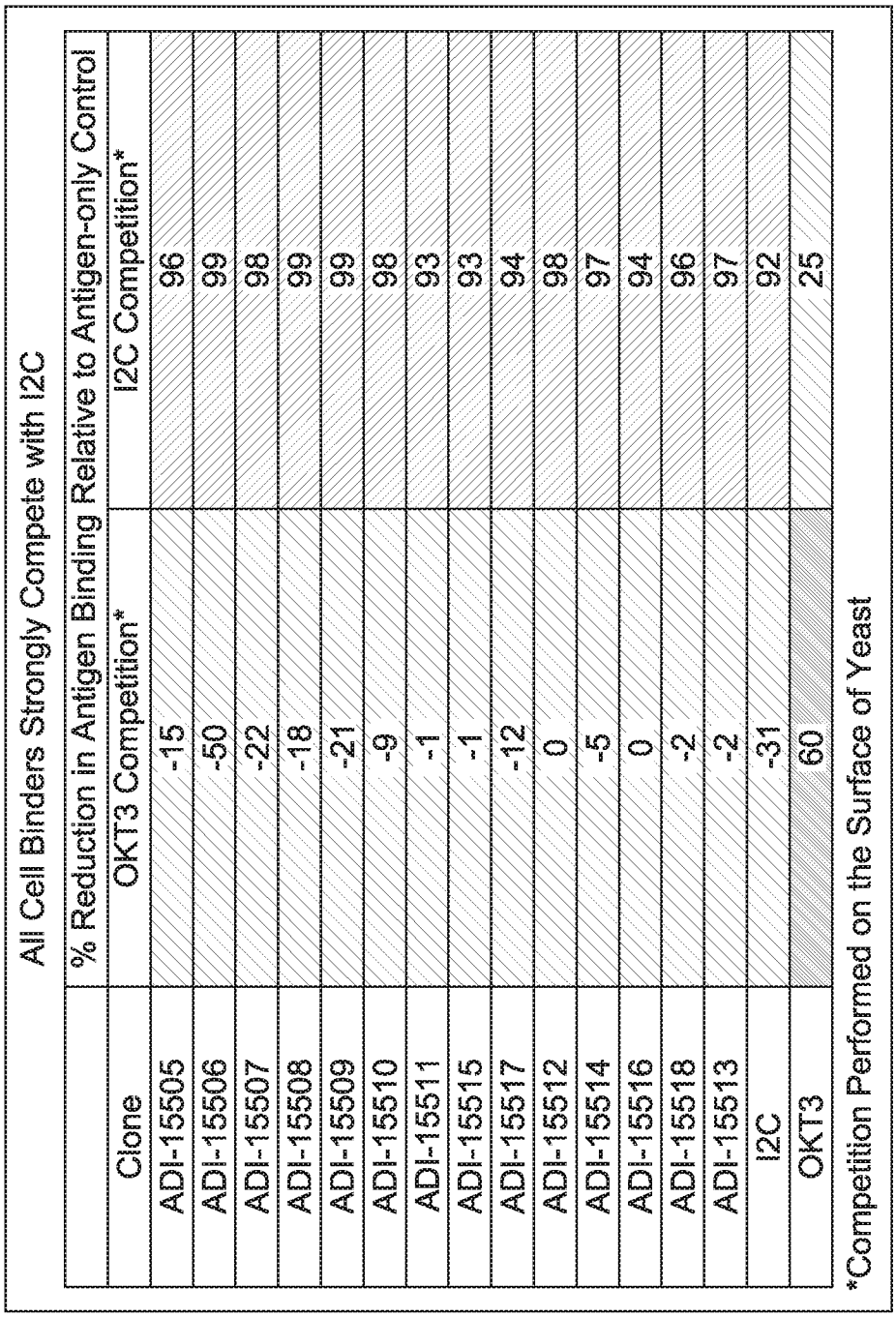
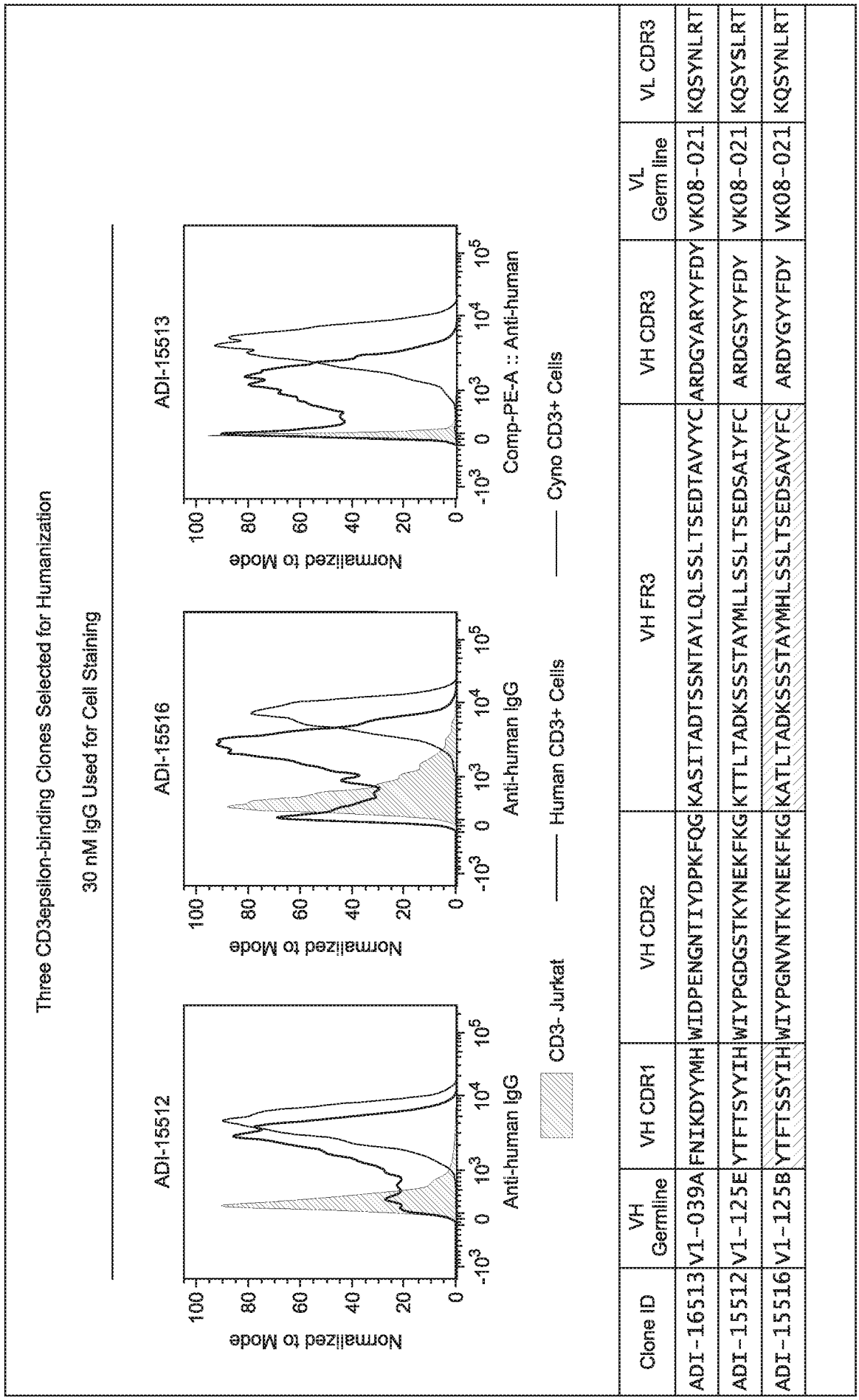

All Cell Binders Strongly Compete with I2C
% Reduction in Antigen Binding Relative to Antigen-only Control
Clone
OKT3 Competition*
I2C Competition*
ADI-15505 -15 96
ADI-15506 -50 99
ADI-15507 -22 98
ADI-15508 -18 99
ADI-15509 -21 99
ADI-15510 -9 98
ADI-15511 -1 93
ADI-15515 -1 93
ADI-15517 -12 94
ADI-15512 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



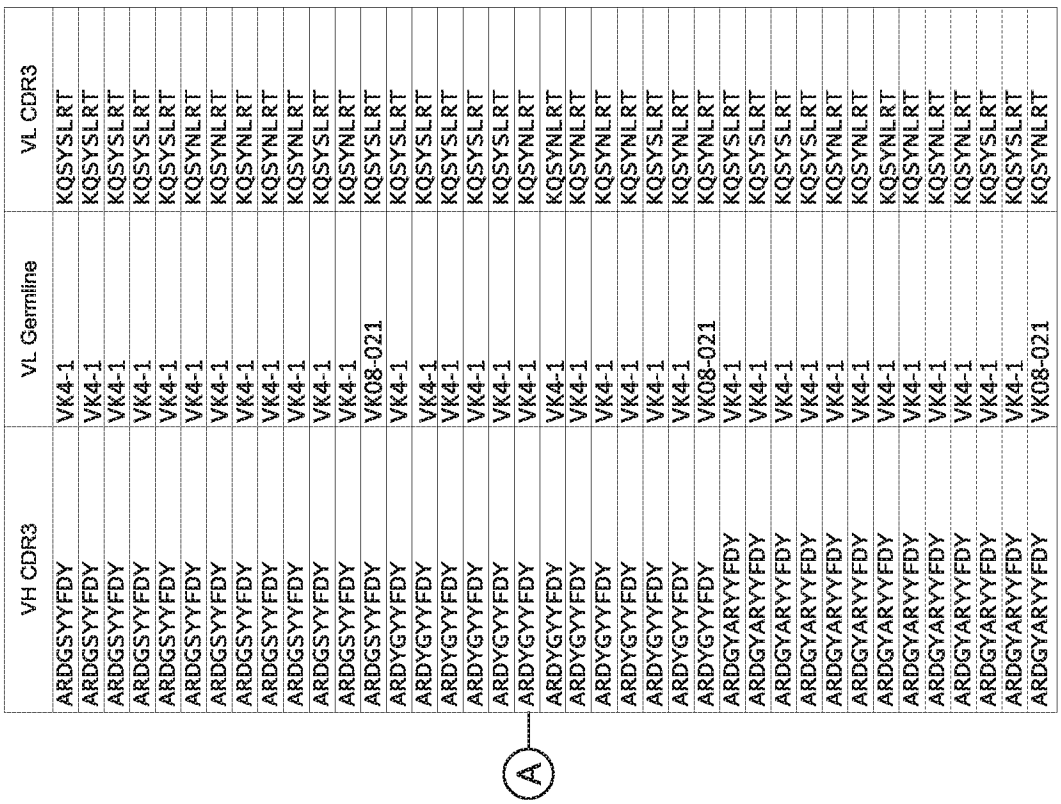
Clone ID	VH Germline	VH CDR1	VH CDR2	VH FR3	VH CDR3	VL Germ line	VL CDR3
ADI-16513	V1-039A	FNIKDYYMH	WIDPENGNTIYDPKFQG	KASITADTSSNTAYLQLSSLTSEDTAVYYC	ARDGYARYYFDY	VK08-021	KQSYNLRT
ADI-15512	V1-125E	YTFTSYYIH	WIYPGDGSTKYNEKFKG	KTTLTADKSSSTAYMLLSSLTSEDSAIYFC	ARDGSYYFDY	VK08-021	KQSYSLRT
ADI-15516	V1-125B	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

A

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	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	KQSYSLRT
ARDGYARYYFDY	VK4-1	KQSYSLRT
ARDGYARYYFDY	VK08-021	KQSYNLRT

Figure 10A (Continued)

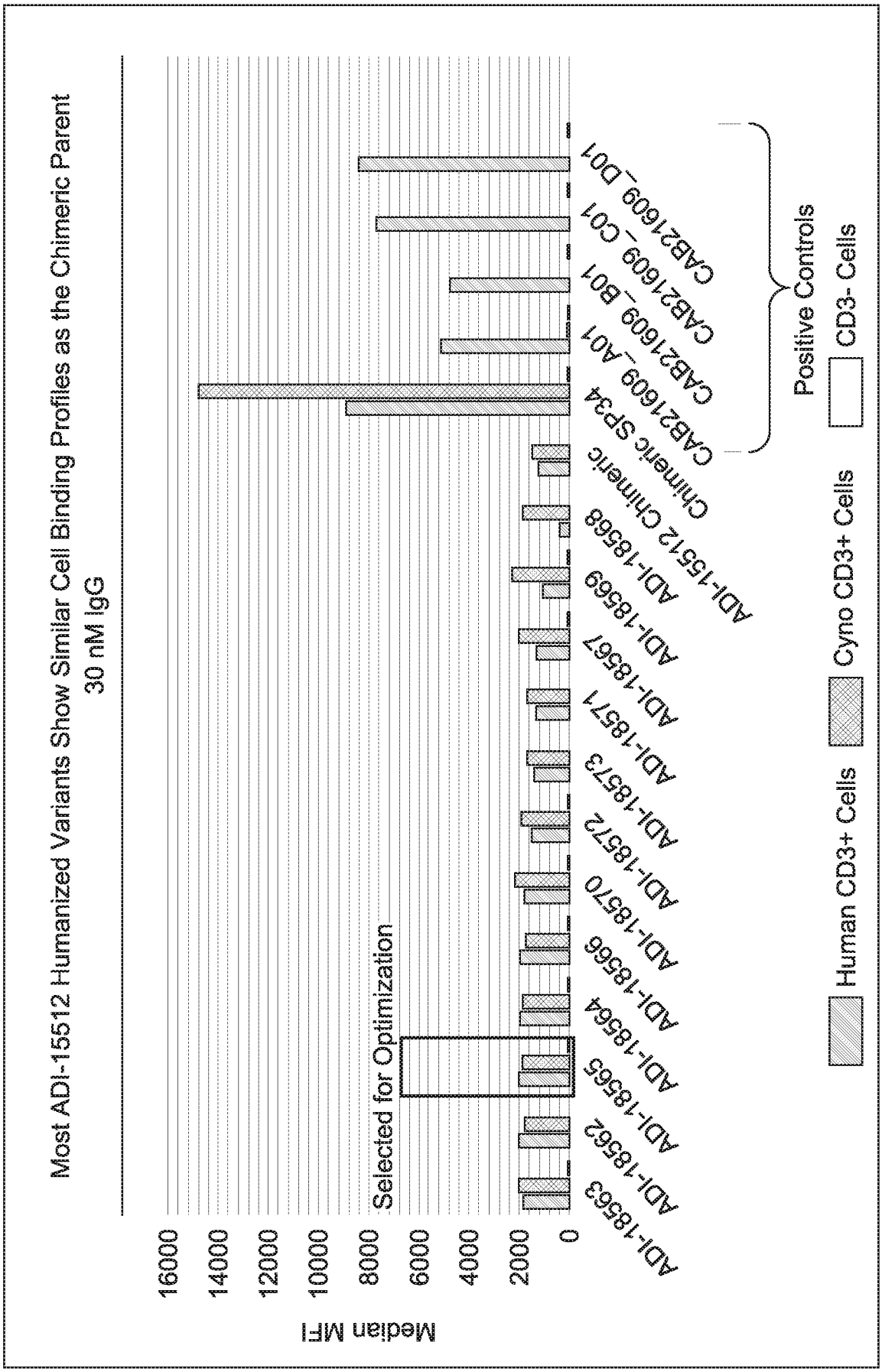

Most ADI-15512 Humanized Variants Show Similar Cell Binding Profiles as the Chimeric Parent
30 nM IgG
Median MFI
16000
14000
12000
10000
8000
6000
4000
2000
0
Selected for Optimization
ADI-18563
ADI-18562
ADI-18565
ADI-18564
ADI-18566
ADI-18570
ADI-18572
ADI-18573
ADI-18571
ADI-18567
ADI-18569
ADI-18568
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

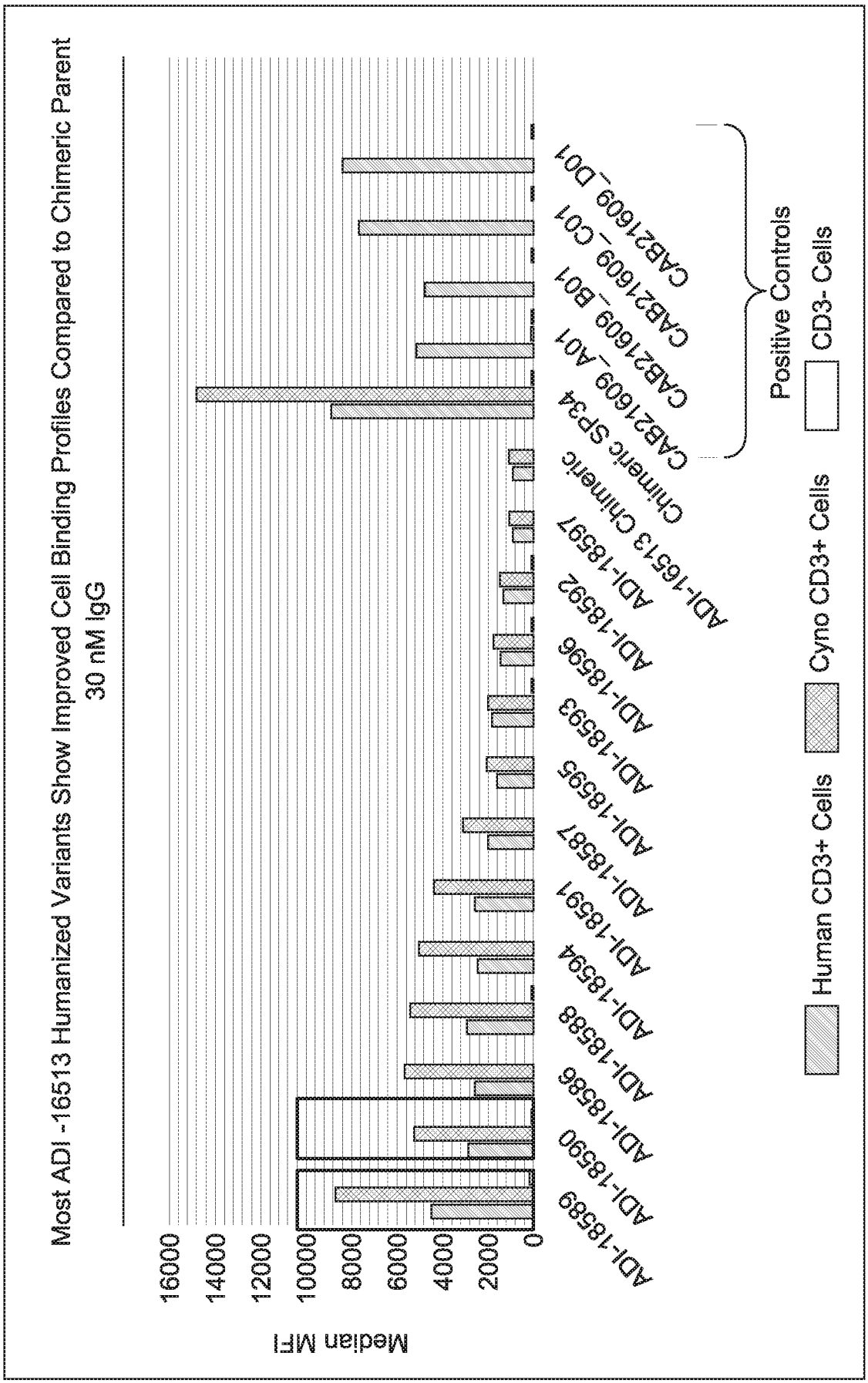

Most ADI -16513 Humanized Variants Show Improved Cell Binding Profiles Compared to Chimeric Parent
30 nM IgG
Median MFI
16000
14000
12000
10000
8000
6000
4000
2000
0
ADI-18589
ADI-18590
ADI-18586
ADI-18588
ADI-18594
ADI-18591
ADI-18587
ADI-18595
ADI-18593
ADI-18596
ADI-18592
ADI-18597
ADI-16513 Chimeric
CAB21609 SP34
CAB21609_A01
CAB21609_B01
CAB21609_C01
CAB21609_D01
Positive Controls
Human CD3+ Cells
Cyno CD3+ Cells
CD3- Cells

Figure 10C

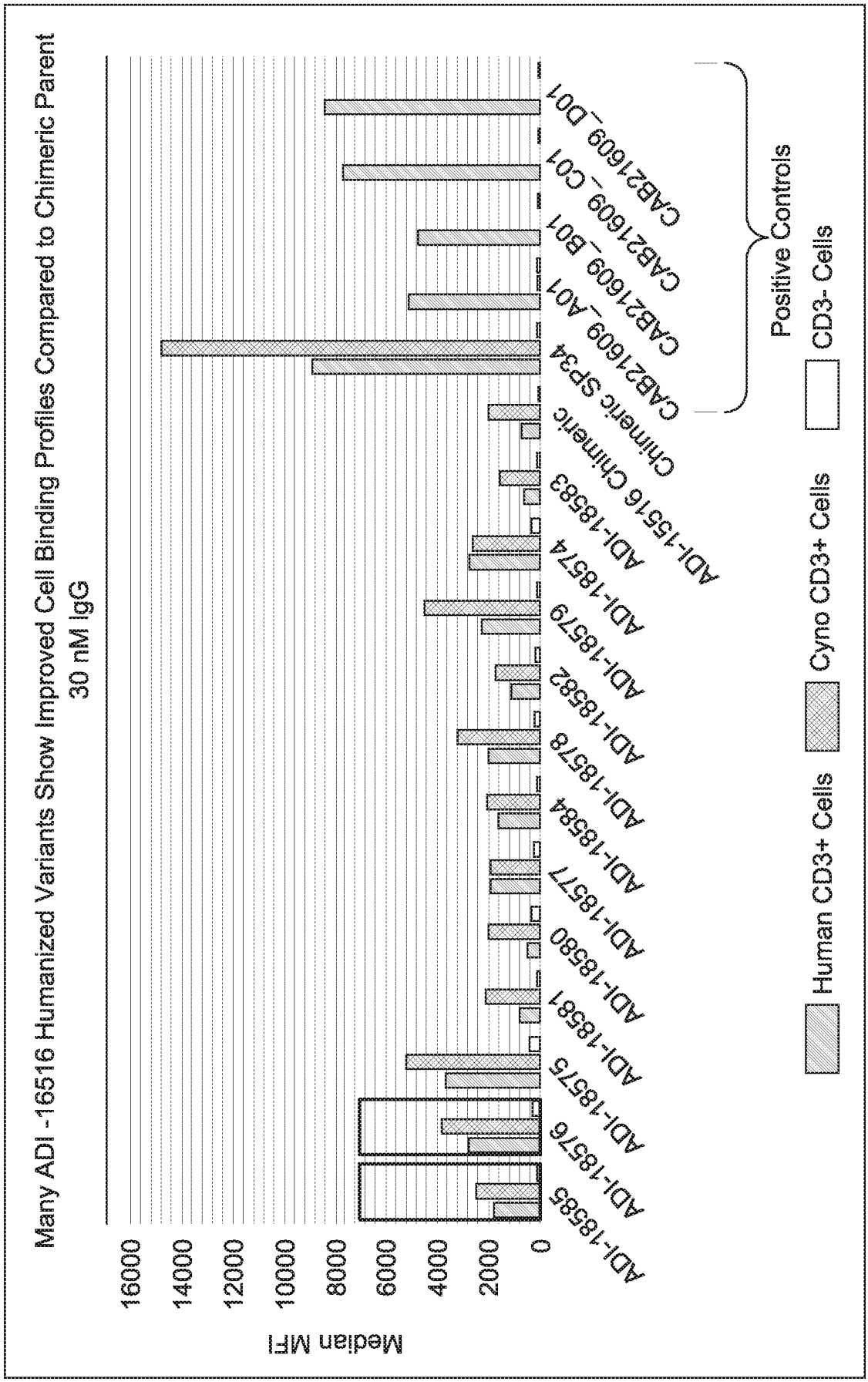

Many ADI -16516 Humanized Variants Show Improved Cell Binding Profiles Compared to Chimeric Parent
30 nM IgG
Median MFI
16000
14000
12000
10000
8000
6000
4000
2000
0
ADI-18585
ADI-18576
ADI-18575
ADI-18581
ADI-18580
ADI-18577
ADI-18584
ADI-18578
ADI-18582
ADI-18579
ADI-18574
ADI-18583
ADI-15516 Chimeric
Chimeric SP34
CAB21609_A01
CAB21609_B01
CAB21609_C01
CAB21609_D01
Positive Controls
Human CD3+ Cells
Cyno CD3+ Cells
CD3- Cells

Figure 10D

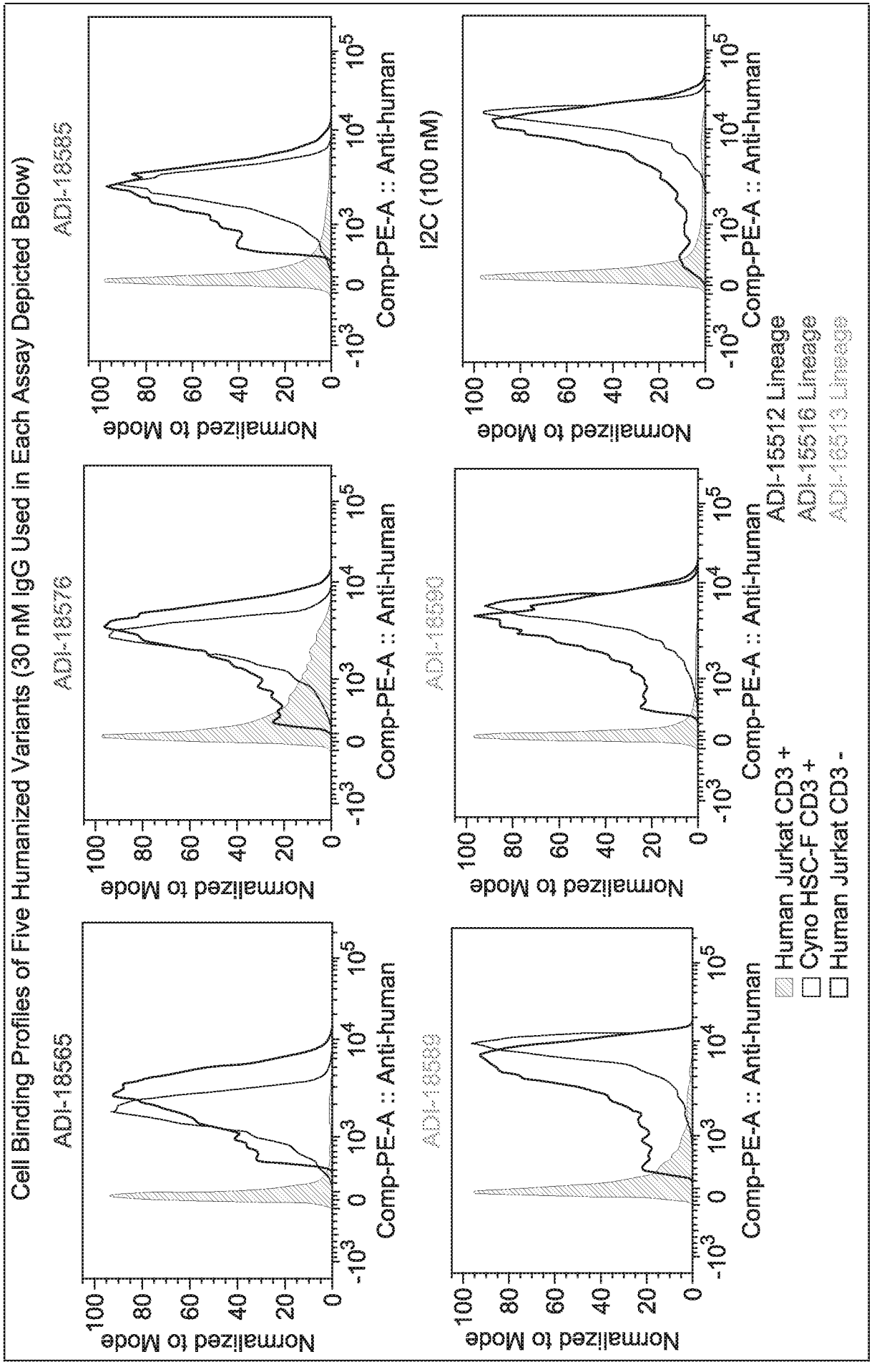

Cell Binding Profiles of Five Humanized Variants (30 nM IgG Used in Each Assay Depicted Below)
ADI-18565
ADI-18576
ADI-18585
ADI-18588
ADI-18590
I2C (100 nM)
Normalized to Mode
Comp-PE-A :: Anti-human
Human Jurkat CD3 +
Cyno HSC-F CD3 +
Human Jurkat CD3 -
ADI-15512 Lineage
ADI-15516 Lineage
ADI-18513 Lineage

Figure 11A

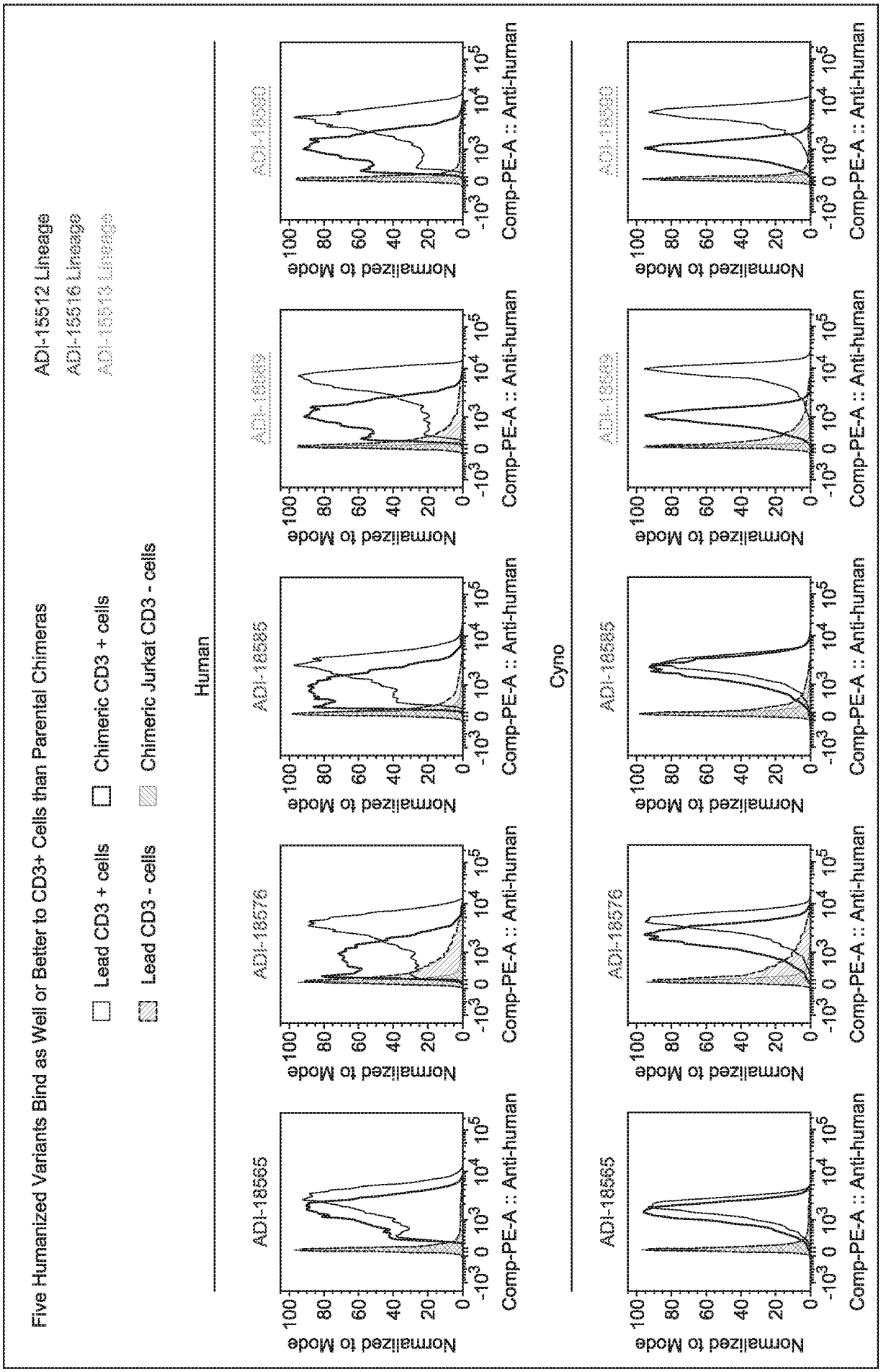

Five Humanized Variants Bind as Well or Better to CD3+ Cells than Parental Chimeras
Lead CD3 + cells
Chimeric CD3 + cells
Lead CD3 - cells
Chimeric Jurkat CD3 - cells
ADI-15512 Lineage
ADI-15516 Lineage
ADI-18513 Lineage
Human
Cyno
ADI-18565
ADI-18576
ADI-18585
ADI-18589
ADI-18590
Normalized to Mode
Comp-PE-A :: Anti-human

Figure 11B

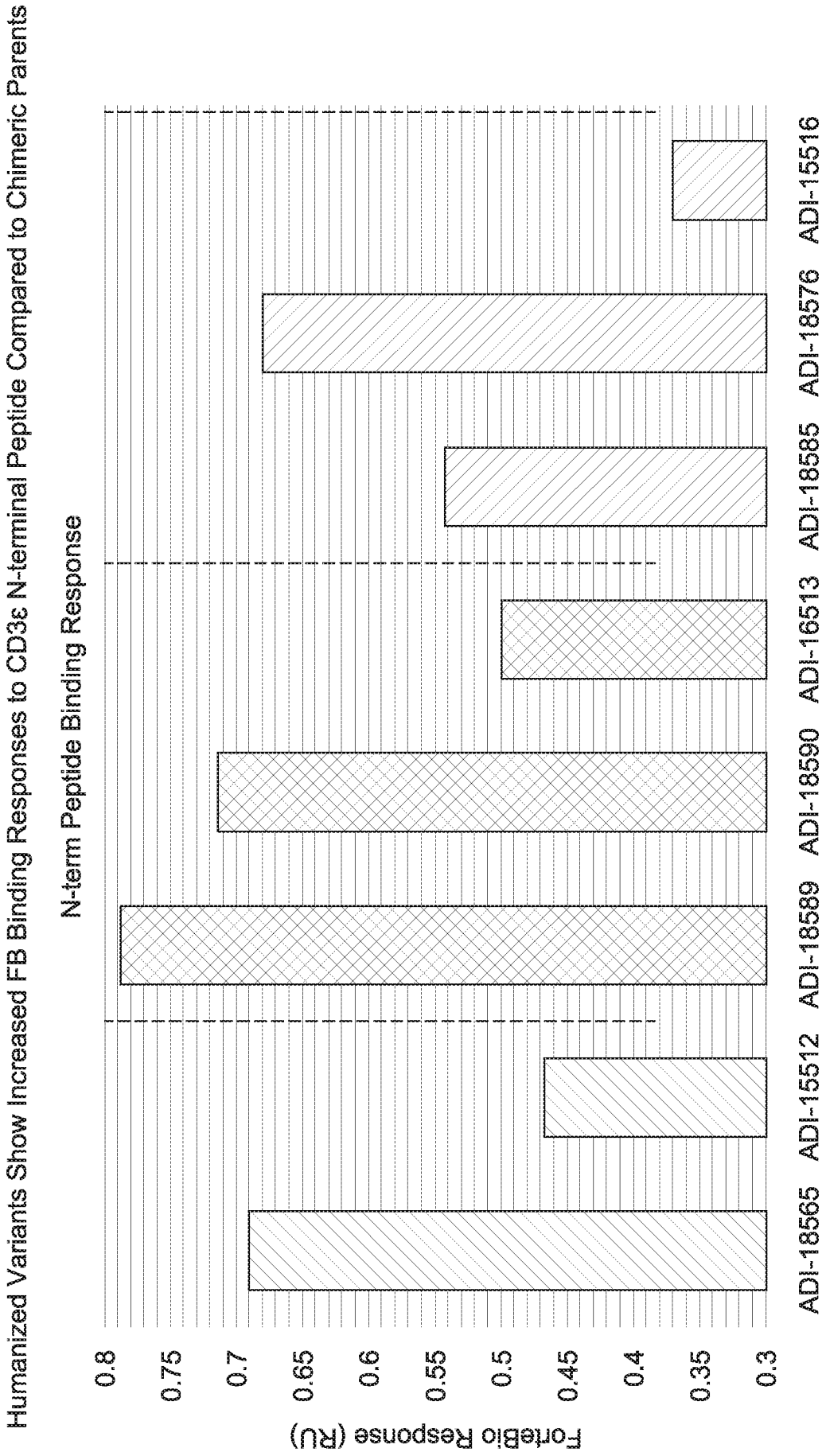

Humanized Variants Show Increased FB Binding Responses to CD3ε N-terminal Peptide Compared to Chimeric Parents
N-term Peptide Binding Response
ForteBio Response (RU)
0.8
0.75
0.7
0.65
0.6
0.55
0.5
0.45
0.4
0.35
0.3
ADI-18565
ADI-15512
ADI-18589
ADI-18590
ADI-16513
ADI-18585
ADI-18576
ADI-15516

Figure 11C

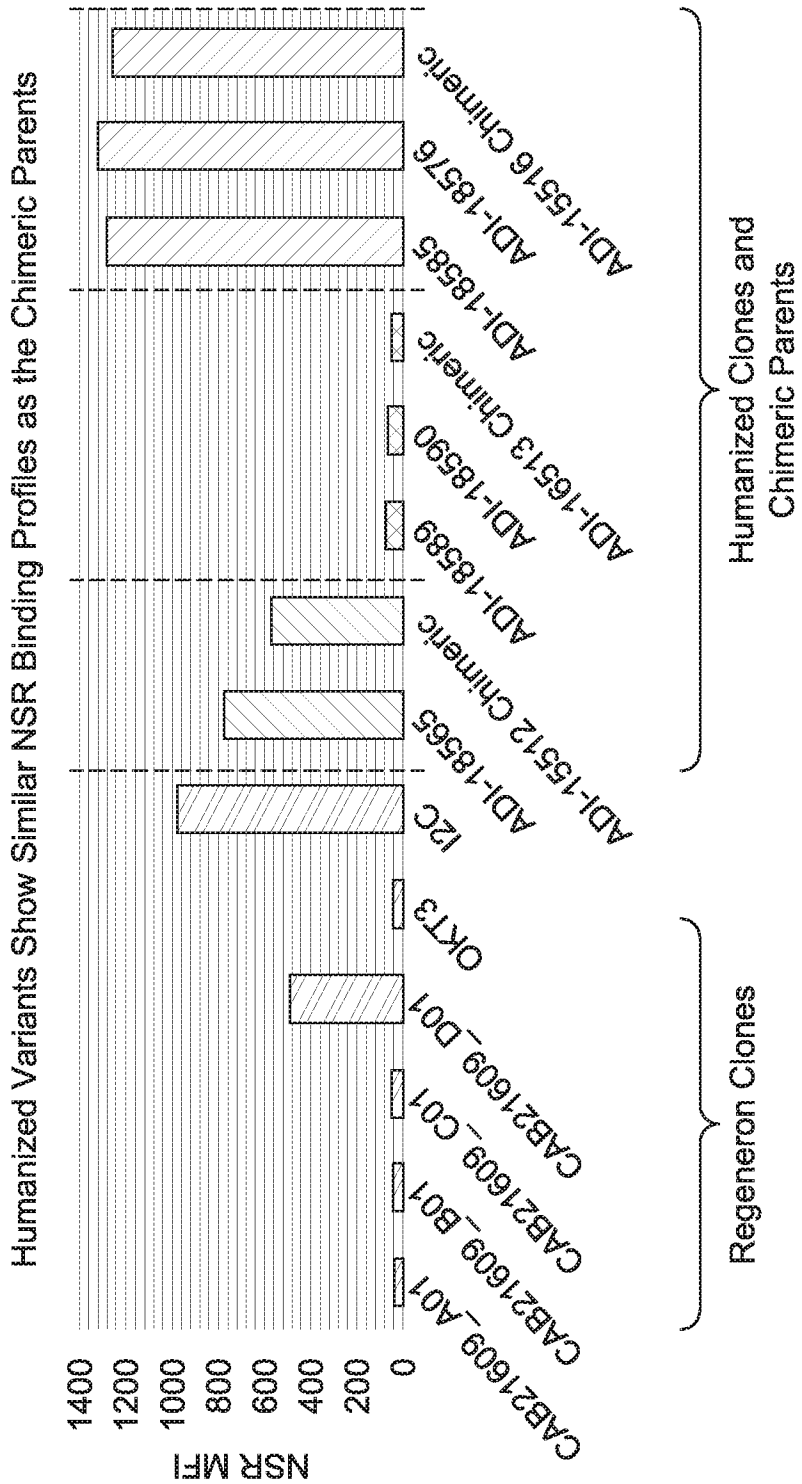

Humanized Variants Show Similar NSR Binding Profiles as the Chimeric Parents
NSR MFI
1400
1200
1000
800
600
400
200
0
CAB21609_A01
CAB21609_B01
CAB21609_C01
CAB21609_D01
OKT3
12C
ADI-18565
ADI-15512 Chimeric
ADI-18589
ADI-18590
ADI-16513 Chimeric
ADI-18585
ADI-18576
ADI-15516 Chimeric
Regeneron Clones
Humanized Clones and
Chimeric Parents

Figure 12A

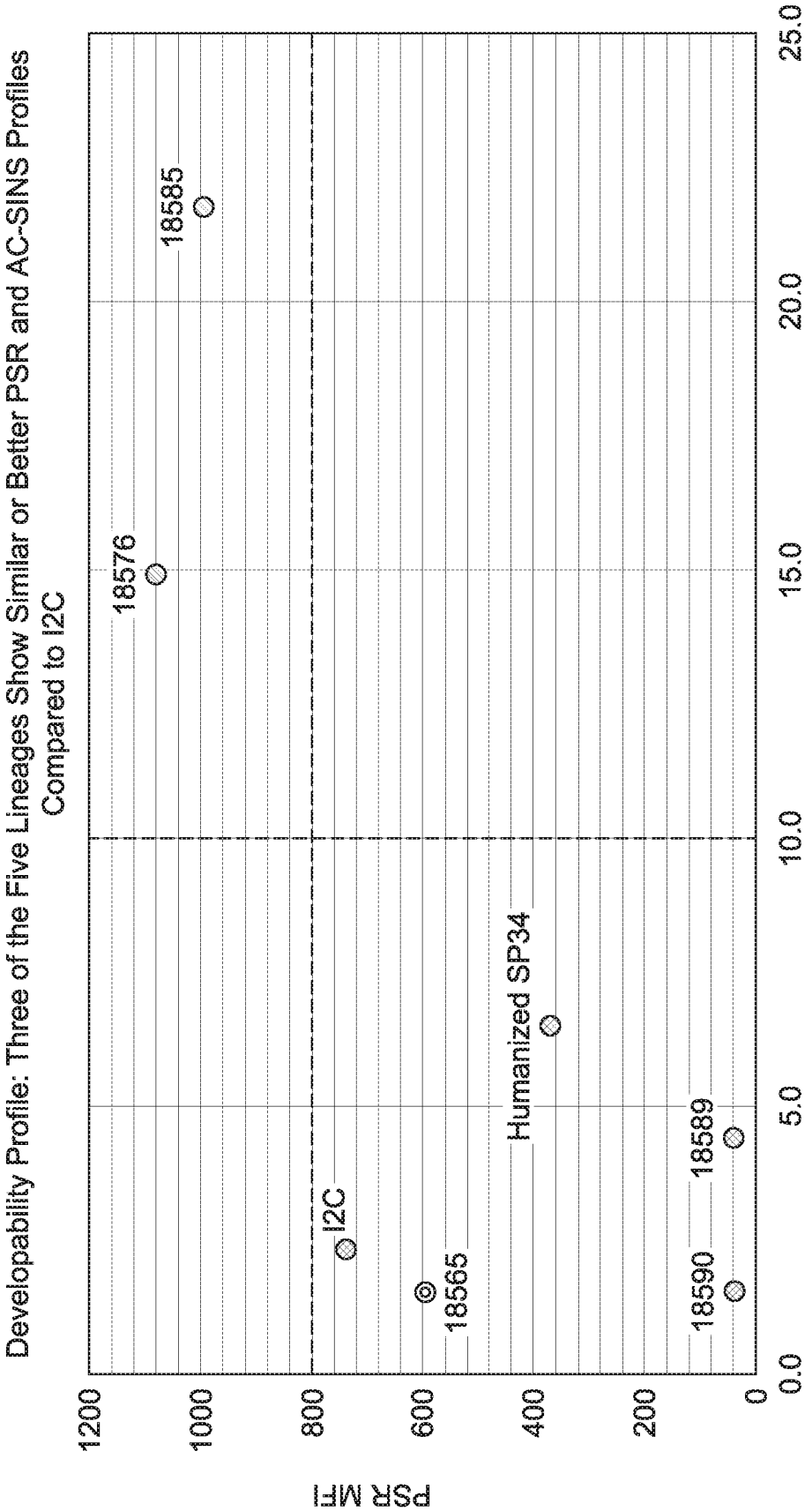

Developability Profile: Three of the Five Lineages Show Similar or Better PSR and AC-SINS Profiles Compared to I2C
PSR MFI
AC-SINS (Δλmax)
0
200
400
600
800
1000
1200
0.0
5.0
10.0
15.0
20.0
25.0
18576
18585
I2C
18565
Humanized SP34
18589
18590

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)

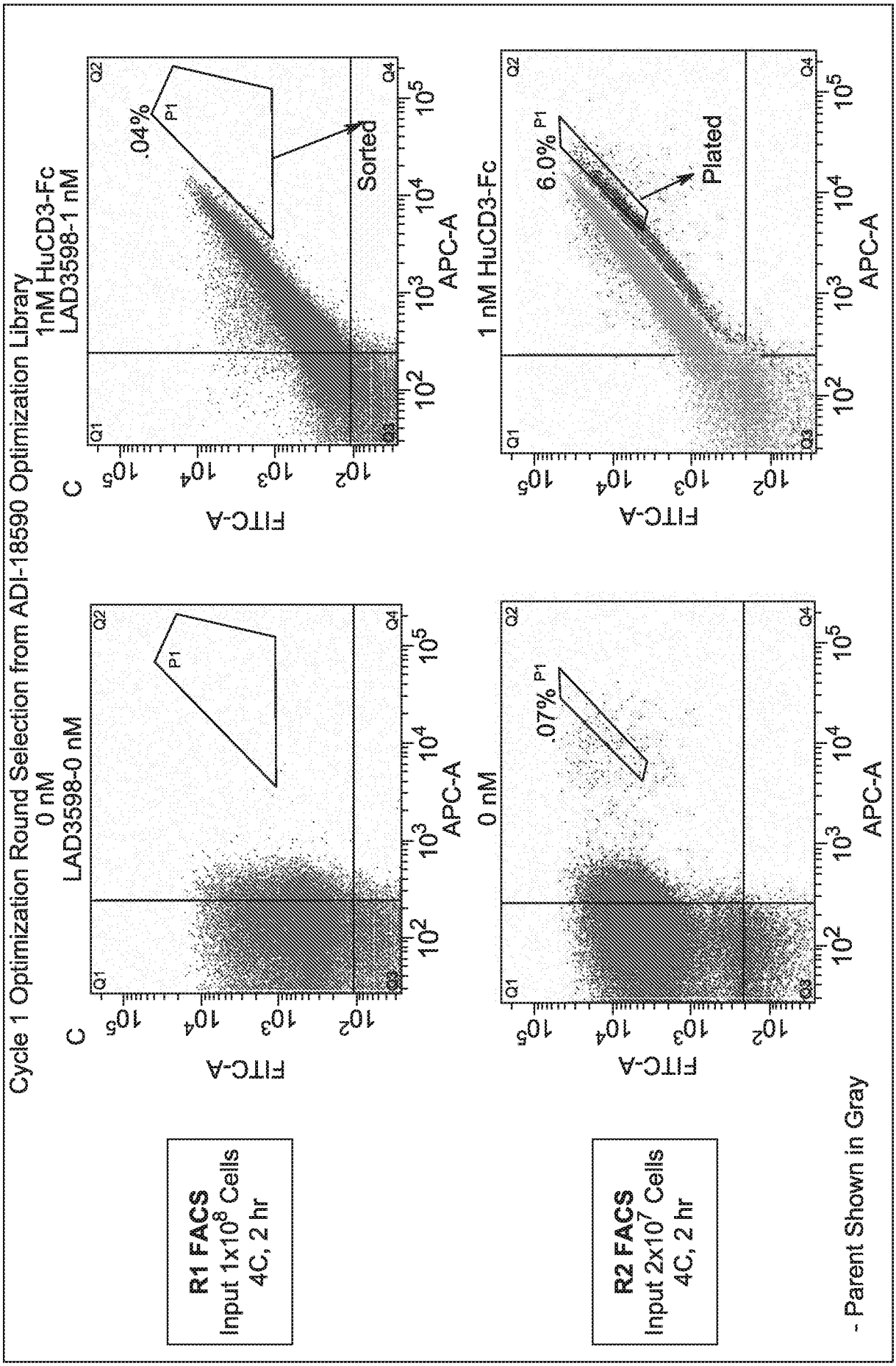

Cycle 1 Optimization Round Selection from ADI-18590 Optimization Library
1nM HuCD3-Fc
LAD3598-1 nM
0 nM
LAD3598-0 nM
1 nM HuCD3-Fc
0 nM
.04%
P1
Sorted
6.0%
Plated
.07%
R1 FACS
Input 1x10^8 Cells
4C, 2 hr
R2 FACS
Input 2x10^7 Cells
4C, 2 hr
- Parent Shown in Gray
FITC-A
APC-A
Q1
Q2
Q3
Q4

Figure 14

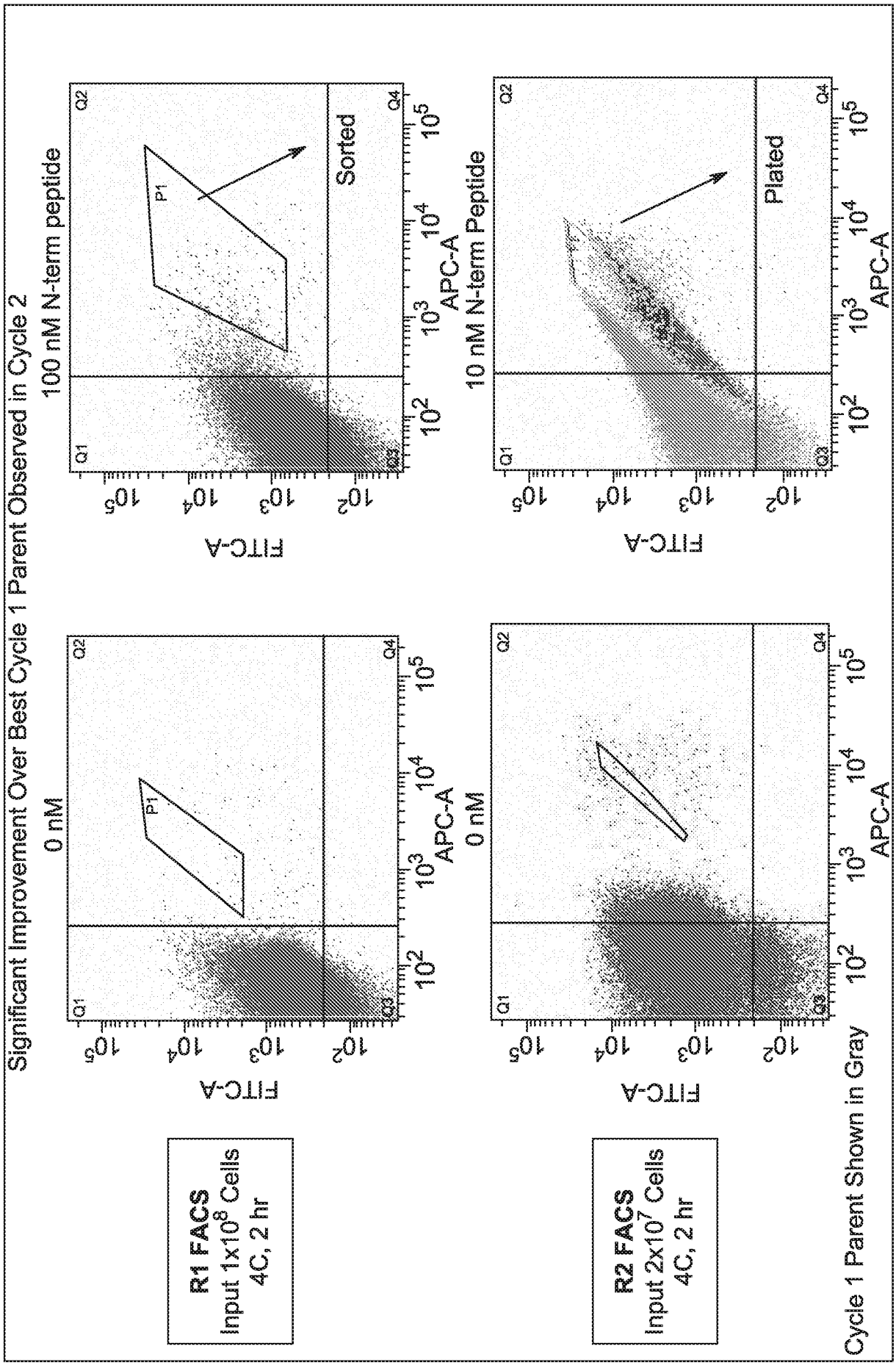

Significant Improvement Over Best Cycle 1 Parent Observed in Cycle 2
100 nM N-term peptide
Sorted
10 nM N-term Peptide
Plated
0 nM
0 nM
R1 FACS
Input 1x10^8 Cells
4C, 2 hr
R2 FACS
Input 2x10^7 Cells
4C, 2 hr
Cycle 1 Parent Shown in Gray
FITC-A
APC-A
P1
Q1
Q2
Q3
Q4

Figure 15

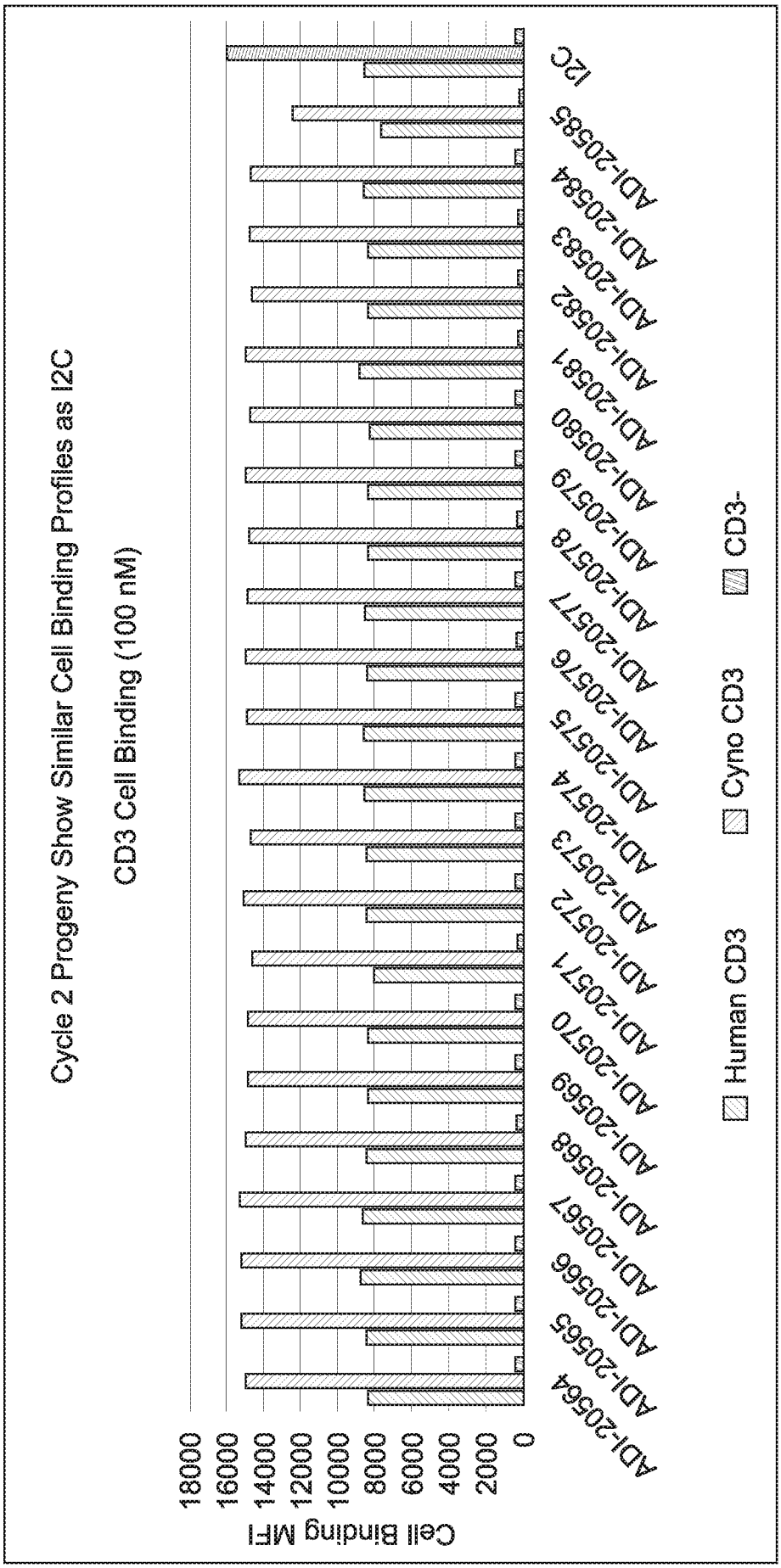

Cycle 2 Progeny Show Similar Cell Binding Profiles as I2C
CD3 Cell Binding (100 nM)
Cell Binding MFI
18000
16000
14000
12000
10000
8000
6000
4000
2000
0
Human CD3
Cyno CD3
CD3-
ADI-20564
ADI-20565
ADI-20566
ADI-20567
ADI-20568
ADI-20569
ADI-20570
ADI-20571
ADI-20572
ADI-20573
ADI-20574
ADI-20575
ADI-20576
ADI-20577
ADI-20578
ADI-20579
ADI-20580
ADI-20581
ADI-20582
ADI-20583
ADI-20584
ADI-20585
I2C

Figure 16

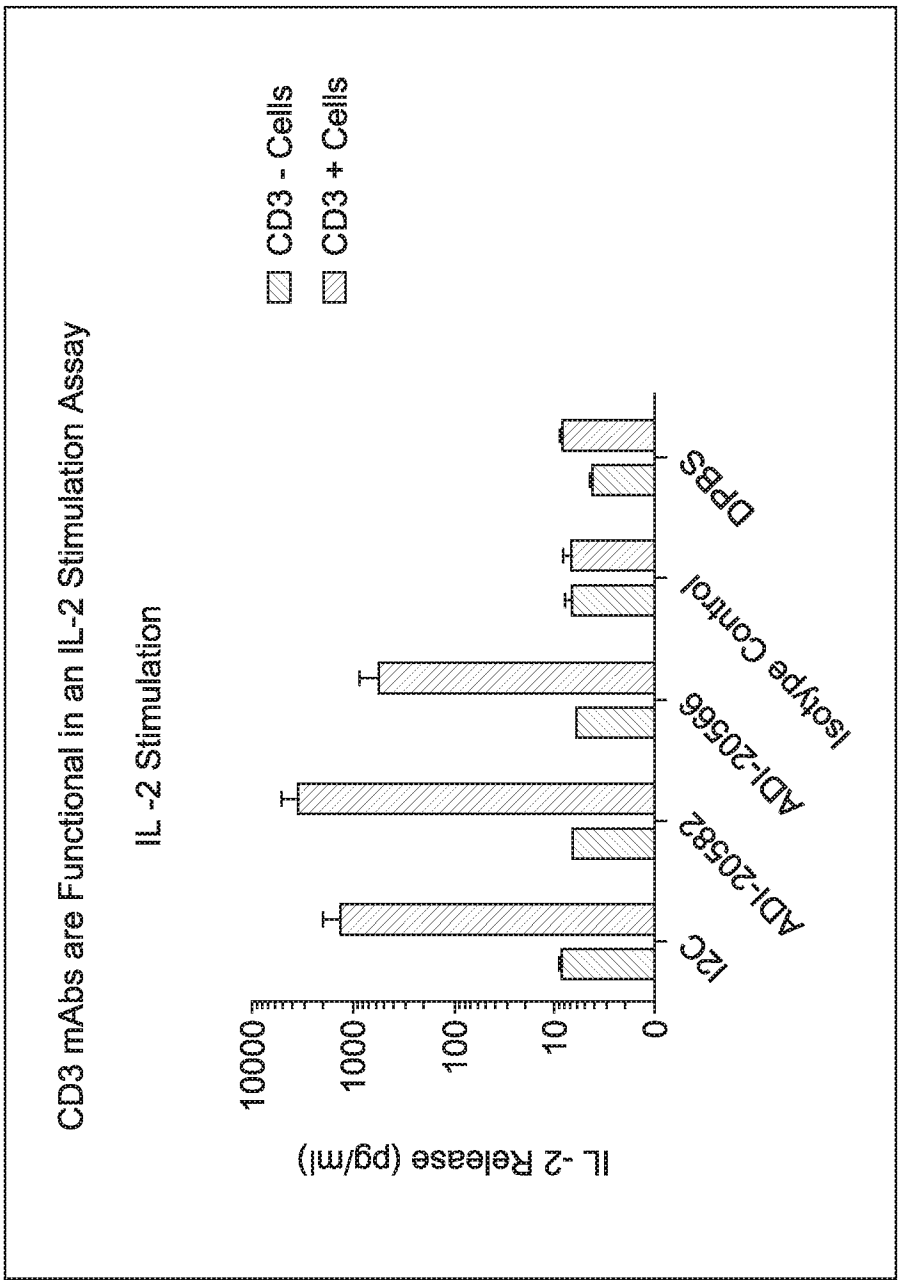

CD3 mAbs are Functional in an IL-2 Stimulation Assay
IL -2 Stimulation
CD3 - Cells
CD3 + Cells
IL -2 Release (pg/ml)
10000
1000
100
10
0
12C
ADI-20582
ADI-20566
Isotype Control
DPBS

Figure 17

Recombinant Heterodimeric CD3 Fc Fusion Antigens
Hu QDGNEEMGGIT...
Cy QDGNEEMGSIT...
α
β
ε
γ
δ
ε
δ
ε
δ
ε
TCR/CD3 complex
Hu CD3εδ Fc
Cy CD3εδ Fc
Hu CD3ε Fc
QDGNEEMGGITQTPYKVSISGTTVILTCPQYPGSEILWQHNDKNIGGDEDDKNIGSDEDHLSLKEFSELEQSGYYVCYPRGSKPEDANFYLYLRARVCENCMEMD
GGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKC
KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS
VMHEALHNHYTQKSLSLSPGK
Hu CD3δ Fc-HIS
FKPIEELEDRVFVNCNTSITWVEGTVGTLLSDITRLDLGKRILDPRGIYRCNGTDIYKDKESTVQVHYRMCQSCVELDPGGSDKTHTCPPCPAPELLGGPSVFLFPPK
PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP
PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKHHHHHH
Cy CD3ε Fc
QDGNEEMGSITQTPYQVSISGTTVILTCSQHLGSEAQWQHNGKNKEDSGDRLFLPEFSEMEQSGYYVCYPRGSNPEDASHHLYLKARVCENCMEMD
GGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKV
SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE
ALHNHYTQKSLSLSPGK
Cy CD3δ Fc-HIS
FKPVEELEDRVFVNCNTSVTWVEGTVGTLLTNNTRLDLGKRILDPRGIYRCNGTDIYKDKESAVQVHYRMCQNCVELDPGGSDKTHTCPPCPAPELLGGPSVFLFPPK
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	DTAVYYCARDXYARXYFDYWGQGTLVTVSS
DTAVYYCXRXGYARYYFDYWGQGTLVTVSS	DTAVYYCARDXYARYXFDYWGQGTLVTVSS
DTAVYYCXRDXYARYYFDYWGQGTLVTVSS	DTAVYYCARDXYARYYXDYWGQGTLVTVSS
DTAVYYCXRDGXARYYFDYWGQGTLVTVSS	DTAVYYCARDXYARYYFXYWGQGTLVTVSS
DTAVYYCXRDGYXRYYFDYWGQGTLVTVSS	DTAVYYCARDXYARYYFDXWGQGTLVTVSS
DTAVYYCXRDGYAXYYFDYWGQGTLVTVSS	DTAVYYCARDGXXRYYFDYWGQGTLVTVSS
DTAVYYCXRDGYARXYFDYWGQGTLVTVSS	DTAVYYCARDGXAXYYFDYWGQGTLVTVSS
DTAVYYCXRDGYARYXFDYWGQGTLVTVSS	DTAVYYCARDGXARXYFDYWGQGTLVTVSS
DTAVYYCXRDGYARYYXDYWGQGTLVTVSS	DTAVYYCARDGXARYXFDYWGQGTLVTVSS
DTAVYYCXRDGYARYYFXYWGQGTLVTVSS	DTAVYYCARDGXARYYXDYWGQGTLVTVSS
DTAVYYCXRDGYARYYFDXWGQGTLVTVSS	DTAVYYCARDGXARYYFXYWGQGTLVTVSS
DTAVYYCAXXGYARYYFDYWGQGTLVTVSS	DTAVYYCARDGXARYYFDXWGQGTLVTVSS
DTAVYYCAXDXYARYYFDYWGQGTLVTVSS	DTAVYYCARDGYXXYYFDYWGQGTLVTVSS
DTAVYYCAXDGXARYYFDYWGQGTLVTVSS	DTAVYYCARDGYXRXYFDYWGQGTLVTVSS
DTAVYYCAXDGYXRYYFDYWGQGTLVTVSS	DTAVYYCARDGYXRYXFDYWGQGTLVTVSS
DTAVYYCAXDGYAXYYFDYWGQGTLVTVSS	DTAVYYCARDGYXRYYXDYWGQGTLVTVSS
DTAVYYCAXDGYARXYFDYWGQGTLVTVSS	DTAVYYCARDGYXRYYFXYWGQGTLVTVSS
DTAVYYCAXDGYARYXFDYWGQGTLVTVSS	DTAVYYCARDGYXRYYFDXWGQGTLVTVSS
DTAVYYCAXDGYARYYXDYWGQGTLVTVSS	DTAVYYCARDGYAXXYFDYWGQGTLVTVSS
DTAVYYCAXDGYARYYFXYWGQGTLVTVSS	DTAVYYCARDGYAXYXFDYWGQGTLVTVSS
DTAVYYCAXDGYARYYFDXWGQGTLVTVSS	DTAVYYCARDGYAXYYXDYWGQGTLVTVSS
DTAVYYCARXXYARYYFDYWGQGTLVTVSS	DTAVYYCARDGYAXYYFXYWGQGTLVTVSS
DTAVYYCARXGXARYYFDYWGQGTLVTVSS	DTAVYYCARDGYAXYYFDXWGQGTLVTVSS
DTAVYYCARXGYXRYYFDYWGQGTLVTVSS	DTAVYYCARDGYARXXFDYWGQGTLVTVSS
DTAVYYCARXGYAXYYFDYWGQGTLVTVSS	DTAVYYCARDGYARXYXDYWGQGTLVTVSS
DTAVYYCARXGYARXYFDYWGQGTLVTVSS	DTAVYYCARDGYARXYFXYWGQGTLVTVSS
DTAVYYCARXGYARYXFDYWGQGTLVTVSS	DTAVYYCARDGYARXYFDXWGQGTLVTVSS
DTAVYYCARXGYARYYXDYWGQGTLVTVSS	DTAVYYCARDGYARYXXDYWGQGTLVTVSS
DTAVYYCARXGYARYYFXYWGQGTLVTVSS	DTAVYYCARDGYARYXFXYWGQGTLVTVSS
DTAVYYCARXGYARYYFDXWGQGTLVTVSS	DTAVYYCARDGYARYXFDXWGQGTLVTVSS
DTAVYYCARDXXARYYFDYWGQGTLVTVSS	DTAVYYCARDGYARYYXXYWGQGTLVTVSS
DTAVYYCARDXYXRYYFDYWGQGTLVTVSS	DTAVYYCARDGYARYYXDXWGQGTLVTVSS
DTAVYYCARDXYAXYYFDYWGQGTLVTVSS	DTAVYYCARDGYARYYFXXWGQGTLVTVSS

Figure 19

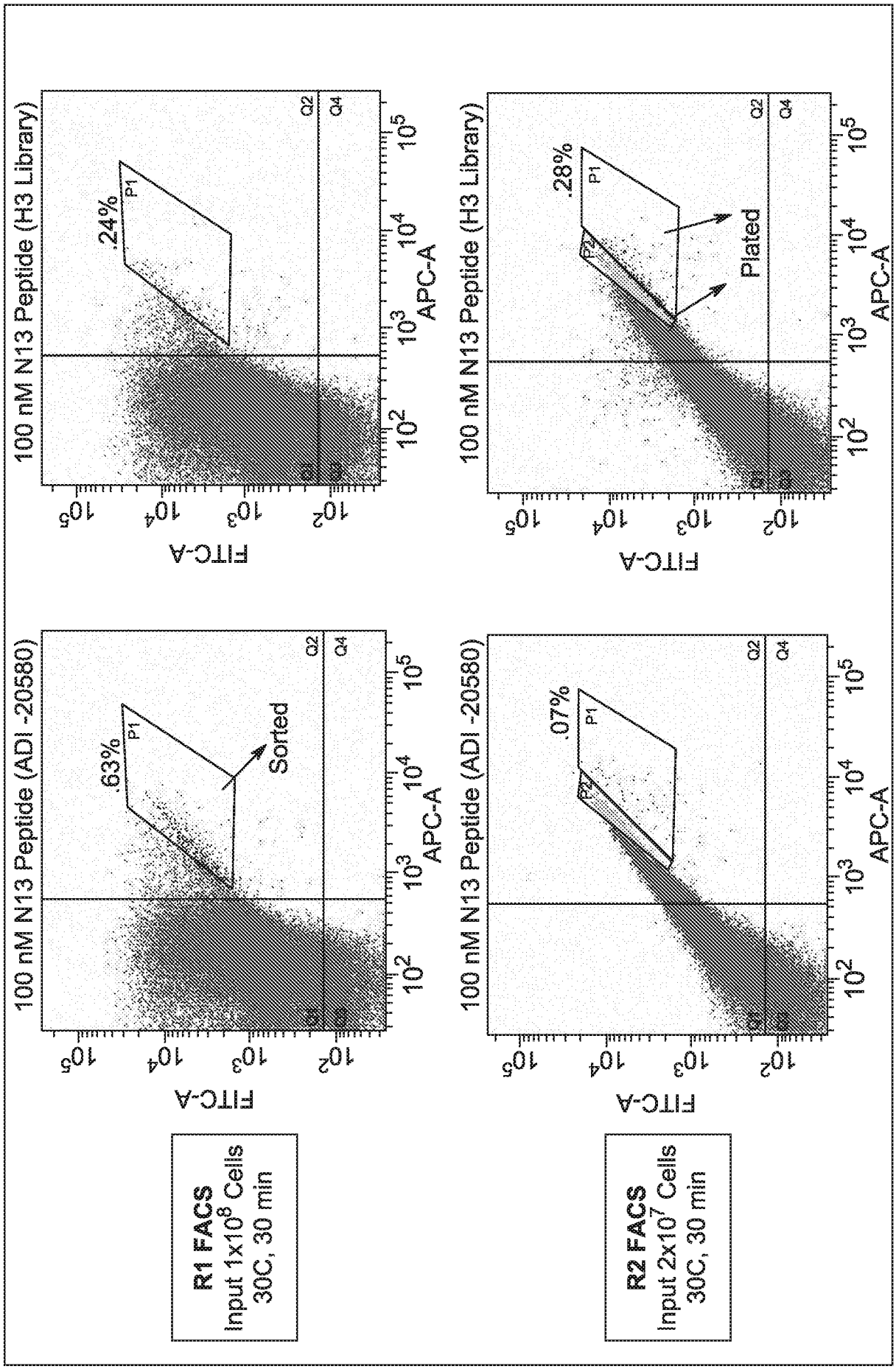

100 nM N13 Peptide (H3 Library)
100 nM N13 Peptide (ADI -20580)
.24%
.28%
.63%
.07%
P1
P2
Q2
Q4
Plated
Sorted
FITC-A
APC-A
R1 FACS
Input 1x10^8 Cells
30C, 30 min
R2 FACS
Input 2x10^7 Cells
30C, 30 min

Figure 20

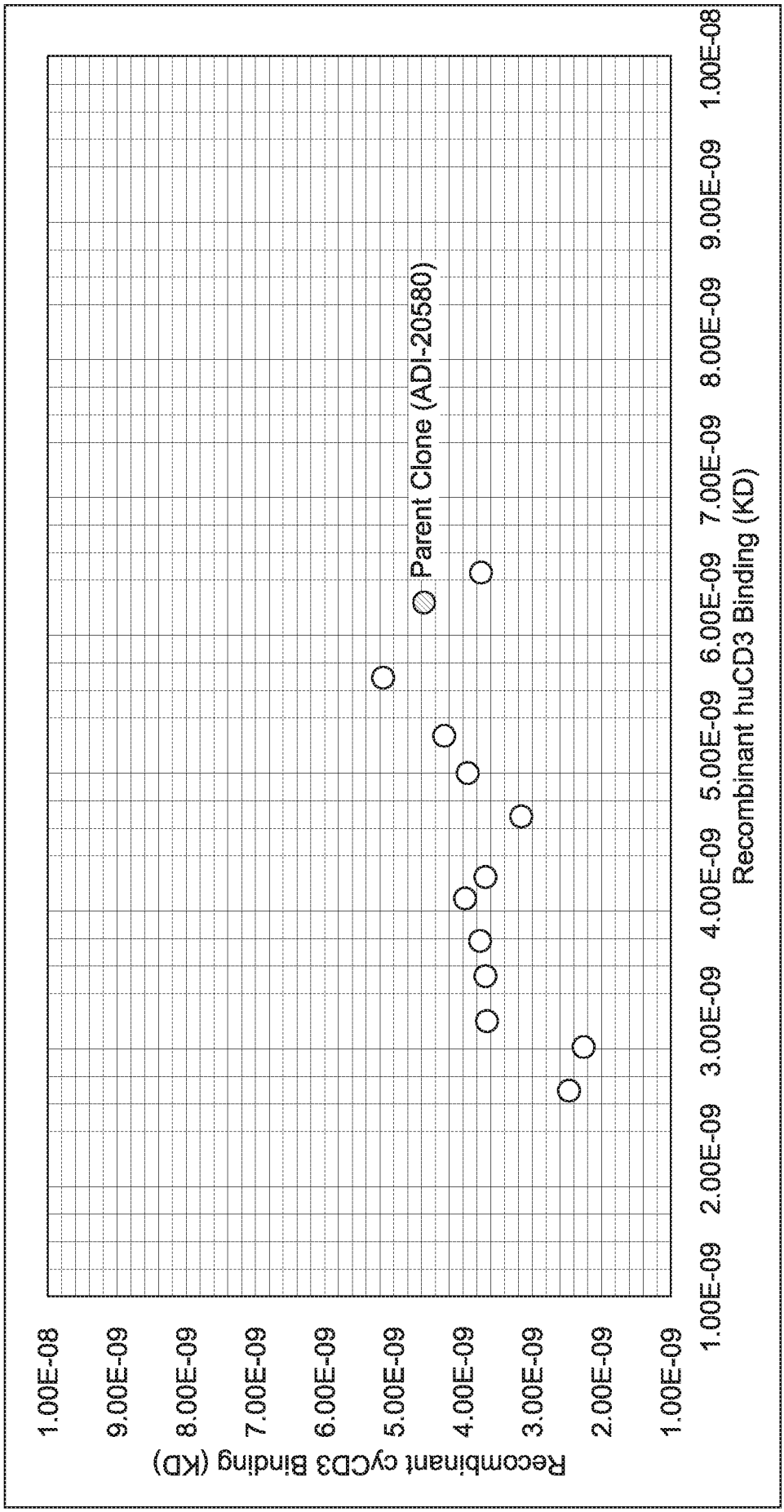

Recombinant cyCD3 Binding (KD)
1.00E-08
9.00E-09
8.00E-09
7.00E-09
6.00E-09
5.00E-09
4.00E-09
3.00E-09
2.00E-09
1.00E-09
Parent Clone (ADI-20580)
1.00E-09
2.00E-09
3.00E-09
4.00E-09
5.00E-09
6.00E-09
7.00E-09
8.00E-09
9.00E-09
1.00E-08
Recombinant huCD3 Binding (KD)

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)	WIDLENANTIYDPKFQG	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

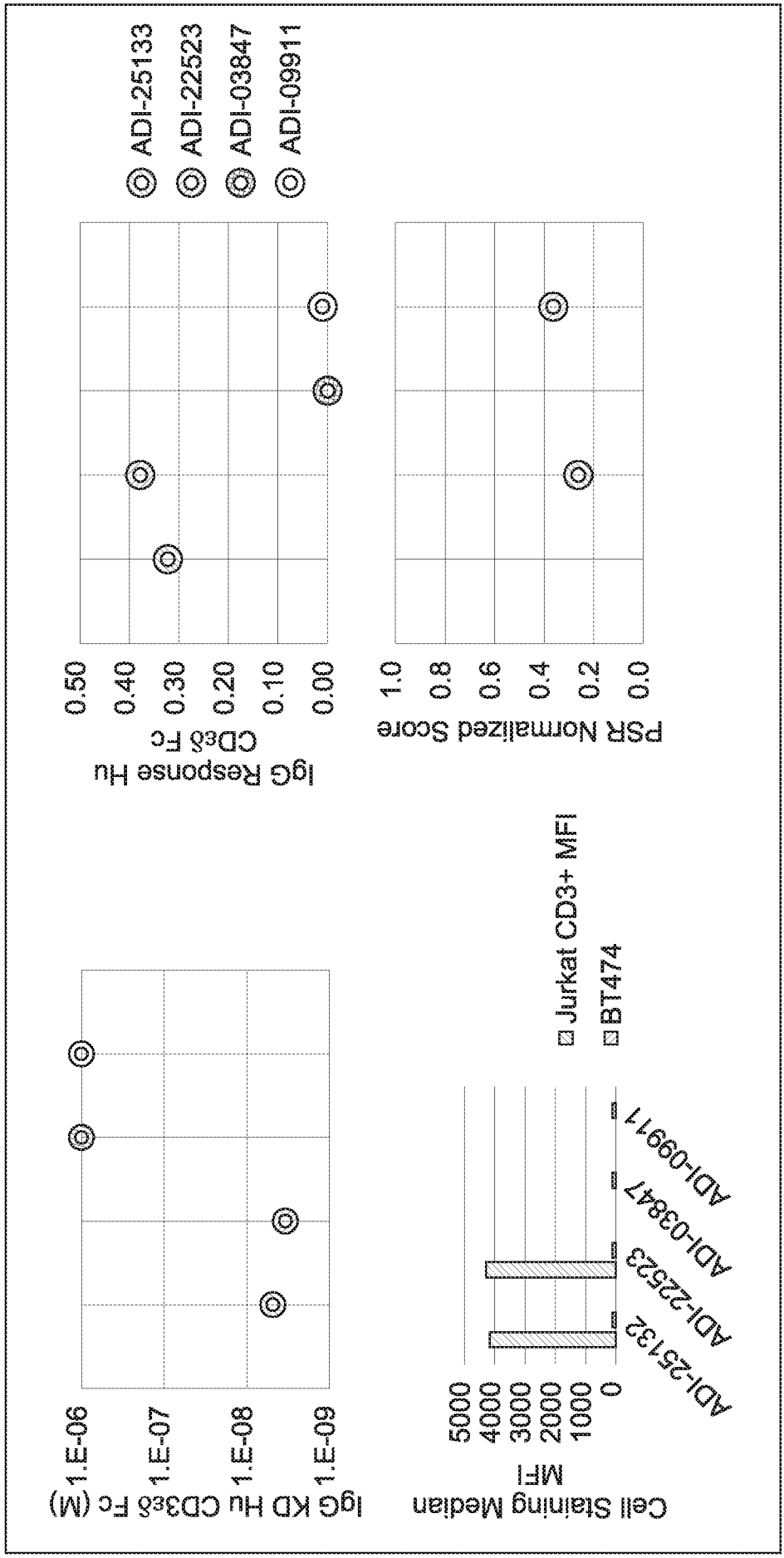

ADI-25133
ADI-22523
ADI-03847
ADI-09911
0.50
0.40
0.30
0.20
0.10
0.00
IgG Response Hu CDεδ Fc
1.0
0.8
0.6
0.4
0.2
0.0
PSR Normalized Score
1.E-06
1.E-07
1.E-08
1.E-09
IgG KD Hu CD3εδ Fc (M)
Jurkat CD3+ MFI
BT474
5000
4000
3000
2000
1000
0
Cell Staining Median MFI
ADI-25132
ADI-22523
ADI-03847
ADI-09911

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
EDTAVYYCARDXXGYGRYFYDVWGQGTLVTVS
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

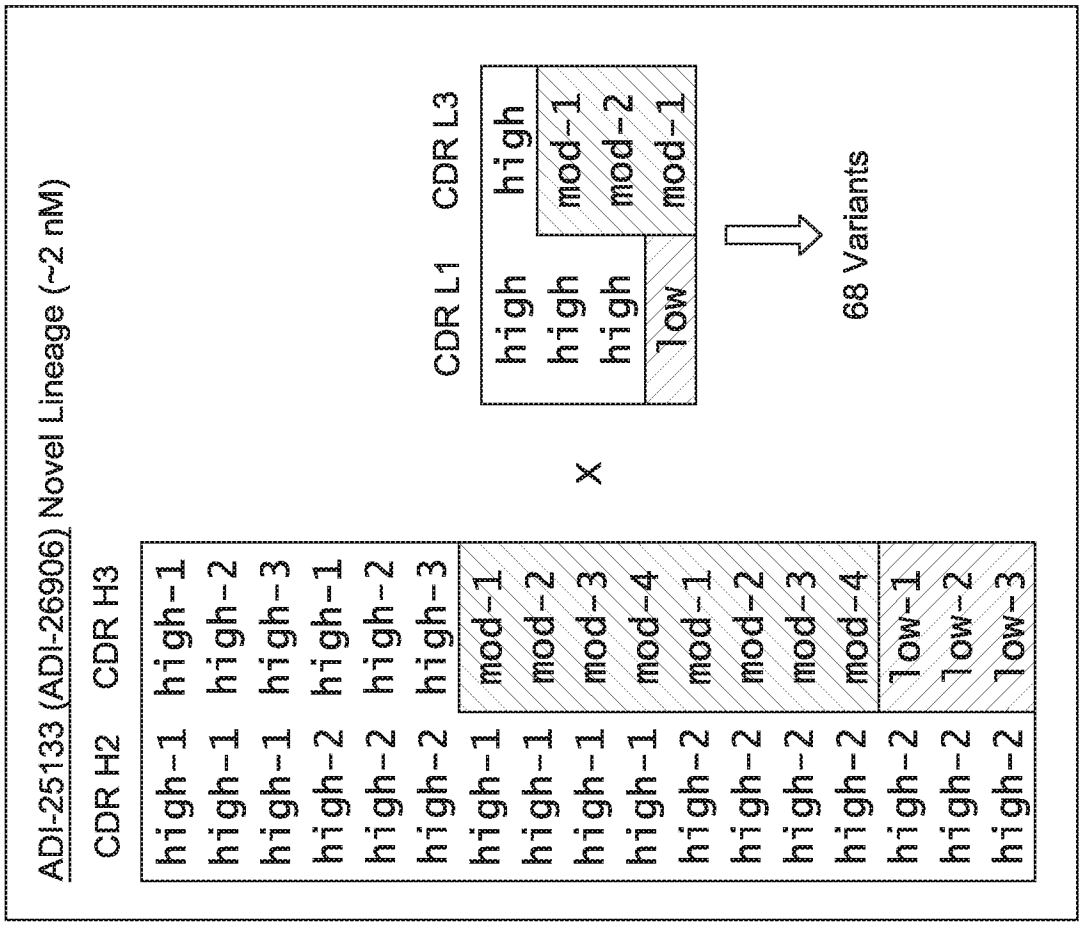

ADI-25133 (ADI-26906) Novel Lineage (~2 nM)
CDR H2
CDR H3
high-1 high-1
high-1 high-2
high-1 high-3
high-2 high-1
high-2 high-2
high-2 high-3
high-1 mod-1
high-1 mod-2
high-1 mod-3
high-1 mod-4
high-2 mod-1
high-2 mod-2
high-2 mod-3
high-2 mod-4
high-2 low-1
high-2 low-2
high-2 low-3
X
CDR L1
CDR L3
high high
high mod-1
high mod-2
low mod-1
68 Variants

Figure 25A

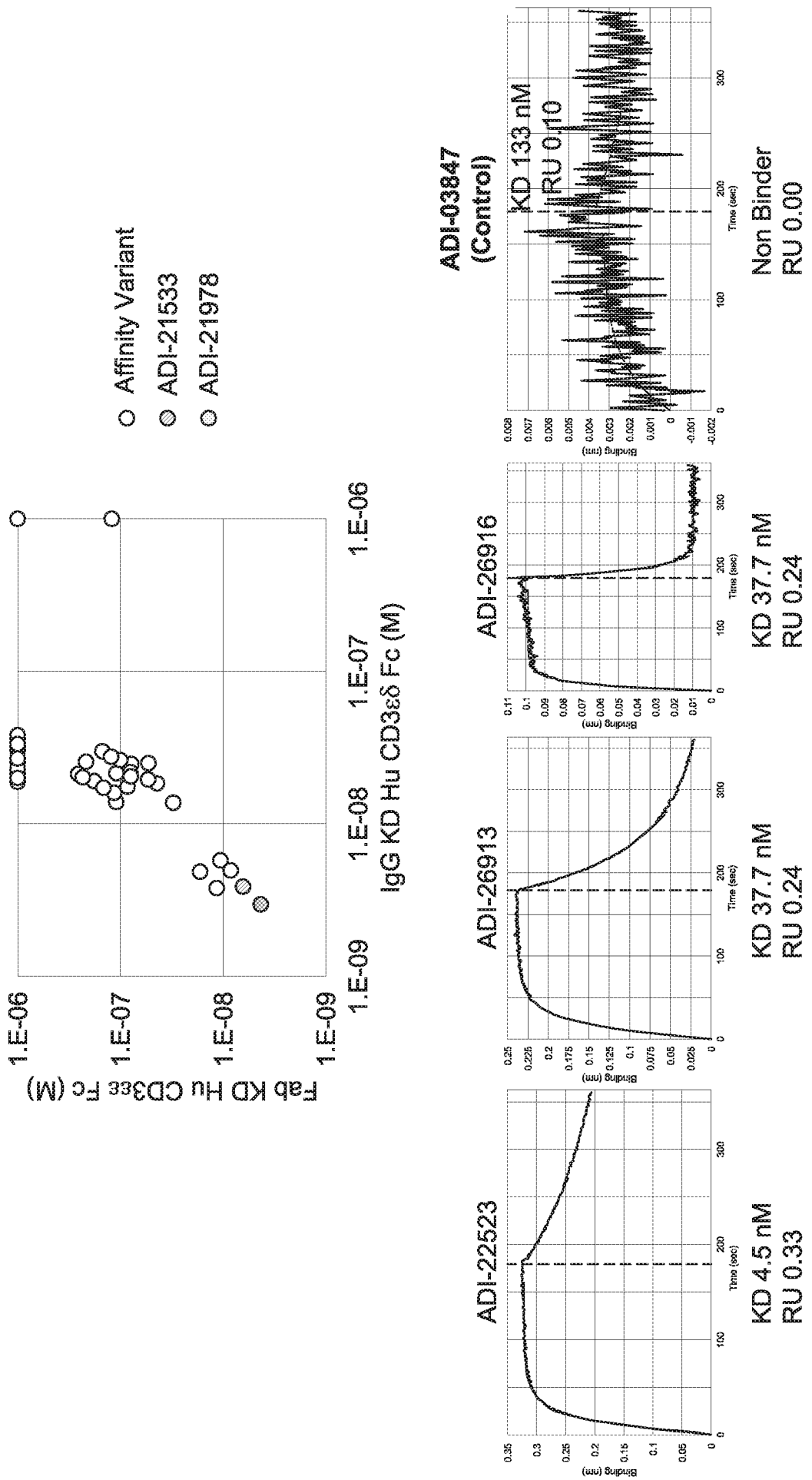

Affinity Variant
ADI-21533
ADI-21978
Fab KD Hu CD3εε Fc (M)
IgG KD Hu CD3εδ Fc (M)
1.E-06
1.E-07
1.E-08
1.E-09
ADI-22523
KD 4.5 nM
RU 0.33
ADI-26913
KD 37.7 nM
RU 0.24
ADI-26916
KD 37.7 nM
RU 0.24
ADI-03847
(Control)
KD 133 nM
RU 0.10
Non Binder
RU 0.00
Binding (nm)
Time (sec)

Figure 25B

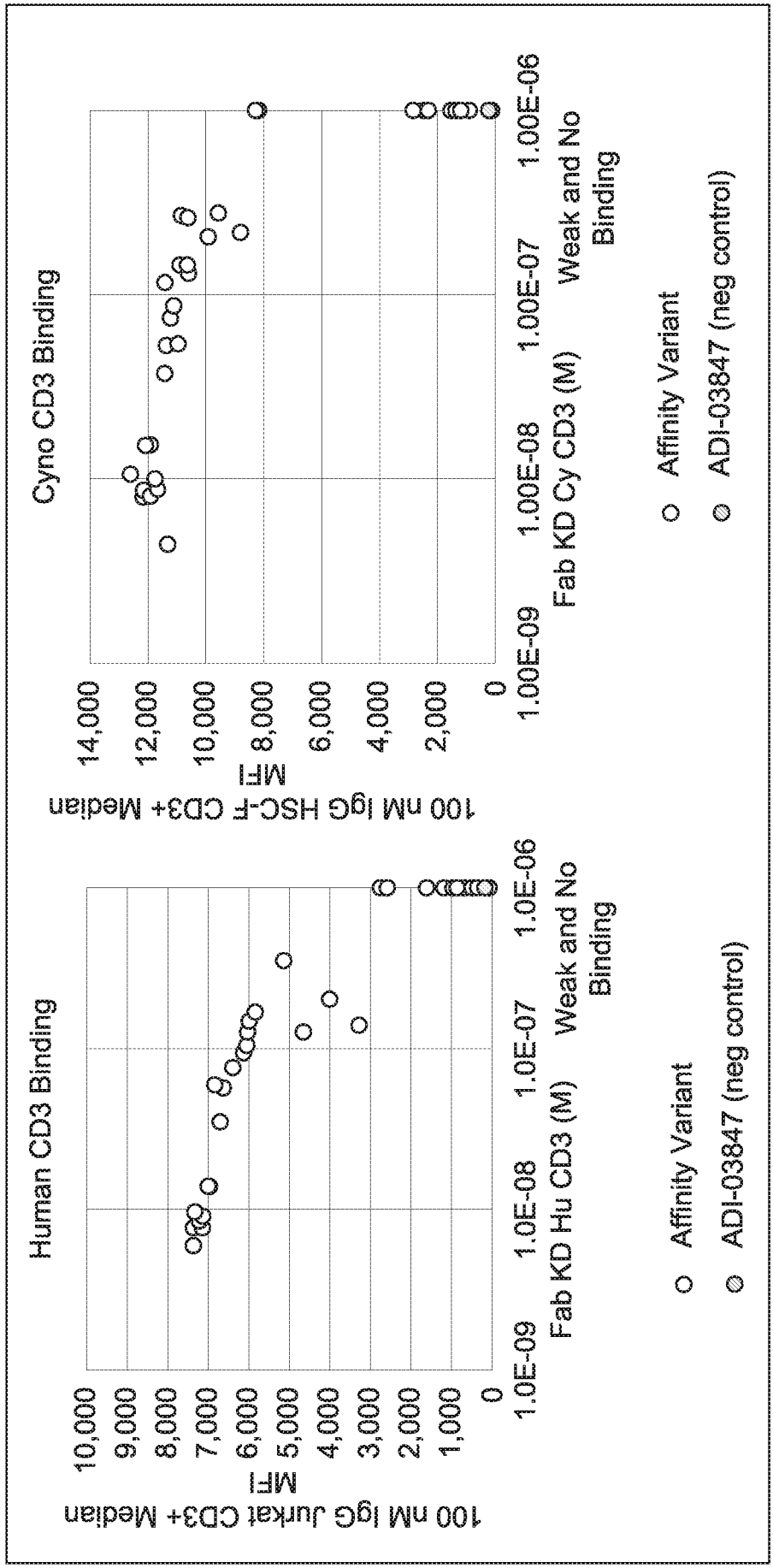

Human CD3 Binding
100 nM IgG Jurkat CD3+ Median MFI
10,000
9,000
8,000
7,000
6,000
5,000
4,000
3,000
2,000
1,000
0
1.0E-09
1.0E-08
1.0E-07
1.0E-06
Fab KD Hu CD3 (M)
Weak and No Binding
Affinity Variant
ADI-03847 (neg control)
Cyno CD3 Binding
100 nM IgG HSC-F CD3+ Median MFI
14,000
12,000
10,000
8,000
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

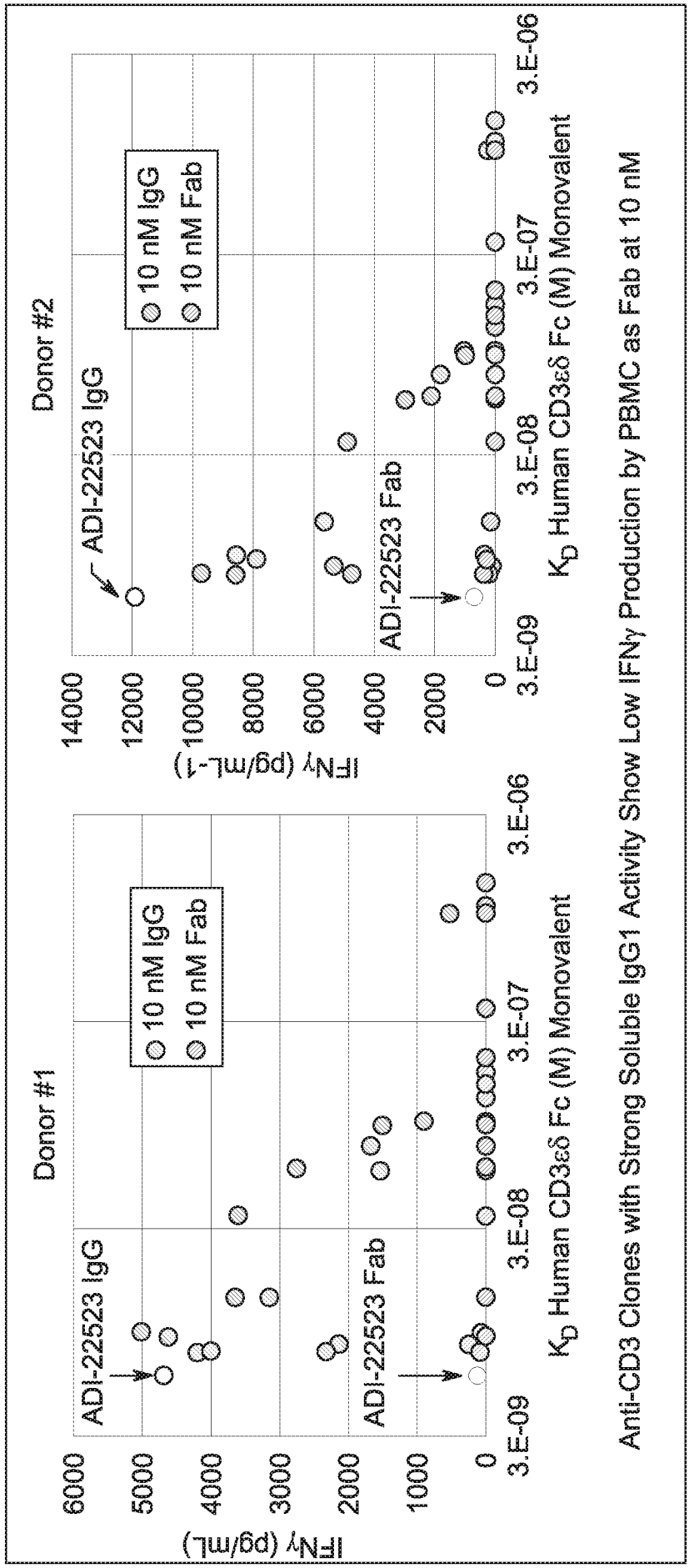
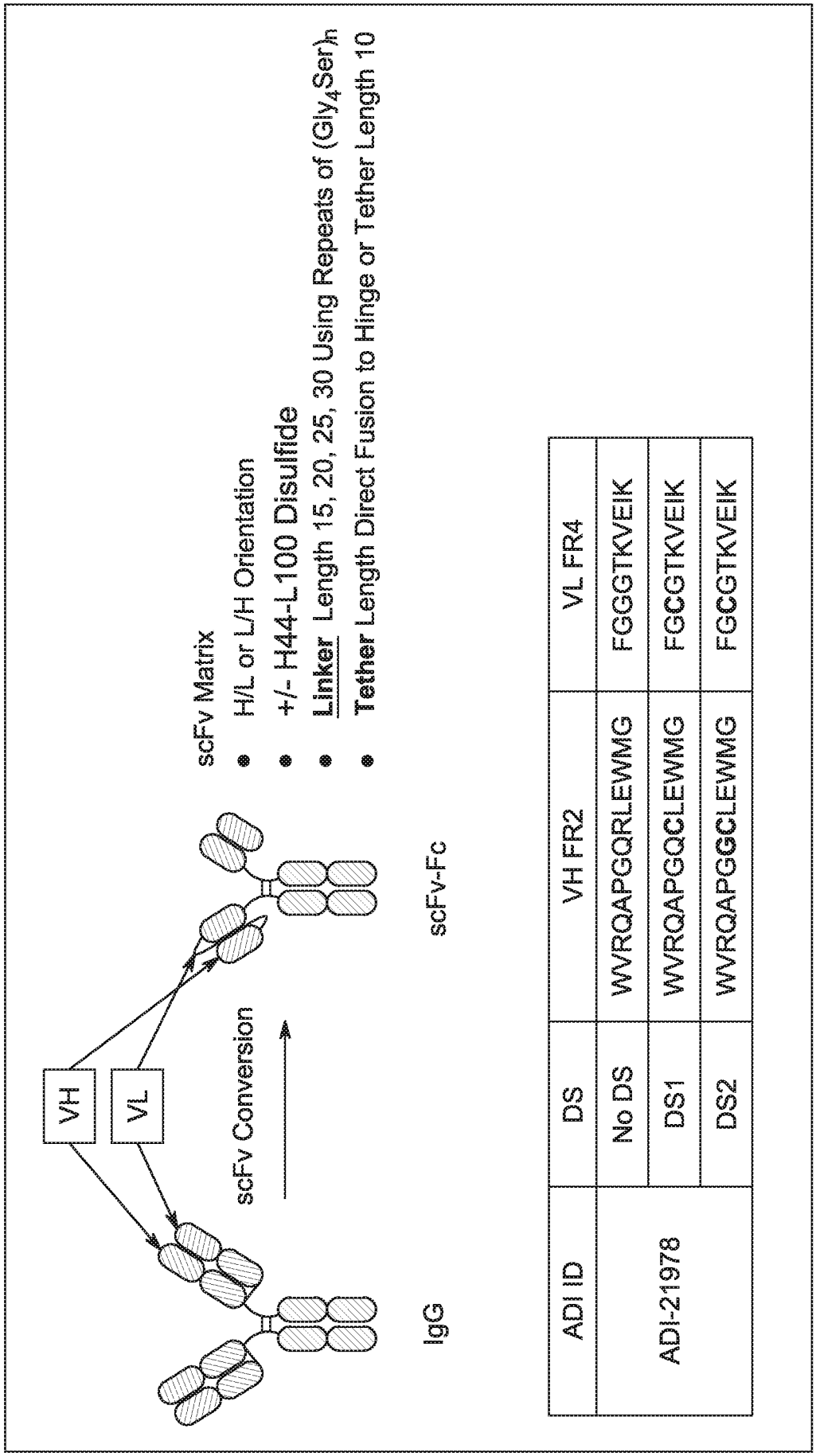

Anti-CD3 Clones with Strong Soluble IgG1 Activity Show Low IFNγ Production by PBMC as Fab at 10 nM
Donor #1
Donor #2
IFNγ (pg/mL)
ADI-22523 IgG
ADI-22523 Fab
10 nM IgG
10 nM Fab
3.E-09
3.E-08
3.E-07
3.E-06
KD Human CD3εδ Fc (M) Monovalent

Figure 25D



ADI ID	DS	VH FR2	VL FR4
ADI-21978	No DS	WVRQAPGQRLEWMG	FGGGTKVEIK
	DS1	WVRQAPGQCLEWMG	FGCGTKVEIK
	DS2	WVRQAPGGCLEWMG	FGCGTKVEIK

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

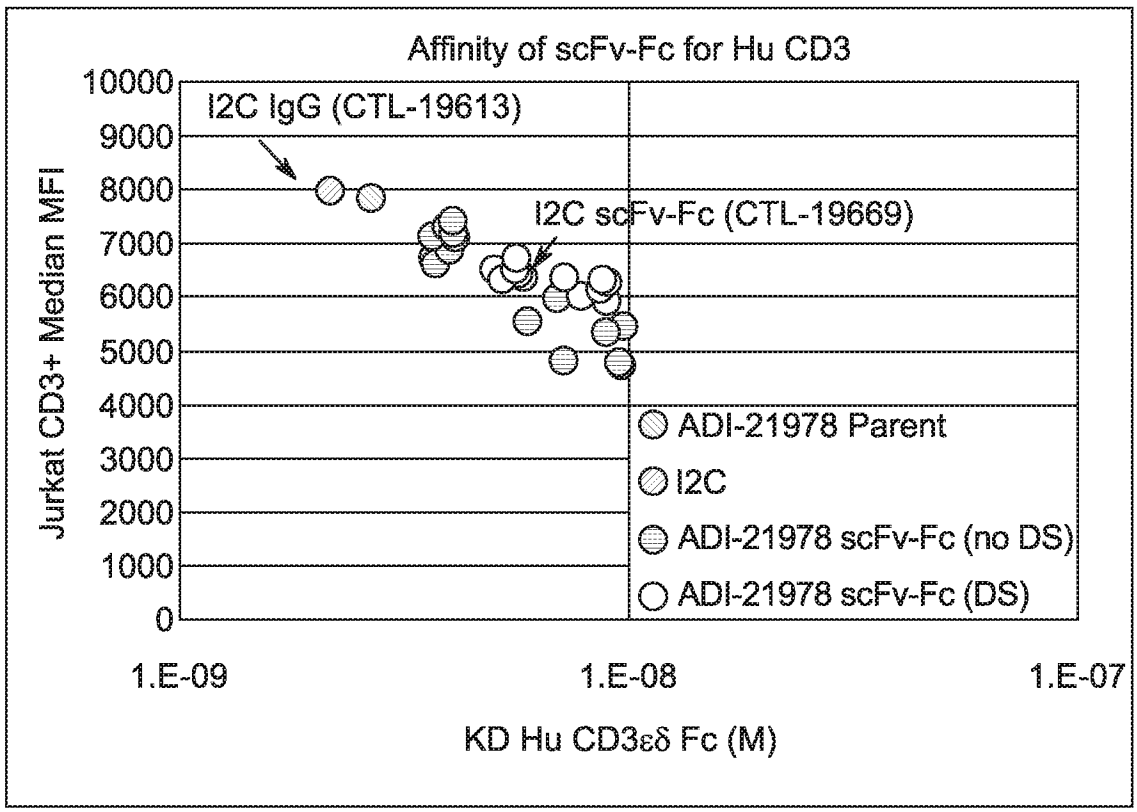


Figure 26C

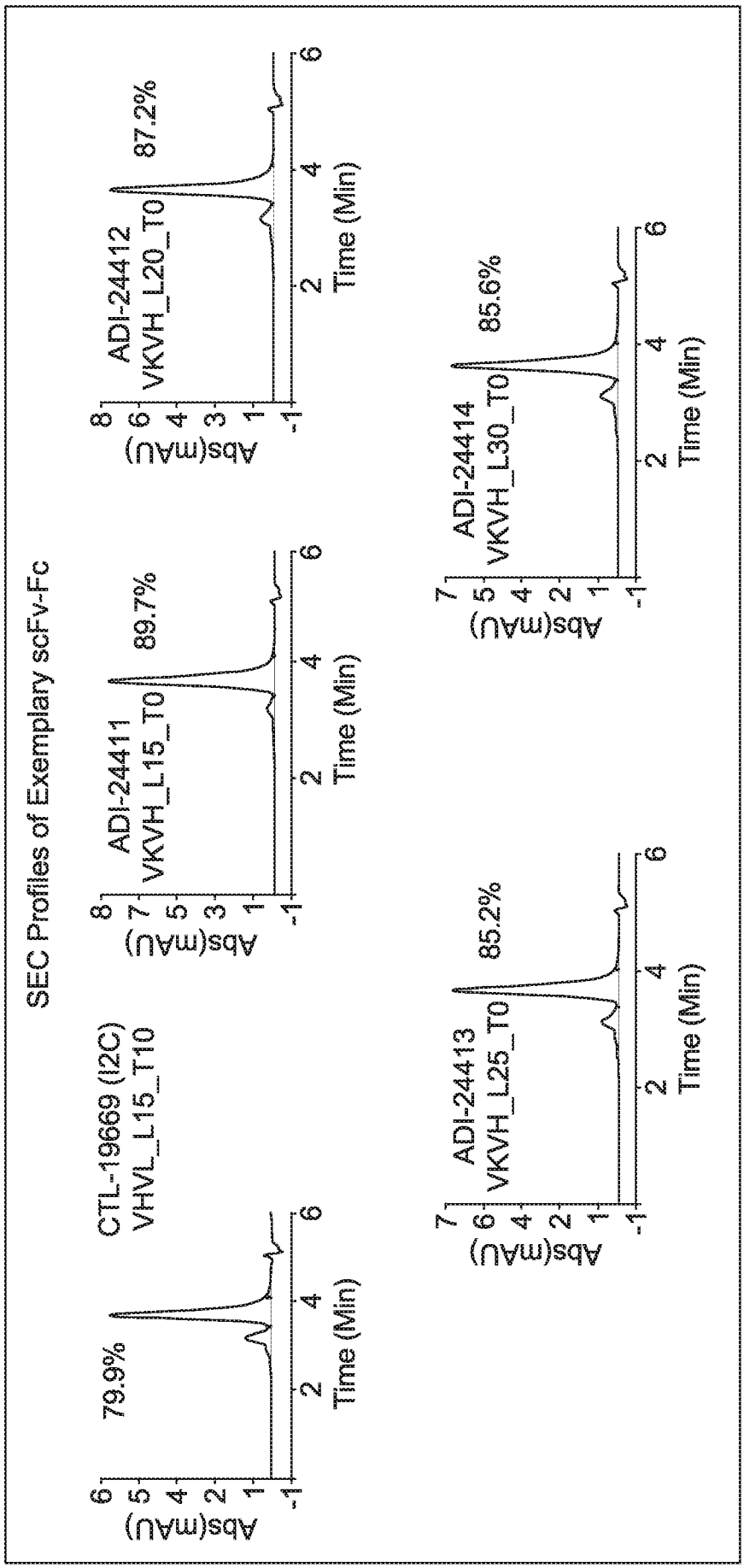

SEC Profiles of Exemplary scFv-Fc
CTL-19669 (I2C)
VHVL_L15_T10
79.9%
ADI-24411
VKVH_L15_T0
89.7%
ADI-24412
VKVH_L20_T0
87.2%
ADI-24413
VKVH_L25_T0
85.2%
ADI-24414
VKVH_L30_T0
85.6%
Abs(mAU)
Time (Min)

Figure 26D

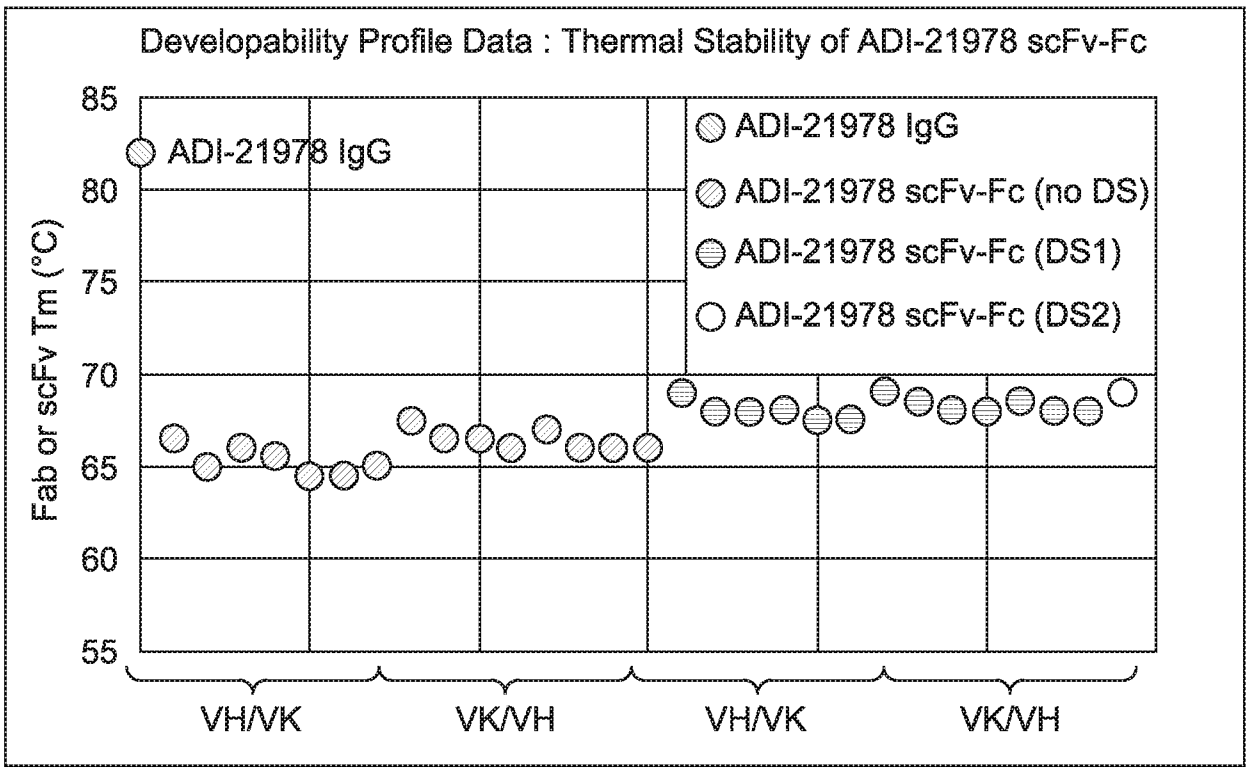


Figure 26E

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

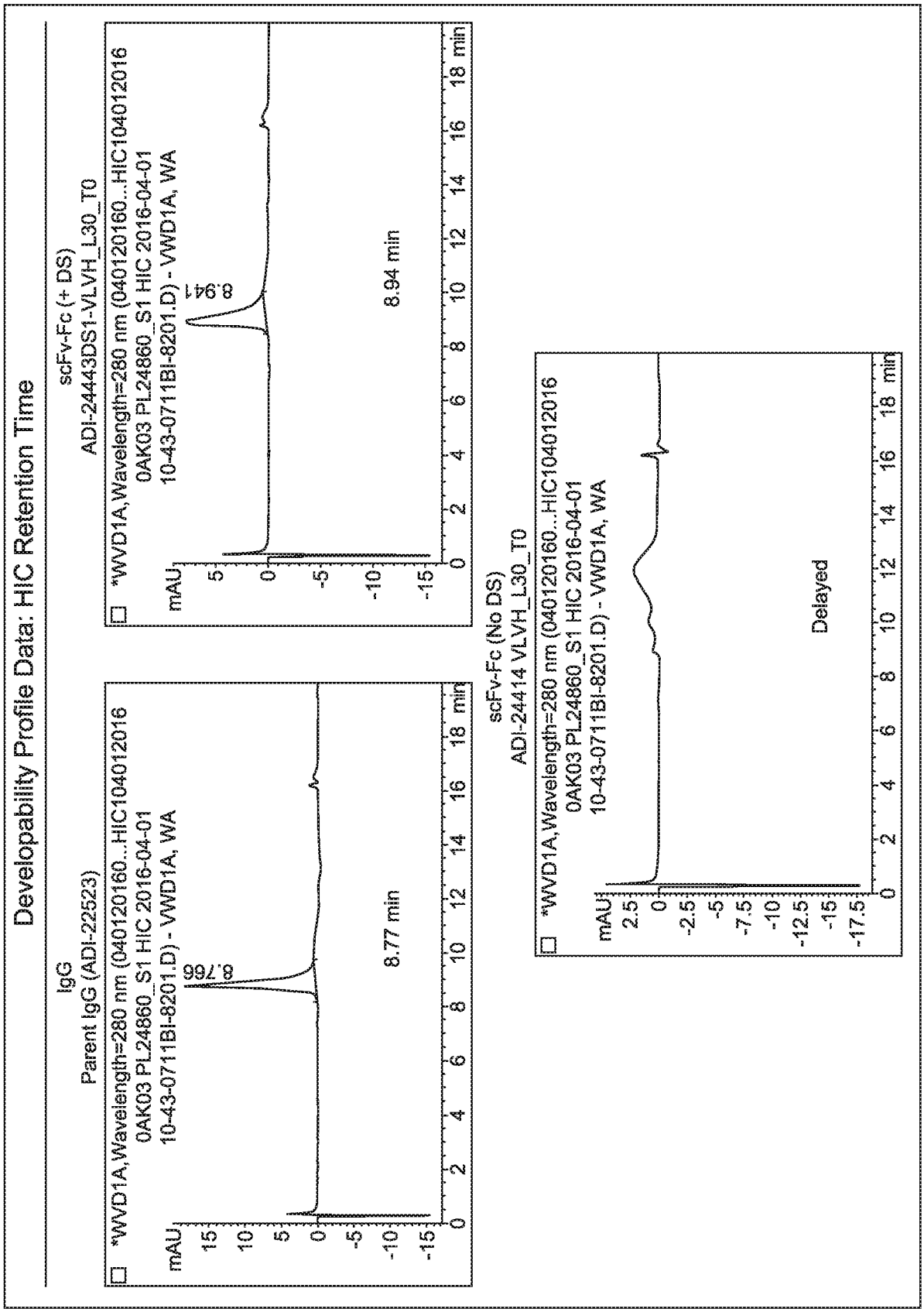

Developability Profile Data: HIC Retention Time
IgG
Parent IgG (ADI-22523)
*WVD1A,Wavelength=280 nm (040120160...HIC104012016
0AK03 PL24860_S1 HIC 2016-04-01
10-43-0711BI-8201.D) - VWD1A, WA
mAU
8.766
8.77 min
min
scFv-Fc (+ DS)
ADI-24443DS1-VLVH_L30_T0
*WVD1A,Wavelength=280 nm (040120160...HIC104012016
0AK03 PL24860_S1 HIC 2016-04-01
10-43-0711BI-8201.D) - VWD1A, WA
mAU
8.941
8.94 min
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
Delayed
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)

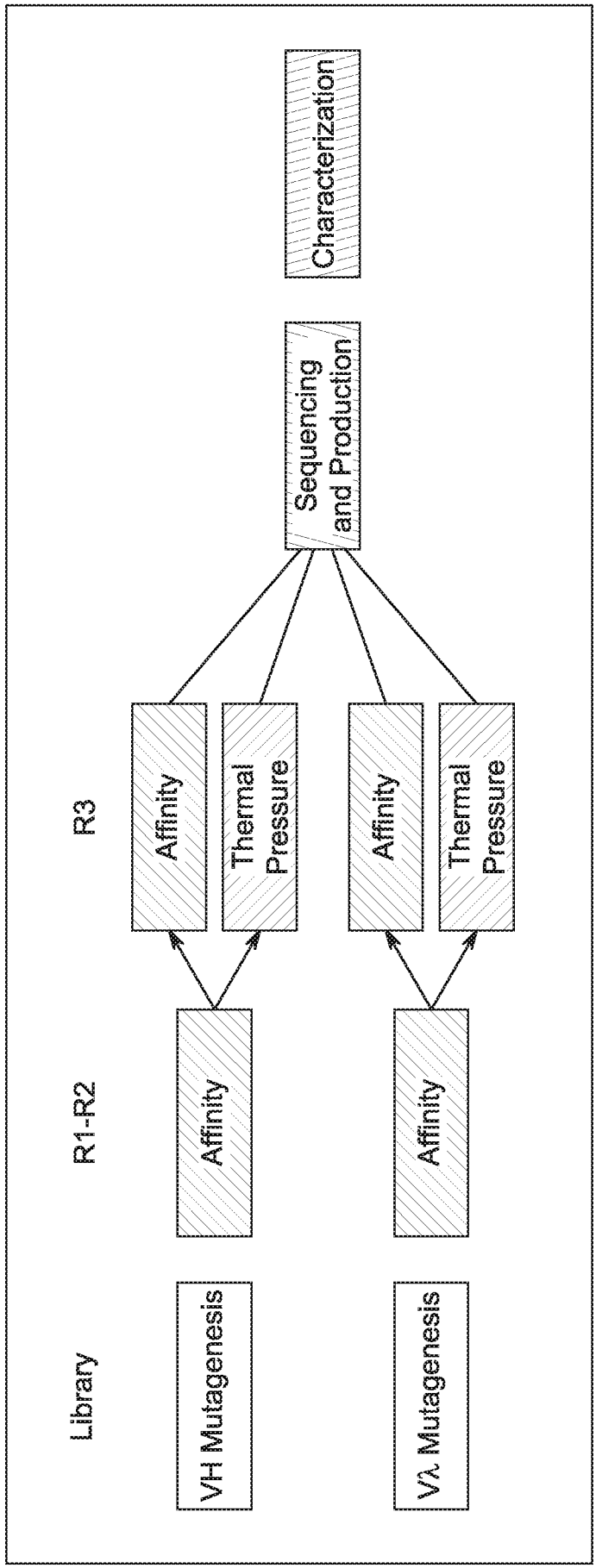

Library
R1-R2
R3
VH Mutagenesis
Vλ Mutagenesis
Affinity
Affinity
Affinity
Thermal Pressure
Thermal Pressure
Sequencing and Production
Characterization

Figure 28A

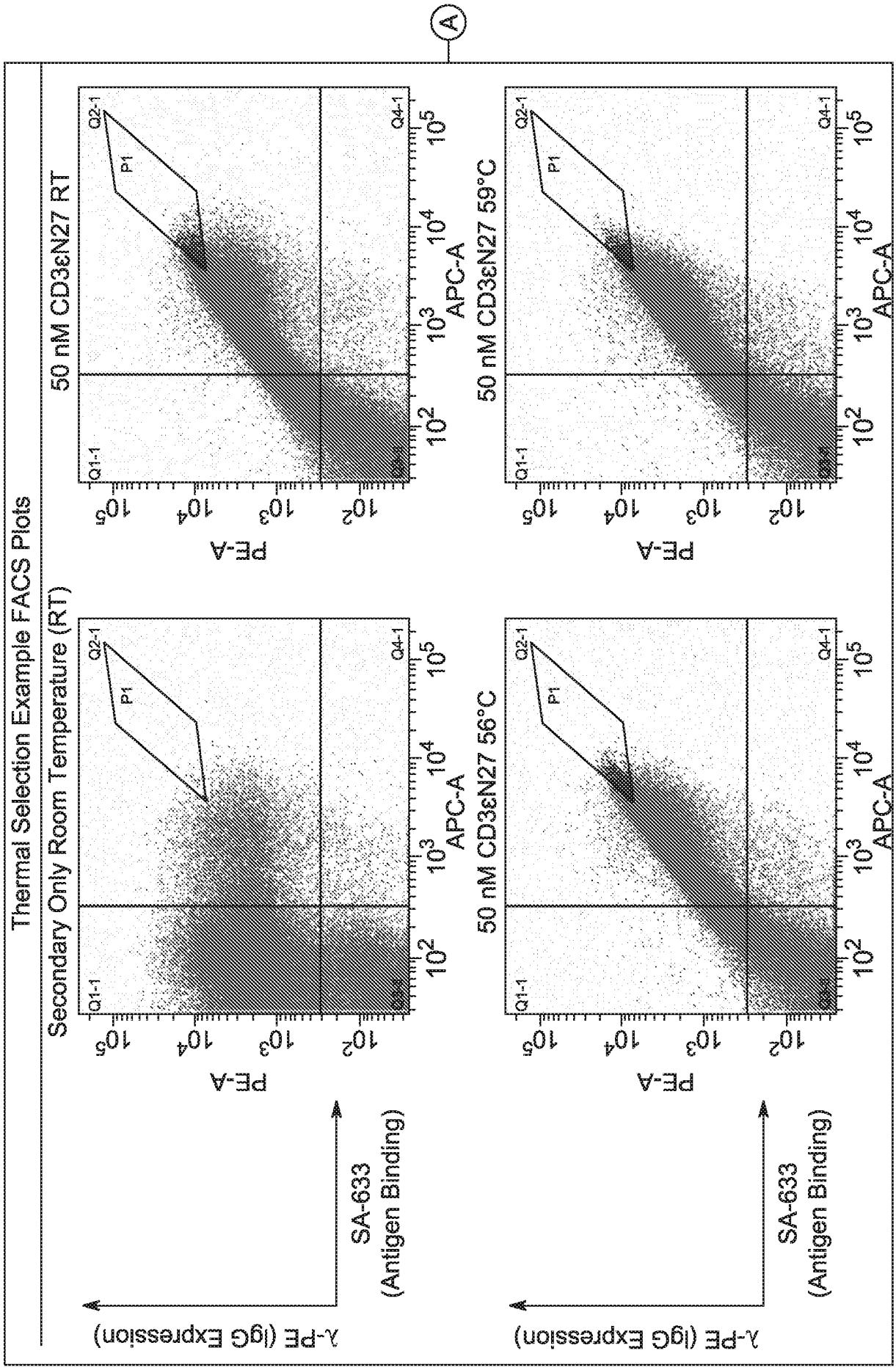

Thermal Selection Example FACS Plots
Secondary Only Room Temperature (RT)
50 nM CD3εN27 RT
50 nM CD3εN27 59°C
50 nM CD3εN27 56°C
λ-PE (IgG Expression)
SA-633 (Antigen Binding)
PE-A
APC-A
P1
Q1-1
Q2-1
Q3-1
Q4-1
A

Figure 28B

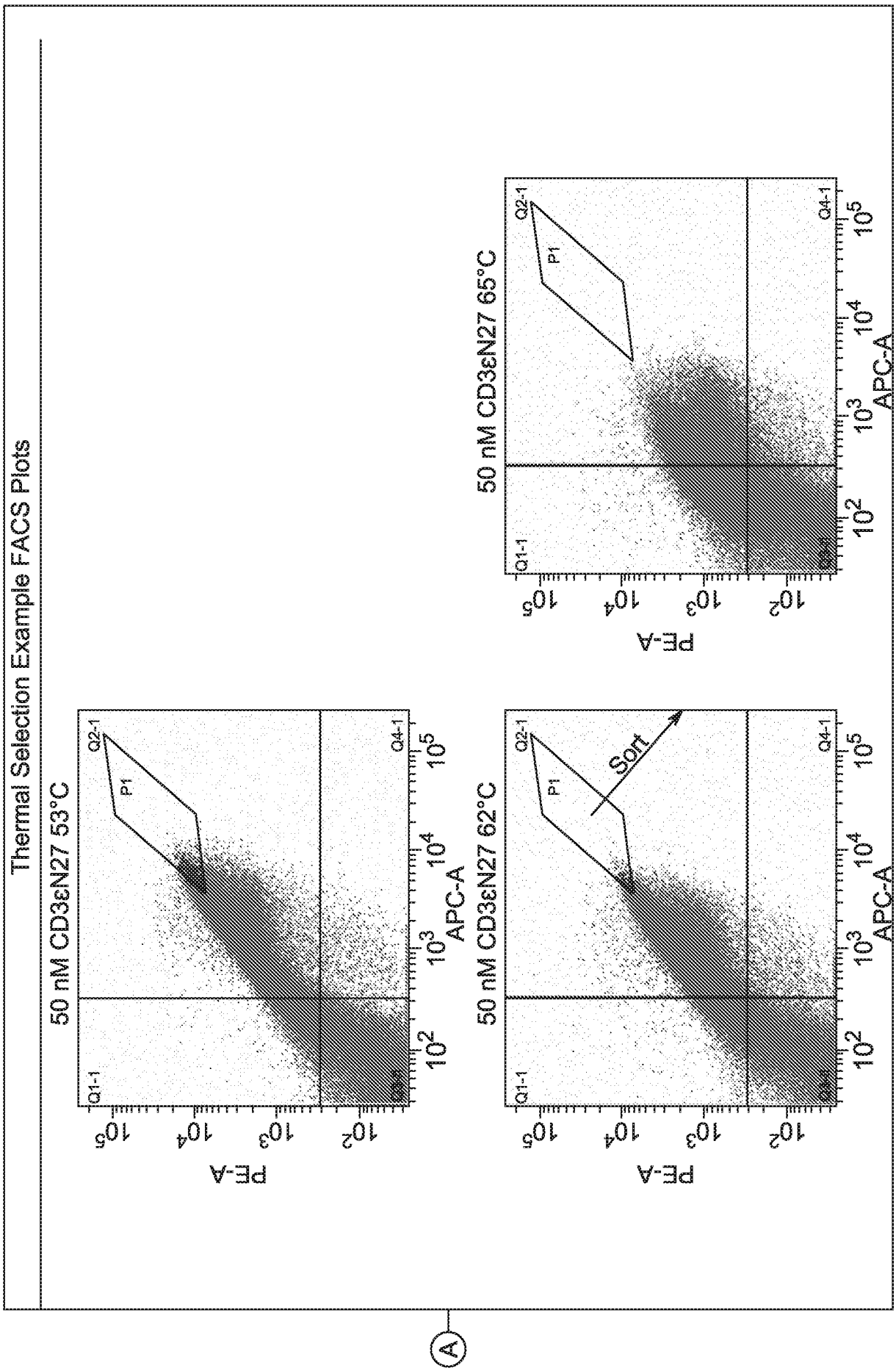


Figure 28B (Continued)

VA Mutagenesis Affinity-pressured Output Sequencing

Parent	VAmut	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	VRHGNFGNSHVSWFAH	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	RIRSKYNMDYATYYADSVKD	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)

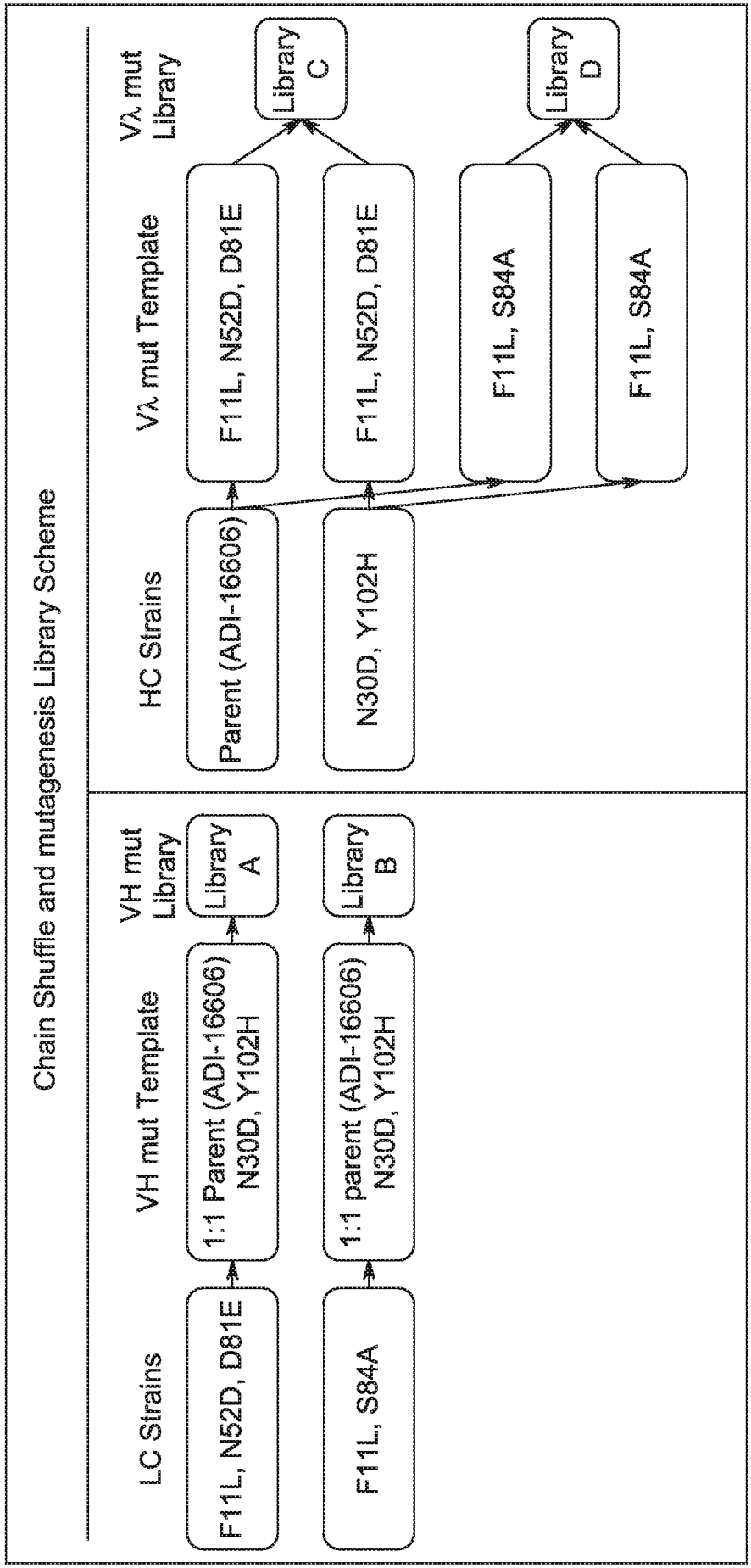

Chain Shuffle and mutagenesis Library Scheme
LC Strains
VH mut Template
VH mut Library
HC Strains
Vλ mut Template
Vλ mut Library
F11L, N52D, D81E
1:1 Parent (ADI-16606) N30D, Y102H
Library A
F11L, S84A
1:1 parent (ADI-16606) N30D, Y102H
Library B
Parent (ADI-16606)
F11L, N52D, D81E
Library C
N30D, Y102H
F11L, N52D, D81E
F11L, S84A
Library D
F11L, S84A

Figure 29A

Parents for Cycle 2 Optimization -Binding and Developability Profile Data

Name	VH mut	VA 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

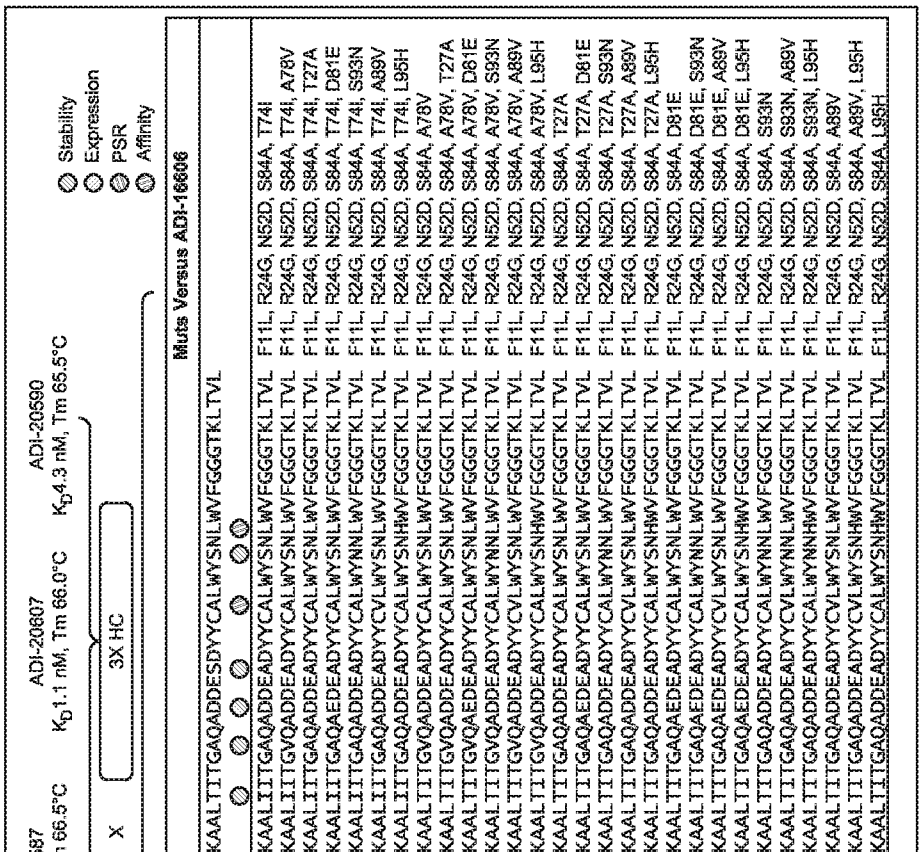

ADI-20587
KD4.1 nM, Tm 66.5°C
ADI-20607
KD1.1 nM, Tm 66.0°C
ADI-20590
KD4.3 nM, Tm 65.5°C
28X VL Rational Combinations
X
3X HC
Stability
Expression
PSR
Affinity
Variant
VL Chain
Muts Versus ADI-16606
ADI-16606 QTVVTQEPSFSVSPGGTVTLTCRSSTGAVTTSNYANWVQQTPGQAPRGLIGGTNKRAPGVPDRFSGSLLGDKAALTITGAQADDESDYYCALWYSNLWVFGGGTKLTVL
LC1 QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGAQADEADYYCALWYSNLWVFGGGTKLTVL F11L, R24G, N52D, S84A, T74I
LC2 QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGVQADDEADYYCALWYSNLWVFGGGTKLTVL F11L, R24G, N52D, S84A, T74I, A78V
LC3 QTVVTQEPSLSVSPGGTVTLTCGSSAGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALIITGAQADEADYYCALWYSNLWVFGGGTKLTVL 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 QTVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQTPGQAPRGLIGGTDKRAPGVPDRFSGSLLGDKAALTITGAQAEDEADYYCALWYNNLWVFGGGTKLTVL 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
DTAVYYCVRHGNFGNXYVSWFAHWGQGTLV
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

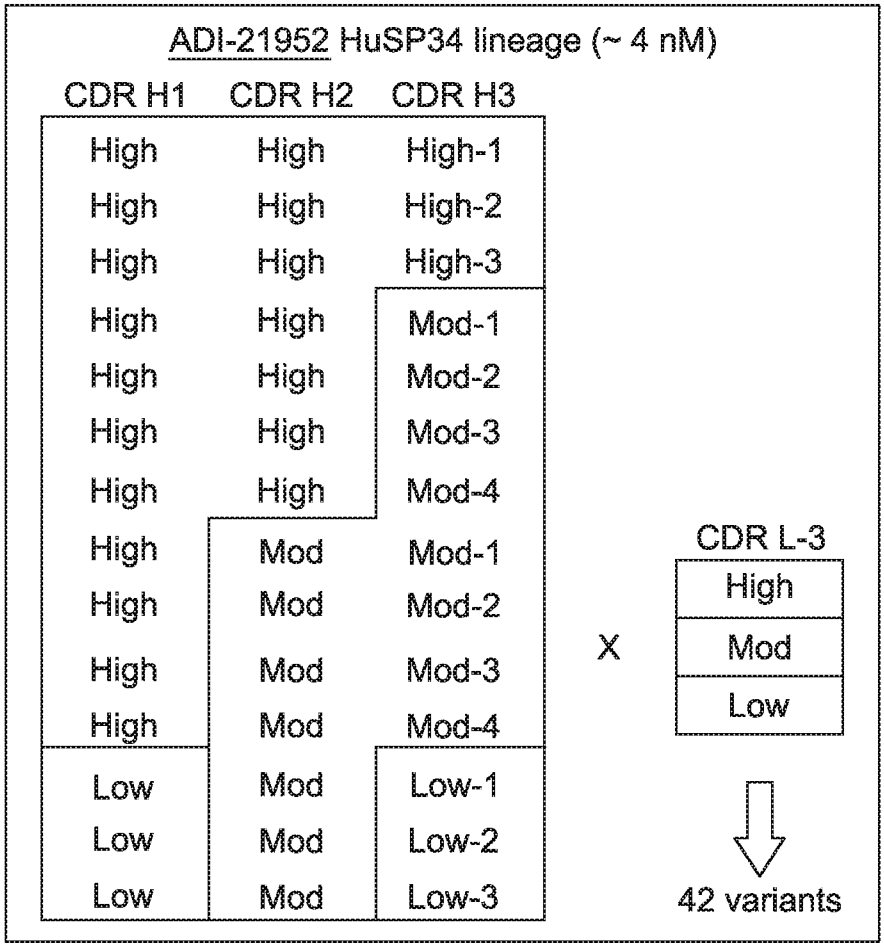


Figure 33A

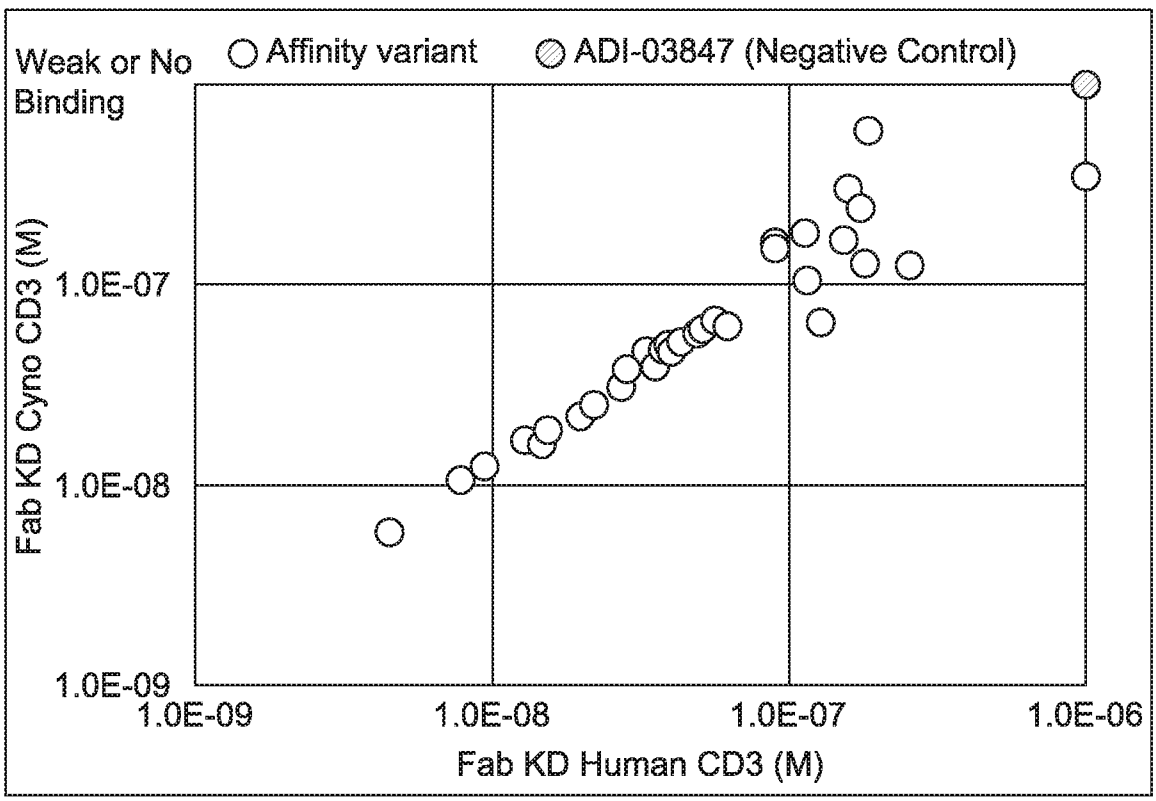


Figure 33B

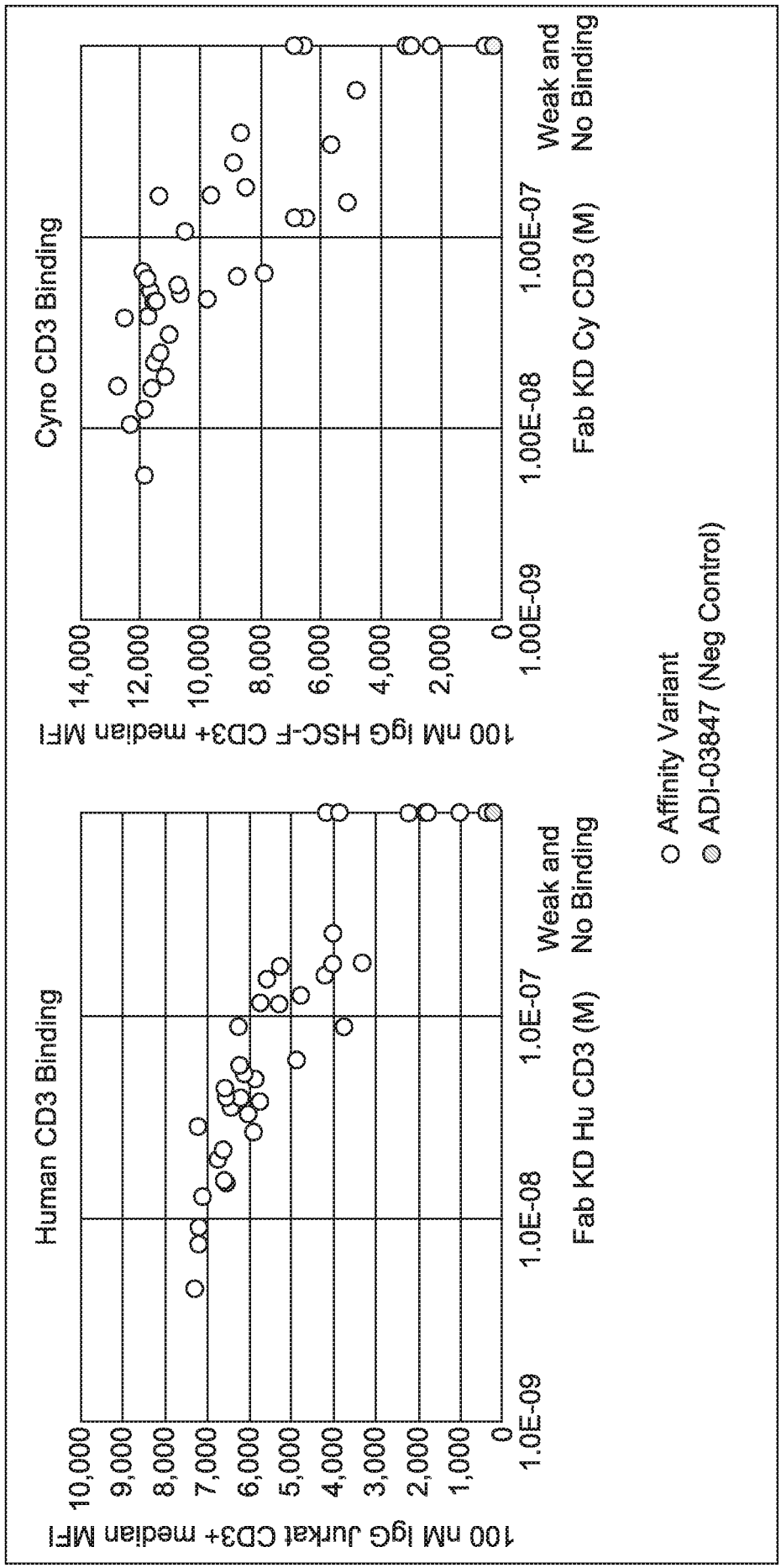

Human CD3 Binding
100 nM IgG Jurkat CD3+ median MFI
10,000
9,000
8,000
7,000
6,000
5,000
4,000
3,000
2,000
1,000
0
1.0E-09
1.0E-08
1.0E-07
Fab KD Hu CD3 (M)
Weak and No Binding
Cyno CD3 Binding
100 nM IgG HSC-F CD3+ median MFI
14,000
12,000
10,000
8,000
6,000
4,000
2,000
0
1.00E-09
1.00E-08
1.00E-07
Fab KD Cy CD3 (M)
Weak and No Binding
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

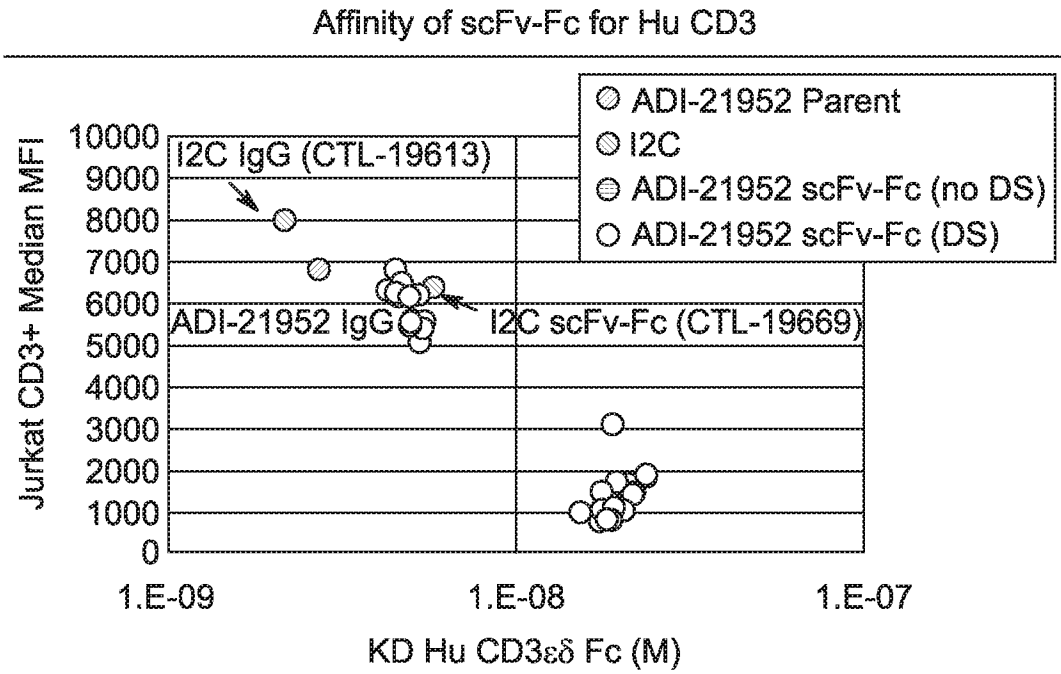


Figure 34A

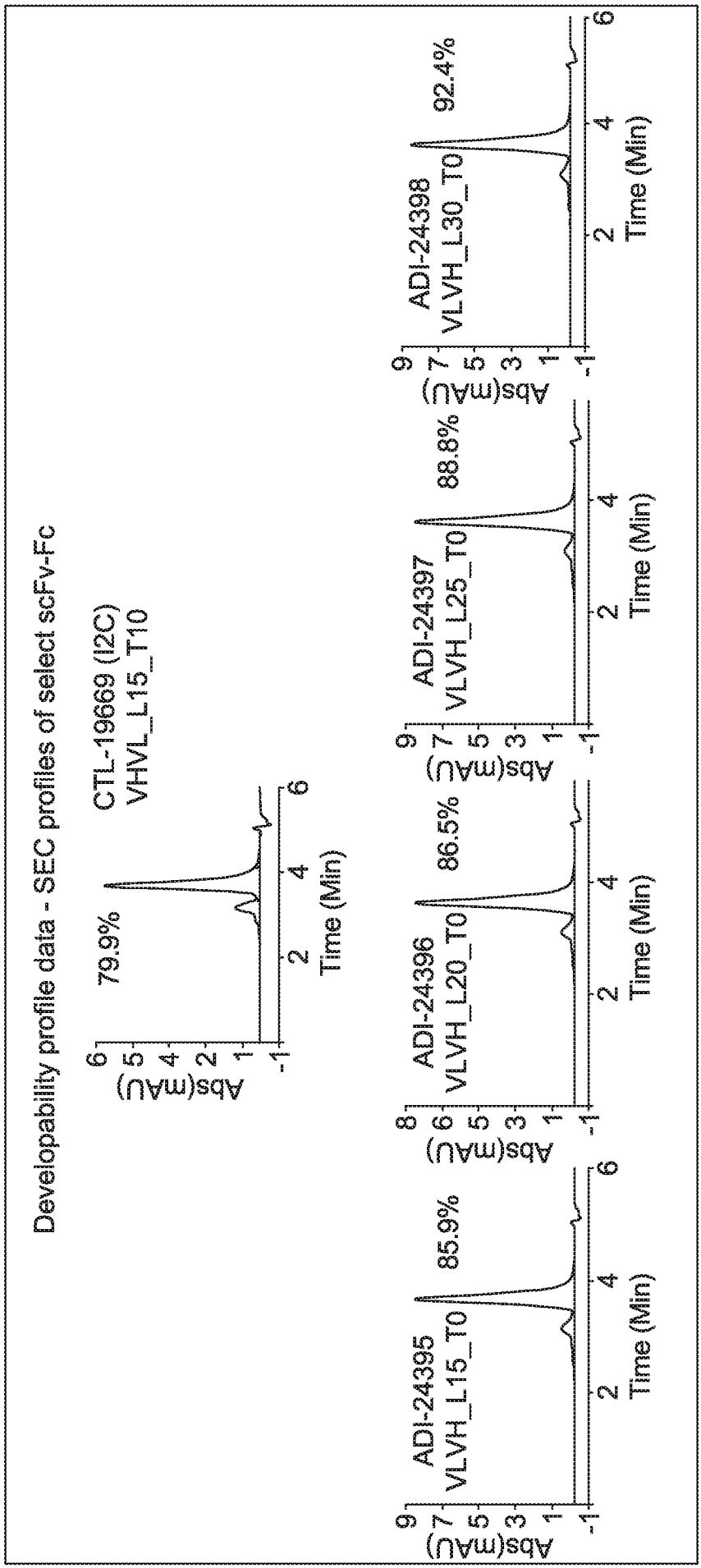

Developability profile data - SEC profiles of select scFv-Fc
CTL-19669 (I2C)
VHVL_L15_T10
79.9%
Abs(mAU)
Time (Min)
ADI-24395
VLVH_L15_T0
85.9%
ADI-24396
VLVH_L20_T0
86.5%
ADI-24397
VLVH_L25_T0
88.8%
ADI-24398
VLVH_L30_T0
92.4%

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

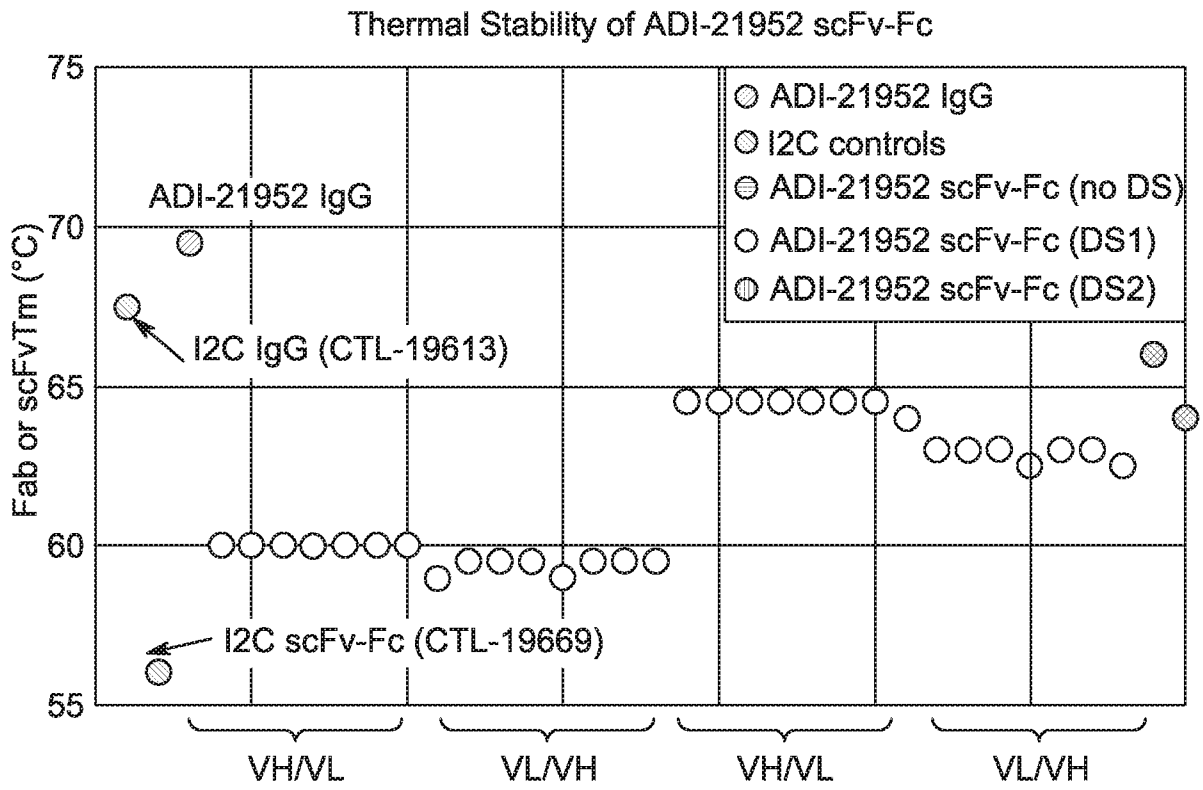


Figure 34C

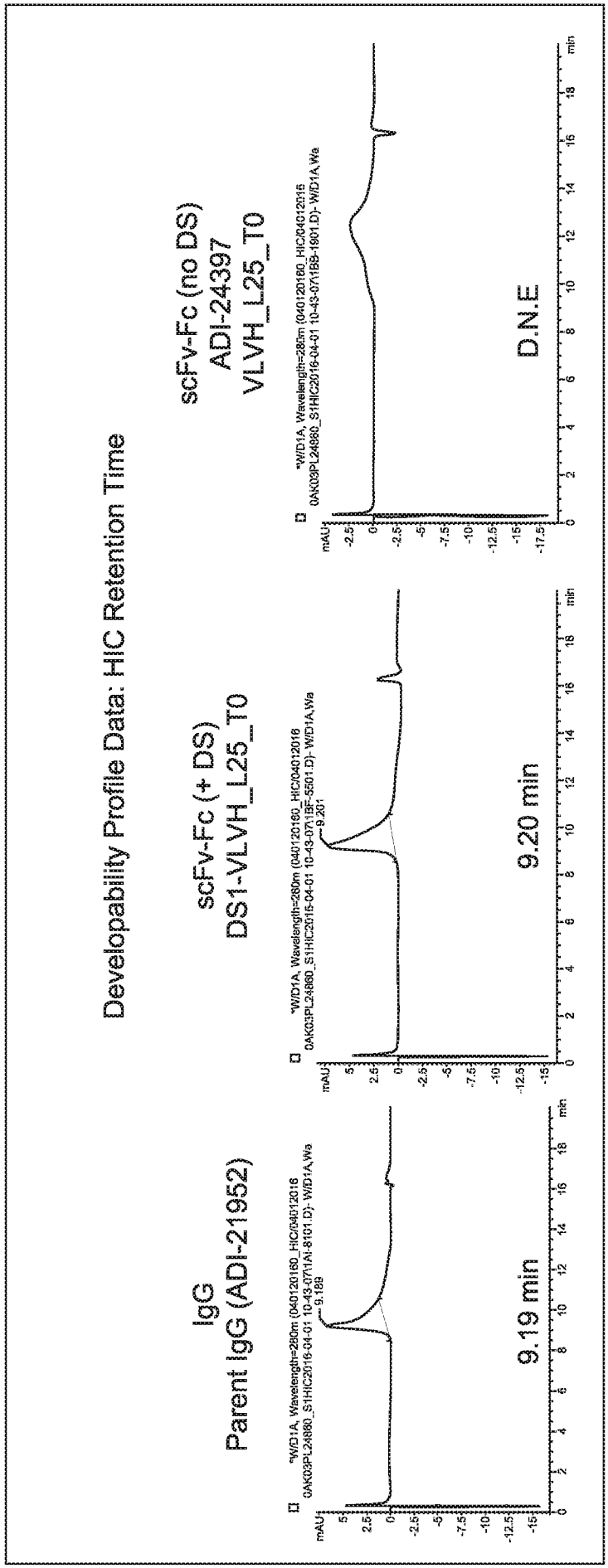

Developability Profile Data: HIC Retention Time
IgG
Parent IgG (ADI-21952)
9.19 min
scFv-Fc (+ DS)
DS1-VLVH_L25_T0
9.20 min
scFv-Fc (no DS)
ADI-24397
VLVH_L25_T0
D.N.E

Figure 34D

Binding and Developability Profile Data

ADI ID	VH CDR H3 sequence	BiaCore Fab K_D (M) Hu CD3ed-Fc Monovalent	BiaCore Fab K_D (M) Cy CD3ed-Fc Monovalent	ForteBio IgG K_D (M) Hu CD3ed-Fc Avid	ForteBio IgG K_D (M) Cy CD3ed-Fc Avid	ForteBio IgG K_D (M) Hu CD28-Fc 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

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 ΔΔmax (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
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

Titer < 50 mg/L

Figure 35A (Continued)

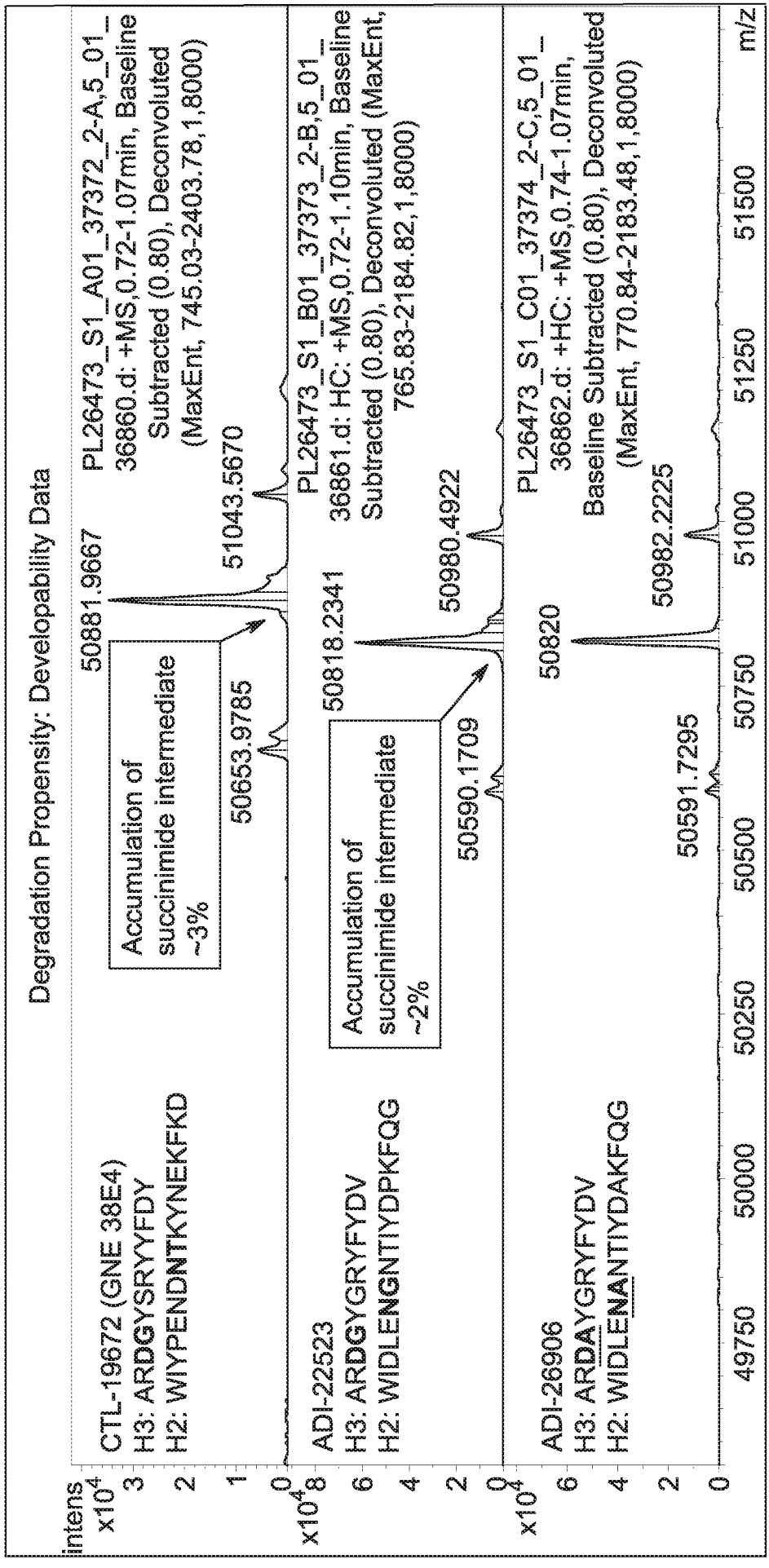

Degradation Propensity: Developability Data
intens
CTL-19672 (GNE 38E4)
H3: ARDGYSRYYFDY
H2: WIYPENDNTKYNEKFKD
PL26473_S1_A01_37372_2-A,5_01_
36860.d: +MS,0.72-1.07min, Baseline
Subtracted (0.80), Deconvoluted
(MaxEnt, 745.03-2403.78,1,8000)
50881.9667
51043.5670
50653.9785
Accumulation of
succinimide intermediate
~3%
ADI-22523
H3: ARDGYGRYFYDV
H2: WIDLENGNTIYDPKFQG
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)
50818.2341
50980.4922
50590.1709
Accumulation of
succinimide intermediate
~2%
ADI-26906
H3: ARDAYGRYFYDV
H2: WIDLENANTIYDAKFQG
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)
50820
50982.2225
50591.7295
m/z

Figure 35B

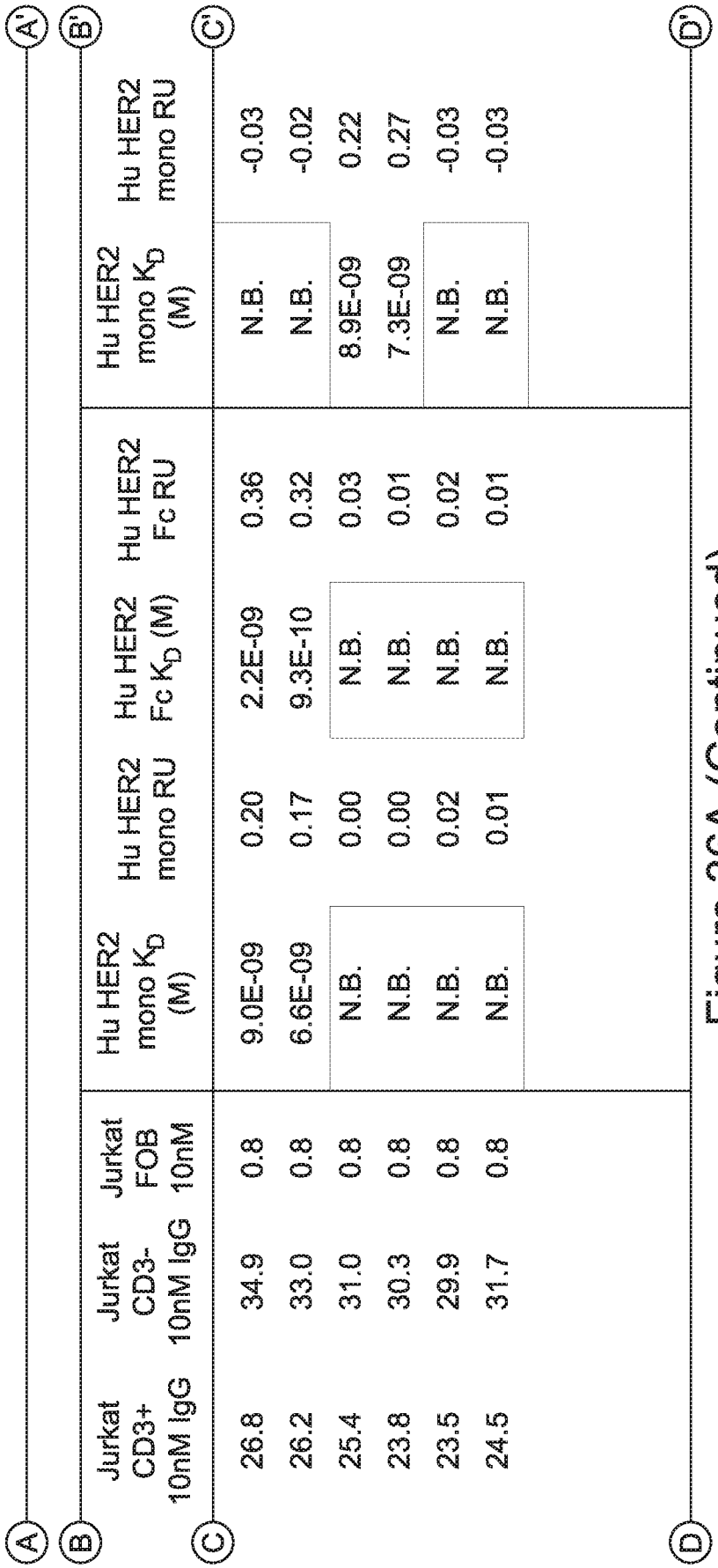
Properties of Monospecific TAA scFv-Fc: Binding and Developability profile data

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

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)

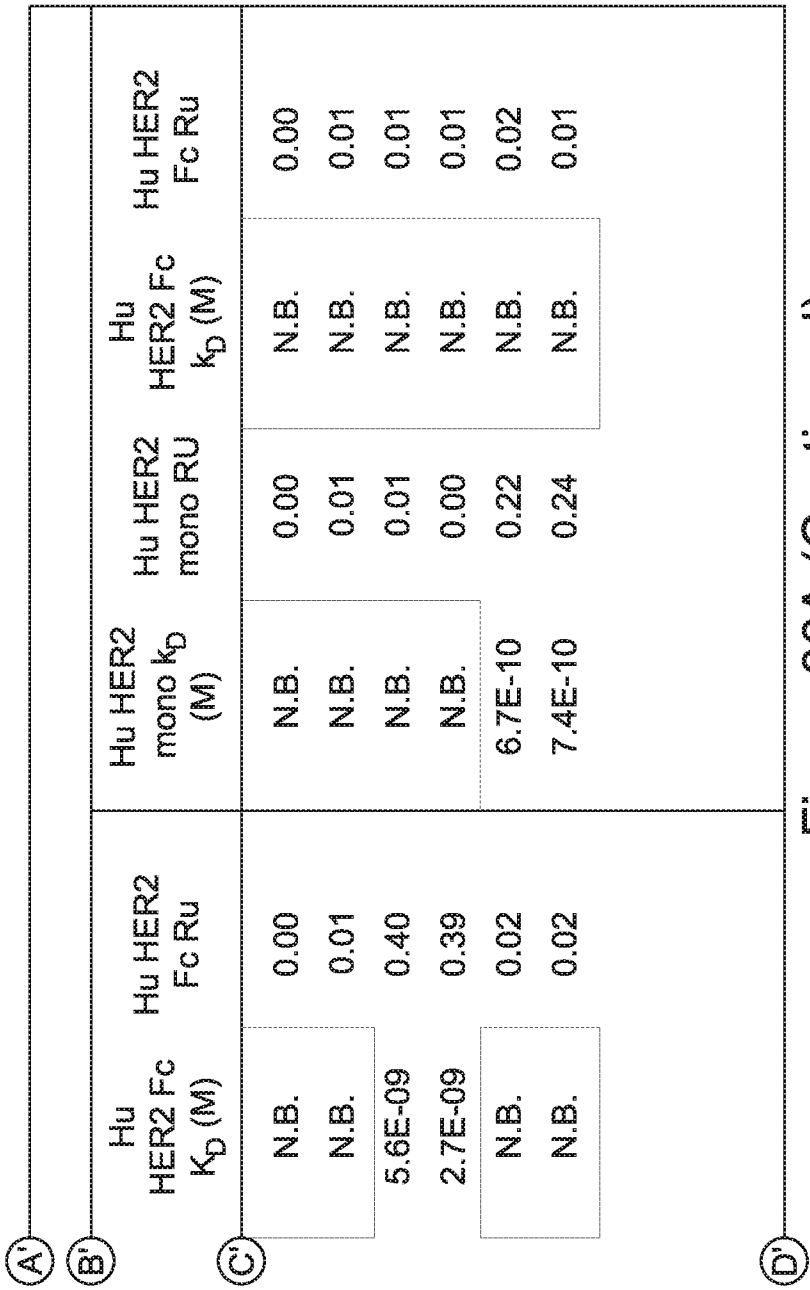


Figure 36A (Continued)

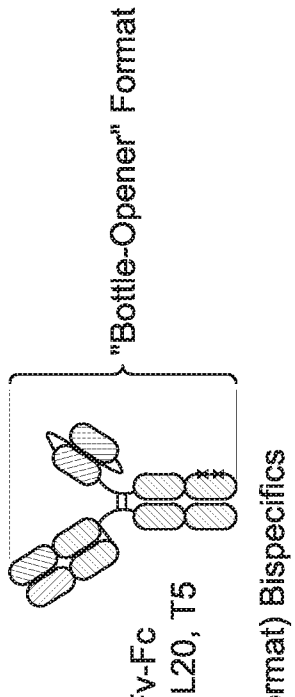

Anti-CD3
Anti-TAA
"Bottle-Opener" Format
scFv-Fc
VK/H, L20, T5
Bispecific Characteristics
IgG4 Ser228Phe
His435->Arg, Tyr436->Phe Mutations (X)
Purification of Fab/scFv-Fc Heterodimer (Aka "Bottle-Opener" Format) Bispecifics

Figure 36B

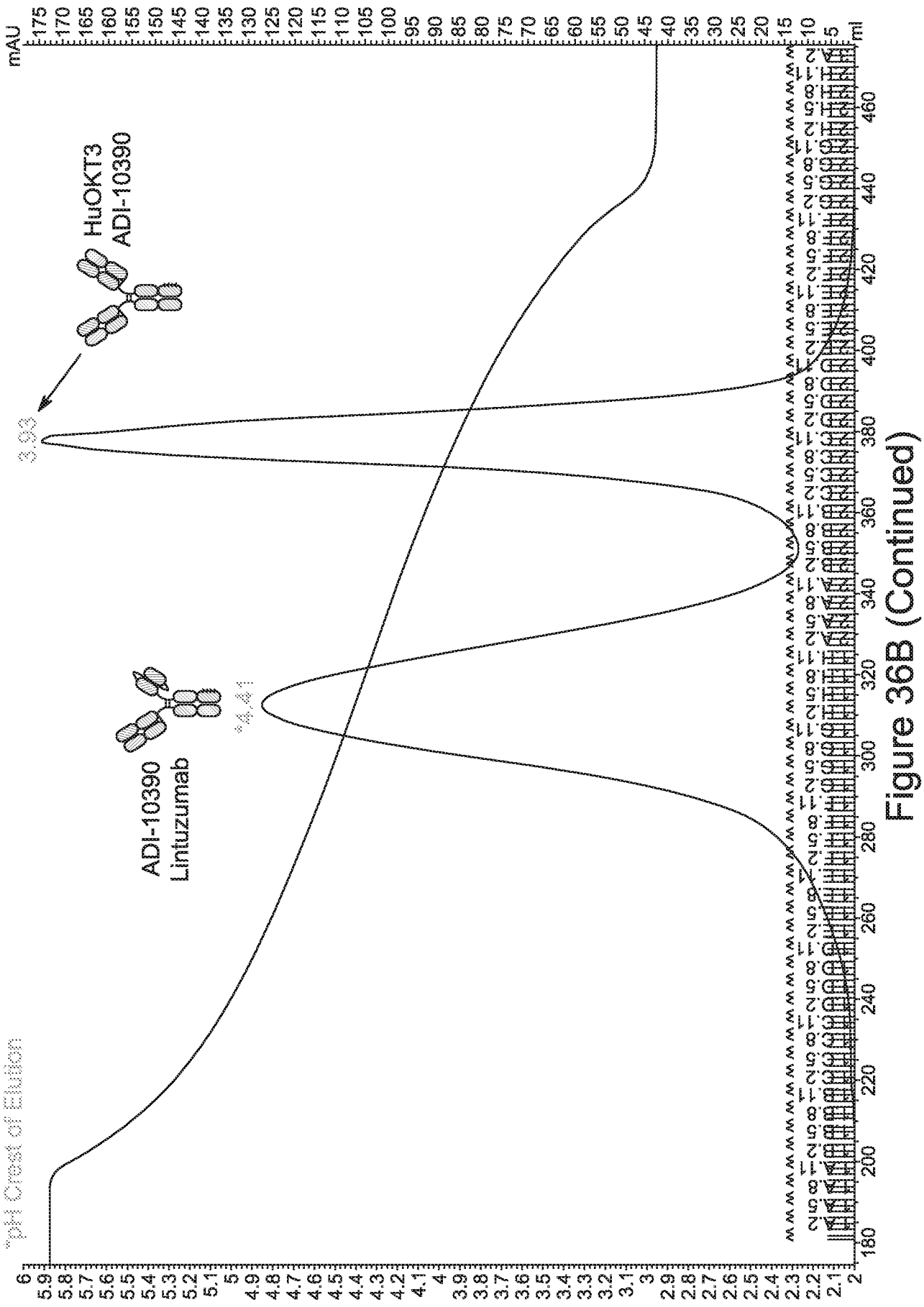


Figure 36B (Continued)

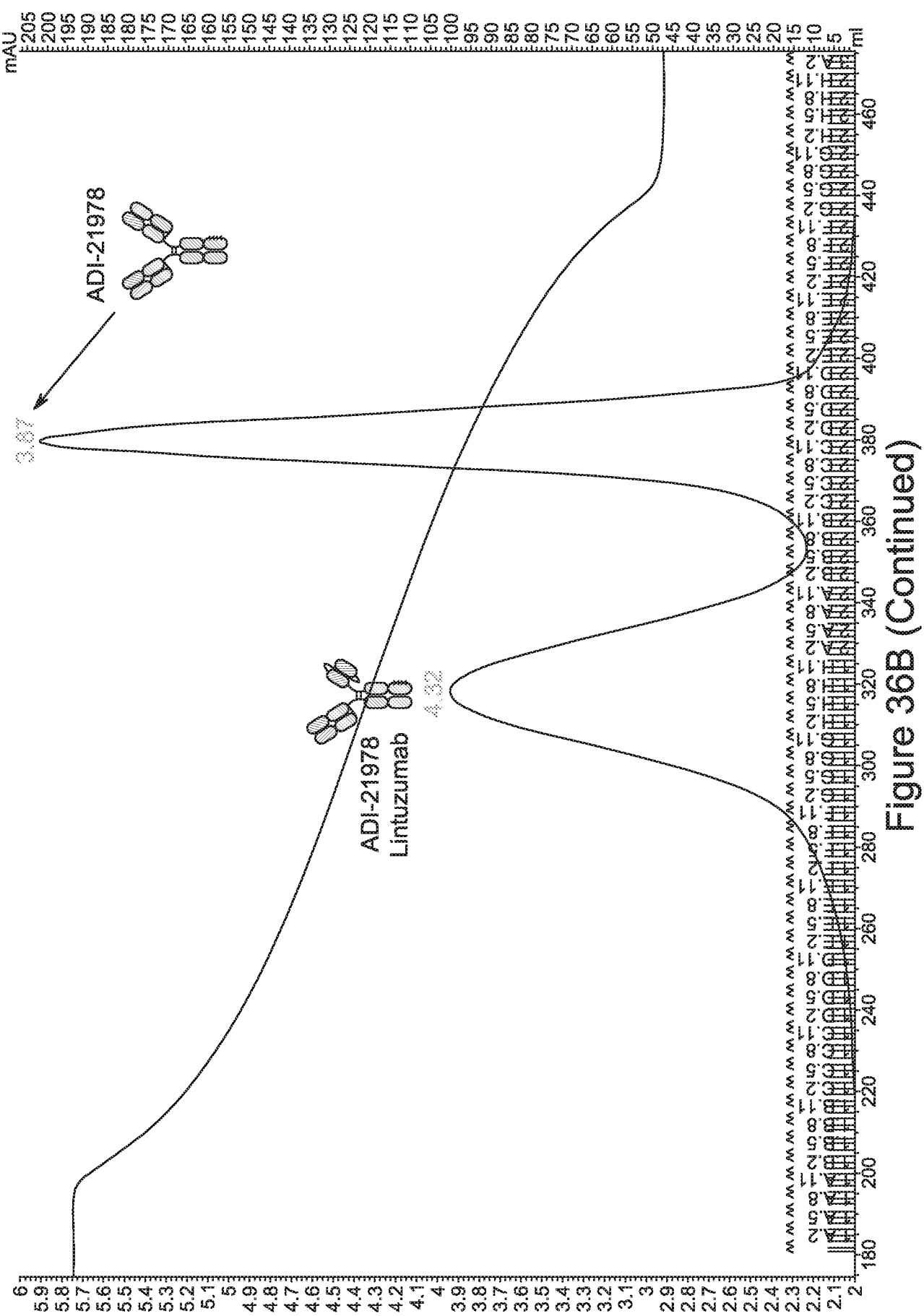


Figure 36B (Continued)

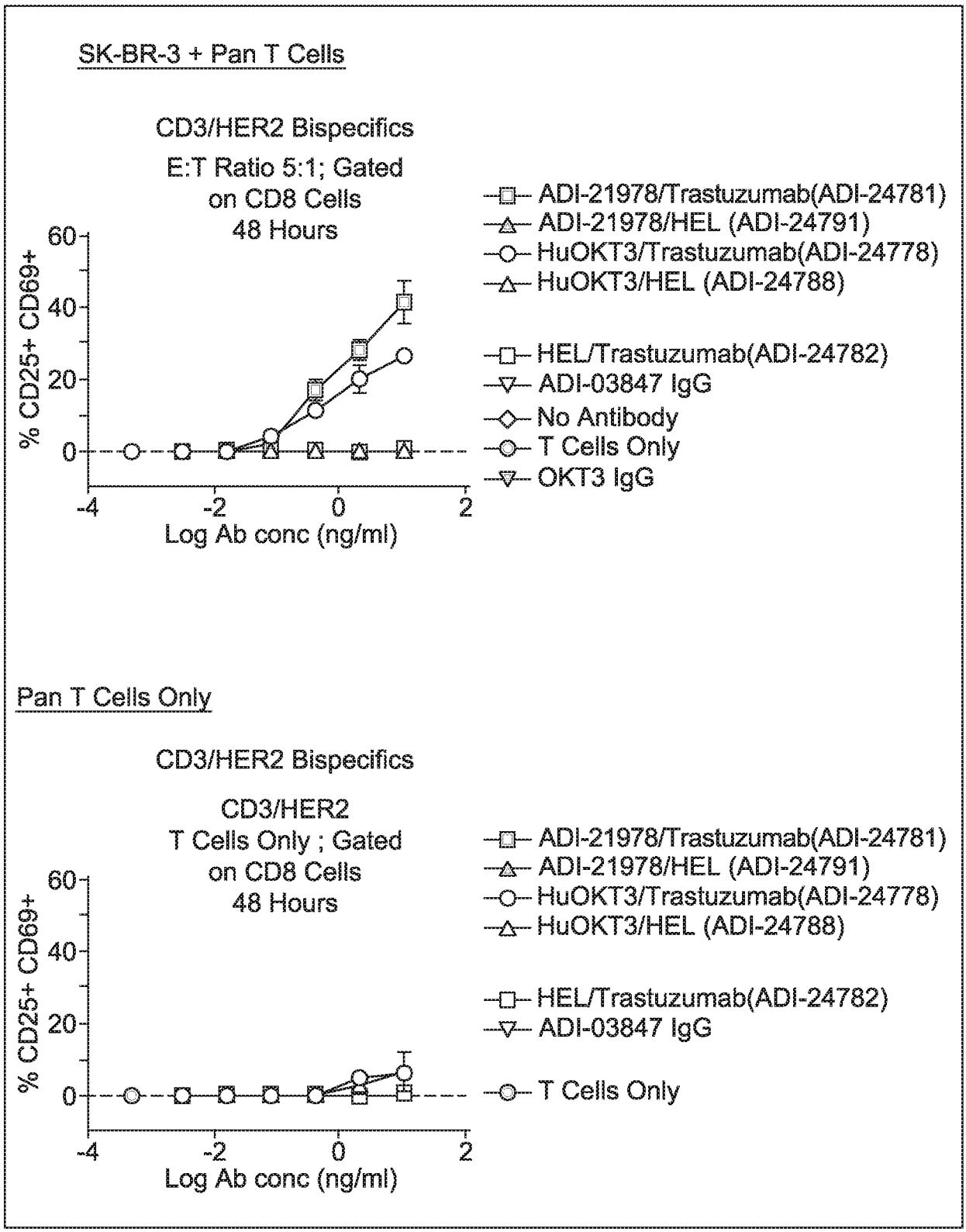
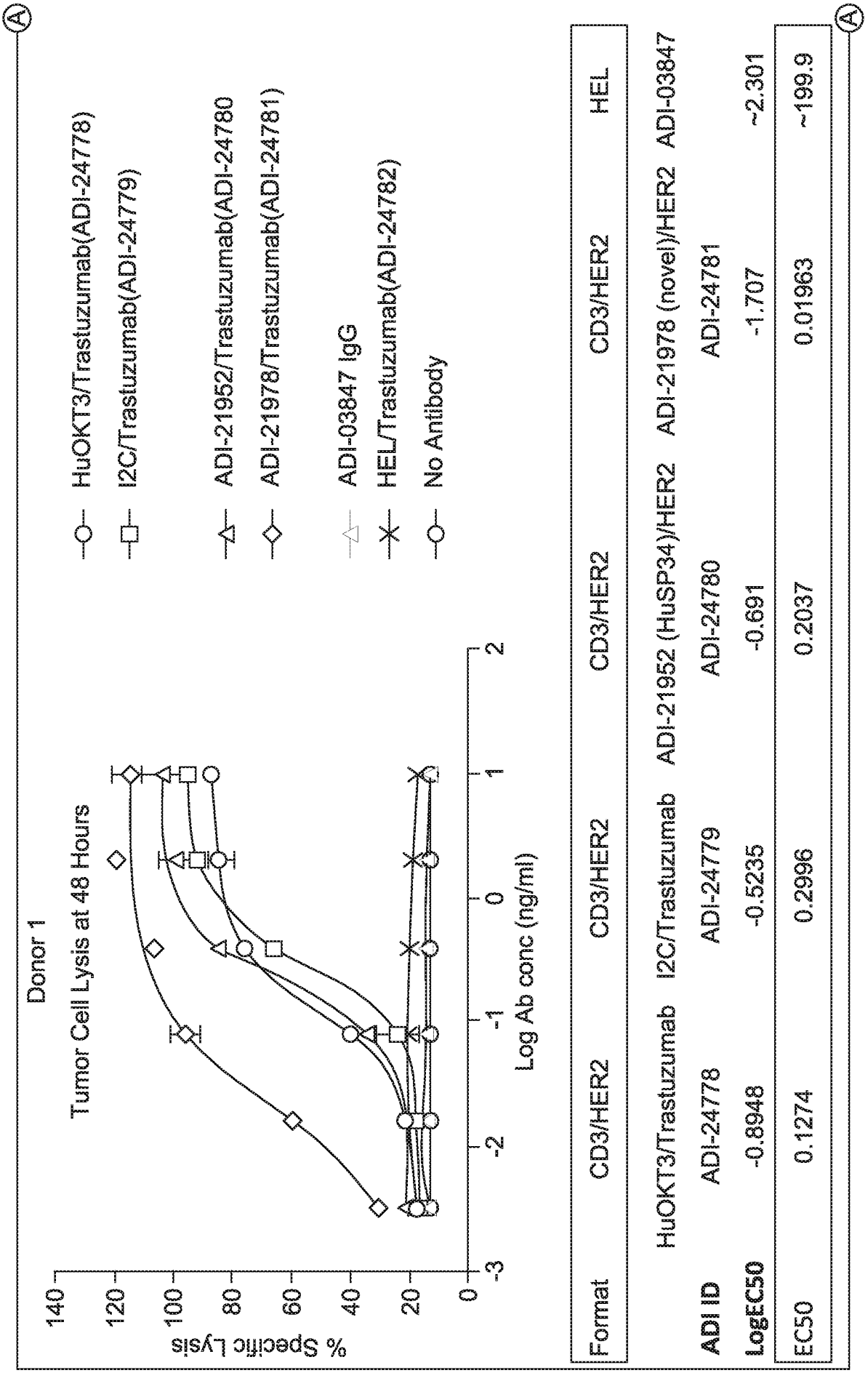
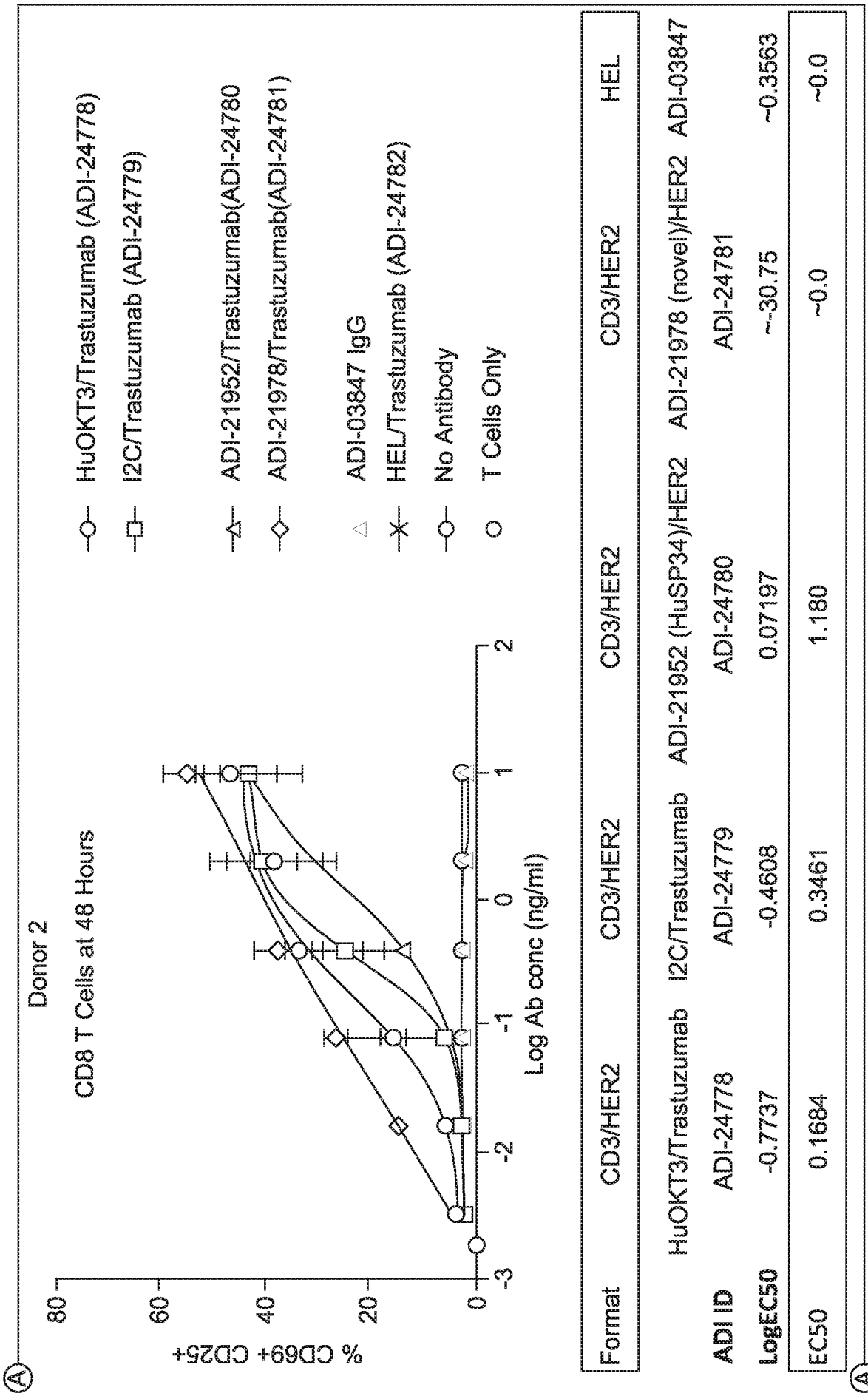

SK-BR-3 + Pan T Cells
CD3/HER2 Bispecifics
E:T Ratio 5:1; Gated
on CD8 Cells
48 Hours
% CD25+ CD69+
60
40
20
0
-4
-2
0
2
Log Ab conc (ng/ml)
ADI-21978/Trastuzumab(ADI-24781)
ADI-21978/HEL (ADI-24791)
HuOKT3/Trastuzumab(ADI-24778)
HuOKT3/HEL (ADI-24788)
HEL/Trastuzumab(ADI-24782)
ADI-03847 IgG
No Antibody
T Cells Only
OKT3 IgG
Pan T Cells Only
CD3/HER2 Bispecifics
CD3/HER2
T Cells Only ; Gated
on CD8 Cells
48 Hours
% CD25+ CD69+
60
40
20
0
-4
-2
0
2
Log Ab conc (ng/ml)
ADI-21978/Trastuzumab(ADI-24781)
ADI-21978/HEL (ADI-24791)
HuOKT3/Trastuzumab(ADI-24778)
HuOKT3/HEL (ADI-24788)
HEL/Trastuzumab(ADI-24782)
ADI-03847 IgG
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)

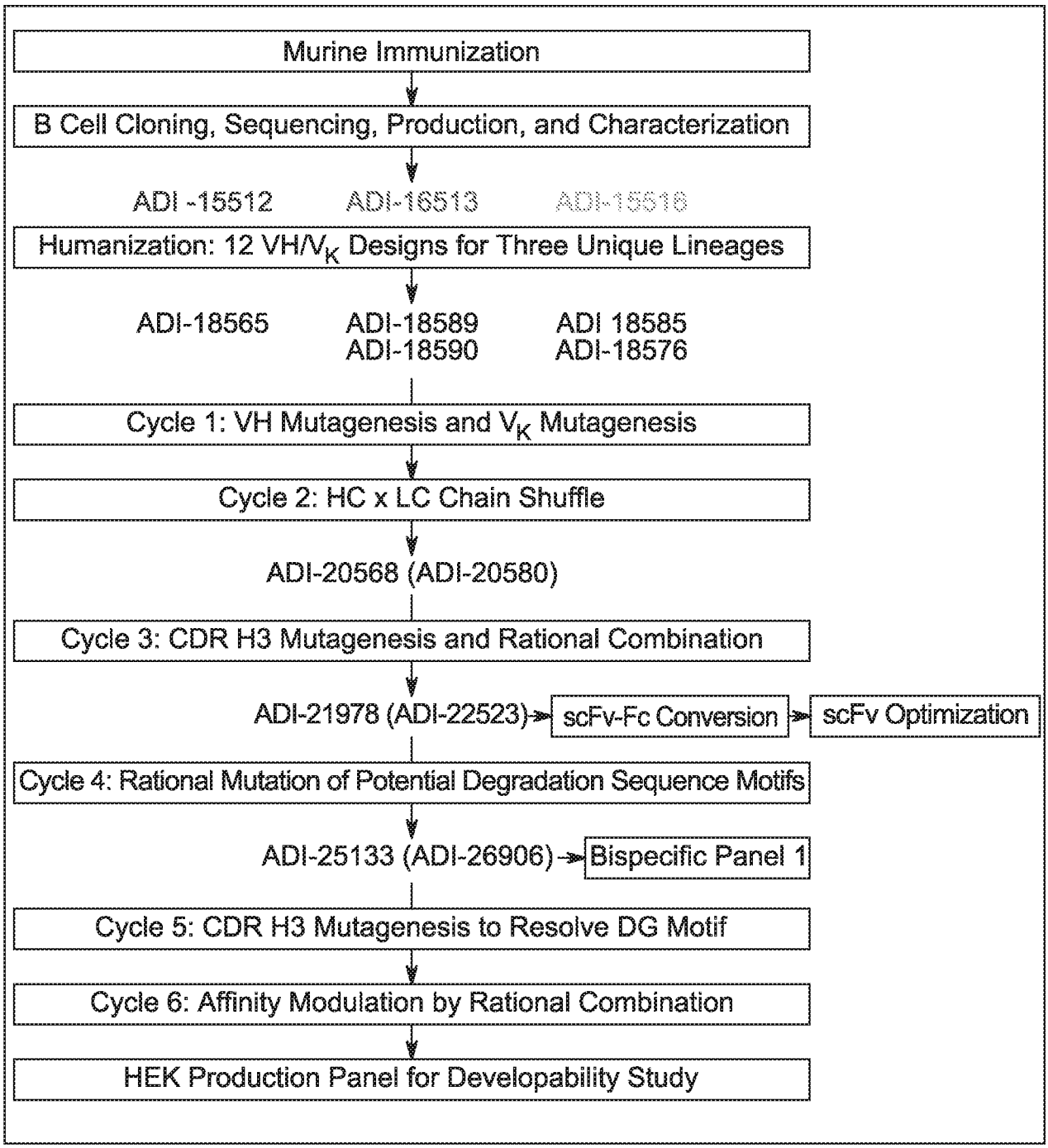

Murine Immunization
B Cell Cloning, Sequencing, Production, and Characterization
ADI -15512
ADI-16513
ADI-15516
Humanization: 12 VH/V_K Designs for Three Unique Lineages
ADI-18565
ADI-18589
ADI-18590
ADI 18585
ADI-18576
Cycle 1: VH Mutagenesis and V_K Mutagenesis
Cycle 2: HC x LC Chain Shuffle
ADI-20568 (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

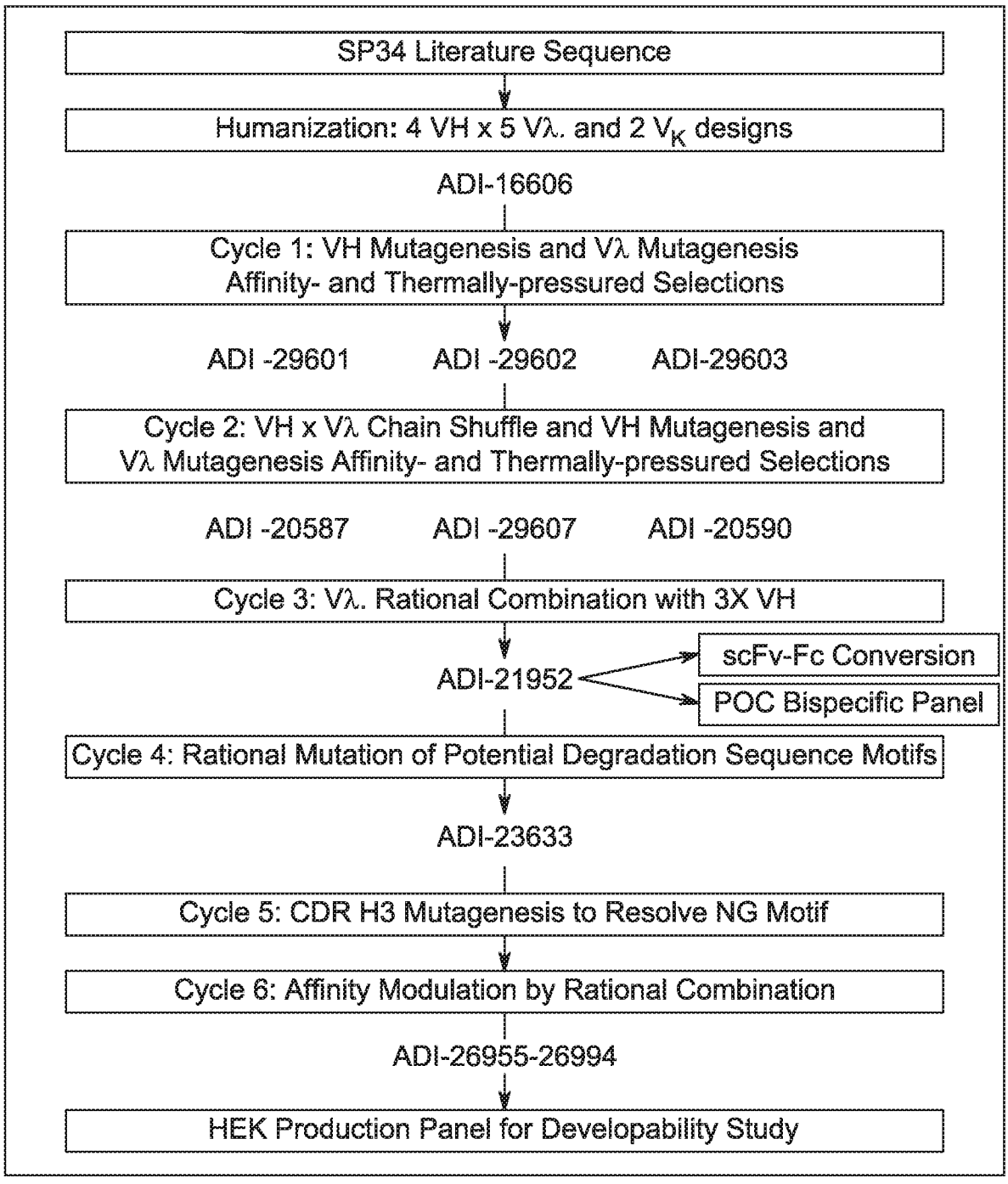

SP34 Literature Sequence
Humanization: 4 VH x 5 Vλ. and 2 V_K designs
ADI-16606
Cycle 1: VH Mutagenesis and Vλ Mutagenesis
Affinity- and Thermally-pressured Selections
ADI -29601
ADI -29602
ADI-29603
Cycle 2: VH x Vλ Chain Shuffle and VH Mutagenesis and
Vλ Mutagenesis Affinity- and Thermally-pressured 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

SEQUENCE LISTING

<110> ADIMAB, LLC

<120> HUMANIZED ANTI-CD3 ANTIBODIES

<130> 2009186-0189

<140>
<141>

<160> 6480

<170> PatentIn version 3.5

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ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

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gtcaccgtct cctca 375

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<211> 125
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<220>
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Heavy chain variable region amino acid sequence

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1 5 10 15

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Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
    50                  55                  60


Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80


Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95


Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
            100                 105                 110


Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
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<211> 9
<212> PRT
<213> Artificial Sequence

<220>
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      Heavy chain variable region CDR H1 amino acid sequence

<400> 3
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1               5


<210> 4
<211> 27
<212> DNA
<213> Artificial Sequence

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      Heavy chain variable region CDR H1 nucleic acid sequence
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Heavy chain variable region CDR H2 amino acid sequence

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Val Lys Asp

<210> 6
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
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Heavy chain variable region CDR H2 nucleic acid sequence

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<210> 7
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
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Heavy chain variable region CDR H3 amino acid sequence

<400> 7
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr
1 5 10 15

<210> 8
<211> 48

<212> DNA
<213> Artificial Sequence

<220>
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Heavy chain variable region CDR H3 nucleic acid sequence

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<210> 9
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
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Light chain variable region nucleic acid sequence

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accccaggcc aggctccacg cggactcatc ggcggcacaa acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

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ggcggaggga ccaagctgac cgtccta 327

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<212> PRT
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Light chain variable region amino acid sequence

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Gln Thr Val Val Thr Gln Glu Pro Ser Phe Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ser Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 11
<211> 14
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Light chain variable region CDR L1 amino acid sequence

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<210> 12
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
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Light chain variable region CDR L1 nucleic acid sequence

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<210> 13
<211> 7
<212> PRT
<213> Artificial Sequence

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Light chain variable region CDR L2 amino acid sequence

<400> 13
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1 5

<210> 14
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
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Light chain variable region CDR L2 nucleic acid sequence

<400> 14
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<210> 15
<211> 9
<212> PRT
<213> Artificial Sequence

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Light chain variable region CDR L3 amino acid sequence

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1 5

<210> 16
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

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<210> 17
<211> 375
<212> DNA

<213> Artificial Sequence

<220>
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Heavy chain variable region nucleic acid sequence

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ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

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gtcaccgtct cctca 375

<210> 18
<211> 125
<212> PRT
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<220>
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Heavy chain variable region amino acid sequence

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1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 19
<211> 9
<212> PRT
<213> Artificial Sequence

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Heavy chain variable region CDR H1 amino acid sequence

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Phe Thr Phe Asp Thr Tyr Ala Met Asn
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<210> 20
<211> 27
<212> DNA
<213> Artificial Sequence

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Heavy chain variable region CDR H1 nucleic acid sequence

<400> 20
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<210> 21
<211> 19
<212> PRT
<213> Artificial Sequence

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Heavy chain variable region CDR H2 amino acid sequence

<400> 21
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 22
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
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Heavy chain variable region CDR H2 nucleic acid sequence

<400> 22
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<210> 23
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<220>
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Heavy chain variable region CDR H3 amino acid sequence

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<210> 24
<211> 48
<212> DNA
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Heavy chain variable region CDR H3 nucleic acid sequence

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<210> 25
<211> 327
<212> DNA
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Light chain variable region nucleic acid sequence

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acttgtagat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcccggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

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ggcggaggga ccaagctgac cgtccta 327

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Light chain variable region amino acid sequence

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1 5 10 15

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ser Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 27
<211> 14
<212> PRT
<213> Artificial Sequence

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Light chain variable region CDR L1 amino acid sequence

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<210> 28
<211> 42
<212> DNA
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Light chain variable region CDR L1 nucleic acid sequence

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<210> 29
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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Light chain variable region CDR L2 amino acid sequence

<400> 29
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1 5

<210> 30
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 30
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<210> 31
<211> 9
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<220>
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Light chain variable region CDR L3 amino acid sequence

<400> 31
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 32
<211> 27
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 32
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Heavy chain variable region nucleic acid sequence

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ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

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gtcaccgtct cctca 375

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Heavy chain variable region amino acid sequence

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
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<213> Artificial Sequence

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Heavy chain variable region CDR H1 amino acid sequence

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<210> 36
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Heavy chain variable region CDR H1 nucleic acid sequence

<400> 36
ttcacctttg acacatatgc catgaat 27

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Heavy chain variable region CDR H2 amino acid sequence

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Val Lys Asp

<210> 38
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Heavy chain variable region CDR H2 nucleic acid sequence

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Heavy chain variable region CDR H3 amino acid sequence

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<210> 40
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

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<210> 41
<211> 327
<212> DNA
<213> Artificial Sequence

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Light chain variable region nucleic acid sequence

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accccaggcc aggctccgcg cggactcatc ggcggcacaa acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

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ggcggaggga ccaagctgac cgtccta 327

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<211> 109

<212> PRT
<213> Artificial Sequence

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Light chain variable region amino acid sequence

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1 5 10 15

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 43
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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Light chain variable region CDR L1 amino acid sequence

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<210> 44
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<212> DNA
<213> Artificial Sequence

<220>
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Light chain variable region CDR L1 nucleic acid sequence

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<210> 45
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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Light chain variable region CDR L2 amino acid sequence

<400> 45
Gly Thr Asn Lys Arg Ala Pro
1 5

<210> 46
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
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Light chain variable region CDR L2 nucleic acid sequence

<400> 46
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<210> 47
<211> 9
<212> PRT
<213> Artificial Sequence

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Light chain variable region CDR L3 amino acid sequence

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Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 48
<211> 27
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 48
gcgctgtggt acagtaacct ttgggtg 27

<210> 49
<211> 375
<212> DNA
<213> Artificial Sequence

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Heavy chain variable region nucleic acid sequence

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tcctgtgcag cctctggatt cacctttaac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attaggtcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

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gtcaccgtct cctca 375

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<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

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1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Ser Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 51
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 51
Phe Thr Phe Asn Thr Tyr Ala Met Asn
1 5

<210> 52
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 52

ttcaccttta acacatatgc catgaat 27

<210> 53
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 53
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 54
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 54
aggattaggt ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 55
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 55
Val Arg His Ser Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala Tyr
1 5 10 15

<210> 56
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 56
gtcaggcaca gtaacttcgg gaacggttat gtatcctggt ttgcttac 48

<210> 57
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 57
cagactgtgg tgacccagga gccatcgctc tcggtgtccc ctggagggac agtcacactc 60

acttgtagat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcccggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaatctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 58
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 58
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ser Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 59
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 59
Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 60
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 60
agatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 61
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region CDR L2 amino acid sequence

<400> 61
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 62
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 62
ggcacagaca agcgcgctcc c 21

<210> 63
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 63
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 64
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 64
gcgctgtggt acagtaacct ttgggtg 27

<210> 65
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 65
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa gggtcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aagtgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 66
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 66
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 67
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 67
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 68
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 68
ttcacctttg acacatatgc catgaat 27

<210> 69
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 69
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Gly

<210> 70
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 70
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaagggt 57

<210> 71
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 71
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 72
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 72
gtcaggcacg gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 73
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 73
cagactgtgg tgacccagga gccatcgctc tcggtgtccc ctggagggac agtcacactc 60

acttgtagat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcccggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaatctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 74
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 74
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ser Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 75
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 75
Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 76
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 76
agatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 77
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 77
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 78
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 78
ggcacagaca agcgcgctcc c 21

<210> 79
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 79
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 80
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 80
gcgctgtggt acagtaacct ttgggtg 27

<210> 81
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 81
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 82
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 82
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 83
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 83
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 84
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 84
ttcacctttg acacatatgc catgaat 27

<210> 85
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 85
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 86
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 86
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 87
<211> 16

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 87
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 88
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 88
gtcaggcacg gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 89
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 89
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtagat caagcactgg cgcagtcact actagtaact acgccaactg gatccagcag 120

accccaggcc aggccccgcg cggactcatc ggcggcacaa acaagcgcgc tcctggggtc 180

cctgatcgcc tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 90
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 90
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Ile Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Asp Arg Leu
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 91
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 91
Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 92
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 92
agatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 93
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 93
Gly Thr Asn Lys Arg Ala Pro
1 5

<210> 94
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 94
ggcacaaaca agcgcgctcc t 21

<210> 95
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 95
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 96
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 96
gcgctgtggt acagtaacct ttgggtg 27

<210> 97
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 97
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccggggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctacg 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtacctgc aaataaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggagccctg 360

gtcaccgtct cctca 375

<210> 98
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 98
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Ile Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Ala Leu Val Thr Val Ser Ser
115 120 125

<210> 99
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 99
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 100
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 100
ttcacctttg acacatatgc catgaat 27

<210> 101
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 101
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 102
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 102
aggattagat ccaagtataa caattacgct acgtactacg cagactccgt gaaggat 57

<210> 103
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 103
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 104
<211> 48
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 104
gtcaggcacg gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 105
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 105
cagactgtgg tgacccagga gccatcgctc tcggtgtccc ctggagggac agtcacactc 60

acttgtagat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcccggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaatctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 106
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 106
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ser Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 107
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 107
Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 108
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 108
agatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 109
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 109
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 110
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 110
ggcacagaca agcgcgctcc c 21

<210> 111
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 111
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 112
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 112
gcgctgtggt acagtaacct ttgggtg 27

<210> 113
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region nucleic acid sequence

<400> 113
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 114
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 114
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 115
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 115
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 116
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 116
ttcacctttg acacatatgc catgaat 27

<210> 117
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 117
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 118
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 118
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 119
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 119
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 120
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 120
gtcaggcacg gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 121
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 121
cagactgtgg tgacccagga gccatcgctc tcggtgtccc ctggagggac agtcacactc 60

acttgtagat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcccggggtc 180

cctgagcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaatctga ttattactgt gtgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 122
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 122
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Glu Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ser Asp Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 123
<211> 14

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 123
Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 124
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 124
agatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 125
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 125
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 126
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 126
ggcacagaca agcgcgctcc c 21

<210> 127
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 127
Val Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 128
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 128
gtgctgtggt acagtaacct ttgggtg 27

<210> 129
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 129
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 130
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 130
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 131
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 131

Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 132
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 132
ttcacctttg acacatatgc catgaat 27

<210> 133
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 133
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 134
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 134
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 135
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 135
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 136
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 136
gtcaggcacg gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 137
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 137
cagactgtgg tgacccagga gccatcgctc tcggtgtccc ctggagggac agtcacactc 60

acttgtagat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcccggggtc 180

cctgatcgct tctctggctc cctgctcggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaatctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 138
<211> 109
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 138
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ser Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 139
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 139
Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 140
<211> 42
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 140
agatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 141
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 141
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 142
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 142
ggcacagaca agcgcgctcc c 21

<210> 143
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 143
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 144
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 144
gcgctgtggt acagtaacca ttgggtg 27

<210> 145
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 145
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc gccatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacagtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 146
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 146
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Ala Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 147
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 147
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 148
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 148
ttcacctttg acacatatgc catgaat 27

<210> 149

<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 149
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 150
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 150
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 151
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 151
Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 152
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 152
gtcaggcaca gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 153
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 153
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtagat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacaa acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 154
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 154
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 155
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 155
Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 156
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 156
agatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 157
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 157
Gly Thr Asn Lys Arg Ala Pro

1 5

<210> 158
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 158
ggcacaaaca agcgcgctcc t 21

<210> 159
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 159
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 160
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 160
gcgctgtggt acagtaacct ttgggtg 27

<210> 161
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 161
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctctgcc acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag tcacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 162
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 162
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Ser Ala Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser His Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 163
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 163
Phe Thr Ser Ala Thr Tyr Ala Met Asn
1 5

<210> 164
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 164
ttcacctctg ccacatatgc catgaat 27

<210> 165
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 165
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 166

<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 166
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 167
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 167
Val Arg His Gly Asn Phe Gly Asn Ser His Val Ser Trp Phe Ala His
1 5 10 15

<210> 168
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 168
gtcaggcacg gtaacttcgg gaacagtcac gtatcctggt ttgctcat 48

<210> 169
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 169
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtagat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacaa acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 170
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 170
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 171
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 171
Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 172
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 172
agatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 173
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 173
Gly Thr Asn Lys Arg Ala Pro
1 5

<210> 174
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 174
ggcacaaaca agcgcgctcc t 21

<210> 175
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 175
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 176
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 176
gcgctgtggt acagtaacct ttgggtg 27

<210> 177
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 177
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttaac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagaacacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttatgtatcc tggtttgctt cttggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 178
<211> 125

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 178
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala Ser Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 179
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 179
Phe Thr Phe Asn Thr Tyr Ala Met Asn
1 5

<210> 180
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 180
ttcaccttta acacatatgc catgaat 27

<210> 181
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 181
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 182
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 182
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 183
<211> 16
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 183
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala Ser
1 5 10 15

<210> 184
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 184
gtcaggcacg gtaacttcgg gaacagttat gtatcctggt ttgcttct 48

<210> 185
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 185
cagactgtgg tgacccagga gccatcgttc tcagtgtccc ctggagggac agtcacactc 60

acttgtggct caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccacg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaatctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 186
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 186
Gln Thr Val Val Thr Gln Glu Pro Ser Phe Ser Val Ser Pro Gly Gly
1   5   10   15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
            20   25   30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
        35   40   45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
    50   55   60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65   70   75   80

Gln Ala Asp Asp Glu Ser Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
                85   90   95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105

<210> 187
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 187
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1   5   10

<210> 188
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 188
ggctcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 189
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 189
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 190
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 190
ggcacagaca agcgcgctcc t 21

<210> 191
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 191
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 192
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 192
gcgctgtggt acagtaacct ttgggtg 27

<210> 193
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 193
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 194
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 194
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 195
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 195
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 196
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 196
ttcacctttg acacatatgc catgaat 27

<210> 197
<211> 19
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 197
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 198
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 198
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 199
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 199
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 200
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 200

gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 201
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 201
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcatcat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 202
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 202
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Ile Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 203
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 203
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 204
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 204
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 205
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 205
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 206
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 206
ggcacagaca agcgcgctcc t 21

<210> 207
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 207
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 208
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 208
gcgctgtggt acagtaacca ttgggtg 27

<210> 209
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 209
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 210
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 210
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 211
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 211
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 212
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 212
ttcacctttg acacatatgc catgaat 27

<210> 213
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 213
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 214
<211> 57
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 214
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 215
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 215
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 216
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 216
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 217
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 217
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggtc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 218
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 218
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Val
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 219
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 219
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 220
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 220
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 221
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 221
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 222
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 222
ggcacagaca agcgcgctcc t 21

<210> 223
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 223
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 224
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 224
gcgctgtggt acagtaacca ttgggtg 27

<210> 225
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 225
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 226
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 226
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 227
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 227
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 228
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 228
ttcacctttg acacatatgc catgaat 27

<210> 229
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 229
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 230
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 230
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 231
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 231
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 232
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 232
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 233
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 233
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcgctgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccacg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gtgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 234
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 234

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Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1               5                   10                  15


Thr Val Thr Leu Thr Cys Gly Ser Ser Ala Gly Ala Val Thr Thr Ser
            20                  25                  30


Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
        35                  40                  45


Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65                  70                  75                  80


Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
                85                  90                  95


Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105


<210> 235
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 235
Gly Ser Ser Ala Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1               5                   10


<210> 236
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 236
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ggatcaagcg ctggcgcagt cactactagt aactacgcca ac 42

<210> 237
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 237
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 238
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 238
ggcacagaca agcgcgctcc t 21

<210> 239
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 239
Val Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 240
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 240
gtgctgtggt acagtaacct ttgggtg 27

<210> 241
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 241
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 242
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 242
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 243
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 243
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 244
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 244
ttcacctttg acacatatgc catgaat 27

<210> 245
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 245
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 246
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 246
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 247
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 247
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 248
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 248
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 249
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 249
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcgctgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccacg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 250
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 250
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Ala Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 251
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 251
Gly Ser Ser Ala Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 252
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 252
ggatcaagcg ctggcgcagt cactactagt aactacgcca ac 42

<210> 253
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 253
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 254

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 254
ggcacagaca agcgcgctcc t 21

<210> 255
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 255
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 256
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 256
gcgctgtggt acagtaacca ttgggtg 27

<210> 257
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 257
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 258
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 258
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 259
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 259
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 260
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 260
ttcacctttg acacatatgc catgaat 27

<210> 261
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 261
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 262
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 262
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 263
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 263
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 264
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 264
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 265
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 265
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acaataacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 266
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 266
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Asn Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 267
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 267
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 268
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 268
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 269
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 269
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 270
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 270
ggcacagaca agcgcgctcc t 21

<210> 271
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 271
Ala Leu Trp Tyr Asn Asn His Trp Val
1 5

<210> 272
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 272
gcgctgtggt acaataacca ttgggtg 27

<210> 273
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 273
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc gccatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacagtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 274
<211> 125
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 274
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Ala Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 275
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 275
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 276
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 276
ttcacctttg acacatatgc catgaat 27

<210> 277
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 277
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 278
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 278
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 279
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 279

Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 280
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 280
gtcaggcaca gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 281
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 281
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcgctgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccacg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gtgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 282
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 282
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Ala Gly Ala Val Thr Thr Ser
            20   25   30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
        35   40   45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
    50   55   60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65   70   75   80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
                85   90   95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105

<210> 283
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 283
Gly Ser Ser Ala Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1   5   10

<210> 284
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 284
ggatcaagcg ctggcgcagt cactactagt aactacgcca ac   42

<210> 285
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 285
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 286
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 286
ggcacagaca agcgcgctcc t 21

<210> 287
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 287
Val Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 288
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 288

gtgctgtggt acagtaacct ttgggtg 27

<210> 289
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 289
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc gccatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacagtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 290
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 290
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Ala Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 291
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 291
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 292
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 292
ttcacctttg acacatatgc catgaat 27

<210> 293
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region CDR H2 amino acid sequence

<400> 293
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 294
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 294
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 295
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 295
Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 296
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 296
gtcaggcaca gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 297

<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 297
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcgctgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccacg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 298
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 298
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Ala Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 299
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 299
Gly Ser Ser Ala Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 300
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 300
ggatcaagcg ctggcgcagt cactactagt aactacgcca ac 42

<210> 301
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 301
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 302
<211> 21
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 302
ggcacagaca agcgcgctcc t 21

<210> 303
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 303
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 304
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 304
gcgctgtggt acagtaacca ttgggtg 27

<210> 305
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 305
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc gccatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacagtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 306
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 306
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Ala Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 307
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 307
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 308
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 308
ttcacctttg acacatatgc catgaat 27

<210> 309
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 309
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 310
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region CDR H2 nucleic acid sequence

<400> 310
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 311
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 311
Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 312
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 312
gtcaggcaca gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 313
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 313
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acaataacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 314
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 314
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Asn Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 315
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 315

Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 316
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 316
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 317
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 317
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 318
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 318
ggcacagaca agcgcgctcc t 21

<210> 319
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 319
Ala Leu Trp Tyr Asn Asn His Trp Val
1 5

<210> 320
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 320
gcgctgtggt acaataacca ttgggtg 27

<210> 321
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 321
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 322
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 322
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
            20   25   30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
    50   55   60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65   70   75   80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85   90   95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
            100   105   110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 323
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 323
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1   5

<210> 324
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 324
ttcacctttg acacatatgc catgaat 27

<210> 325
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 325
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 326
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 326
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 327
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 327
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 328
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 328
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 329
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 329
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gtgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 330
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 330
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 331
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 331
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 332
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 332
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 333

<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 333
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 334
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 334
ggcacagaca agcgcgctcc t 21

<210> 335
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 335
Val Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 336
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 336
gtgctgtggt acagtaacct ttgggtg 27

<210> 337
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 337
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 338
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 338
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 339
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 339
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 340
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 340
ttcacctttg acacatatgc catgaat 27

<210> 341
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 341
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 342
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 342
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 343
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 343
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 344
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 344
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 345
<211> 327
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 345
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 346
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 346
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 347
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 347
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 348
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 348
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 349
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 349
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 350
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 350
ggcacagaca agcgcgctcc t 21

<210> 351
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 351
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 352
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 352
gcgctgtggt acagtaacca ttgggtg 27

<210> 353
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 353
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 354
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 354
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 355
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 355
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 356
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 356
ttcacctttg acacatatgc catgaat 27

<210> 357
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 357
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 358
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 358
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 359
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 359
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 360
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 360
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 361
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 361
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcgctgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccacg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcatcat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 362
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 362
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Ala Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Ile Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 363
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 363
Gly Ser Ser Ala Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 364
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 364
ggatcaagcg ctggcgcagt cactactagt aactacgcca ac 42

<210> 365
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 365
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 366
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 366
ggcacagaca agcgcgctcc t 21

<210> 367
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 367

Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 368
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 368
gcgctgtggt acagtaacct ttgggtg 27

<210> 369
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 369
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 370
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 370

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
            20                  25                  30


Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
    50                  55                  60


Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80


Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95


Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
            100                 105                 110


Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125


<210> 371
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 371
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1               5


<210> 372
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
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<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 372
ttcacctttg acacatatgc catgaat 27

<210> 373
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 373
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 374
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 374
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 375
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 375
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 376
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 376
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 377
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 377
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcgctgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccacg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acaataacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 378
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 378
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Ala Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Asn Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 379
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 379
Gly Ser Ser Ala Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 380
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 380
ggatcaagcg ctggcgcagt cactactagt aactacgcca ac 42

<210> 381
<211> 7
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 381
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 382
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 382
ggcacagaca agcgcgctcc t 21

<210> 383
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 383
Ala Leu Trp Tyr Asn Asn Leu Trp Val
1 5

<210> 384
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 384
gcgctgtggt acaataacct ttgggtg 27

<210> 385

<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 385
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc gccatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacagtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 386
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 386
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Ala Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 387
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 387
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 388
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 388
ttcacctttg acacatatgc catgaat 27

<210> 389
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 389
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser

1 5 10 15

Val Lys Asp

<210> 390
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 390
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 391
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 391
Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 392
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 392
gtcaggcaca gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 393
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 393
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcgctgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccacg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcatcat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 394
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 394
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Ala Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Ile Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 395
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 395
Gly Ser Ser Ala Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 396
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 396
ggatcaagcg ctggcgcagt cactactagt aactacgcca ac 42

<210> 397
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 397
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 398
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region CDR L2 nucleic acid sequence

<400> 398
ggcacagaca agcgcgctcc t 21

<210> 399
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 399
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 400
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 400
gcgctgtggt acagtaacct ttgggtg 27

<210> 401
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 401
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc gccatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacagtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 402
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 402
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Ala Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 403
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 403
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 404
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 404
ttcacctttg acacatatgc catgaat 27

<210> 405
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 405
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 406
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 406
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 407
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 407
Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 408
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 408
gtcaggcaca gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 409
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 409
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcgctgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccacg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acaataacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 410
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 410
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Ala Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Asn Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 411
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 411
Gly Ser Ser Ala Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 412
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 412
ggatcaagcg ctggcgcagt cactactagt aactacgcca ac 42

<210> 413
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 413
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 414
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 414
ggcacagaca agcgcgctcc t 21

<210> 415
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 415
Ala Leu Trp Tyr Asn Asn Leu Trp Val
1 5

<210> 416
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 416
gcgctgtggt acaataacct ttgggtg 27

<210> 417
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 417
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac gcttatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacga ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 418
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 418
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Ala Tyr
            20                  25                  30


Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ala Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp
    50                  55                  60


Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80


Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95


Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
            100                 105                 110


Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125


<210> 419
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 419
Phe Thr Phe Asp Ala Tyr Ala Met Asn
1               5


<210> 420
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence
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<400> 420
ttcacctttg acgcttatgc catgaat 27

<210> 421
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 421
Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 422
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 422
aggattagat ccaagtataa cgattacgct acatactacg cagactccgt gaaggat 57

<210> 423
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 423
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 424
<211> 48

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 424
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 425
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 425
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtgatct gtgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 426
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 426
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asp
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 427
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 427
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 428
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 428
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 429
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 429
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 430
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 430
ggcacagaca agcgcgctcc t 21

<210> 431
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 431
Ala Leu Trp Tyr Ser Asp Leu Trp Val
1 5

<210> 432
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 432
gcgctgtggt acagtgatct gtgggtg 27

<210> 433
<211> 375
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 433
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 434
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 434
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 435
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 435
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 436
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 436
ttcacctttg acacatatgc catgaat 27

<210> 437
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 437
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 438
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 438
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 439
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 439
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 440
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 440
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 441
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region nucleic acid sequence

<400> 441
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtgatct gtgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 442
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 442
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asp
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 443
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 443
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 444
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 444
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 445
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 445
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 446
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 446
ggcacagaca agcgcgctcc t 21

<210> 447
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 447
Ala Leu Trp Tyr Ser Asp Leu Trp Val
1 5

<210> 448
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 448
gcgctgtggt acagtgatct gtgggtg 27

<210> 449
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 449
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 450
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 450
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 451
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 451
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 452
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 452
ttcacctttg acacatatgc catgaat 27

<210> 453
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 453
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 454
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 454
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 455
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 455
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 456
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 456
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 457
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 457
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 458
<211> 109

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 458
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 459
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 459
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 460
<211> 42

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 460
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 461
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 461
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 462
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 462
ggcacagaca agcgcgctcc t 21

<210> 463
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 463
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 464
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 464
gcgctgtggt acagtaacca ttgggtg 27

<210> 465
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 465
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcggggaagg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 466
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 466
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
            20                  25                  30


Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
    50                  55                  60


Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80


Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95


Tyr Cys Val Arg His Gly Asn Phe Gly Glu Gly Tyr Val Ser Trp Phe
            100                 105                 110


Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125


<210> 467
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 467
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1               5


<210> 468
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 468
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ttcacctttg acacatatgc catgaat 27

<210> 469
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 469
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 470
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 470
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 471
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 471
Val Arg His Gly Asn Phe Gly Glu Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 472
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 472
gtcaggcacg gtaacttcgg ggaaggttac gtatcctggt ttgctcat 48

<210> 473
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 473
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 474
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 474
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 475
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 475
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 476
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 476
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 477
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region CDR L2 amino acid sequence

<400> 477
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 478
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 478
ggcacagaca agcgcgctcc t 21

<210> 479
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 479
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 480
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 480
gcgctgtggt acagtaacca ttgggtg 27

<210> 481
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 481
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcggggaagg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 482
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 482
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Glu Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 483
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 483
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 484
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 484
ttcacctttg acacatatgc catgaat 27

<210> 485
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 485
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 486
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 486
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 487
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 487
Val Arg His Gly Asn Phe Gly Glu Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 488
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 488
gtcaggcacg gtaacttcgg ggaaggttac gtatcctggt ttgctcat 48

<210> 489
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 489
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 490
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 490
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 491
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 491
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 492
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 492
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 493
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 493
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 494
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 494
ggcacagaca agcgcgctcc t 21

<210> 495
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 495
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 496
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 496
gcgctgtggt acagtaacca ttgggtg 27

<210> 497
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 497
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacgc tctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 498
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 498
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 499
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 499
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 500
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 500
ttcacctttg acacatatgc catgaat 27

<210> 501
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 501
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 502
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 502
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 503
<211> 16

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 503
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 504
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 504
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 505
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 505
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 506
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 506
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 507
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 507
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 508
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 508
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 509
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 509
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 510
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 510
ggcacagaca agcgcgctcc t 21

<210> 511
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 511
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 512
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 512
gcgctgtggt acagtaacca ttgggtg 27

<210> 513
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 513
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgc ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 514
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 514
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ala Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 515
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 515
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 516
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 516
ttcacctttg acacatatgc catgaat 27

<210> 517
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 517
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 518
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 518
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 519
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 519
Val Arg His Gly Asn Phe Gly Asn Ala Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 520
<211> 48
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 520
gtcaggcacg gtaacttcgg gaacgcttac gtatcctggt ttgctcat 48

<210> 521
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 521
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 522
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 522
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 523
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 523
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 524
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 524
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 525
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 525
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 526
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 526
ggcacagaca agcgcgctcc t 21

<210> 527
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 527
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 528
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 528
gcgctgtggt acagtaacca ttgggtg 27

<210> 529
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region nucleic acid sequence

<400> 529
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacgc tctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgc ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 530
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 530
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ala Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ala Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 531
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 531
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 532
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 532
ttcacctttg acacatatgc catgaat 27

<210> 533
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 533
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 534
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 534
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 535
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 535
Val Arg His Gly Asn Phe Gly Asn Ala Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 536
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 536
gtcaggcacg gtaacttcgg gaacgcttac gtatcctggt ttgctcat 48

<210> 537
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 537
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 538
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 538
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 539
<211> 14

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 539
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 540
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 540
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 541
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 541
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 542
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 542
ggcacagaca agcgcgctcc t 21

<210> 543
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 543
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 544
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 544
gcgctgtggt acagtaacca ttgggtg 27

<210> 545
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 545
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 546
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 546
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 547
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 547

Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 548
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 548
ttcacctttg acacatatgc catgaat 27

<210> 549
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 549
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 550
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 550
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 551
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 551
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 552
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 552
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 553
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 553
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 554
<211> 109
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 554
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 555
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 555
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 556
<211> 42
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 556
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 557
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 557
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 558
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 558
ggcacagaca agcgcgctcc t 21

<210> 559
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 559
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 560
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 560
gcgctgtggt acagtaacca ttgggtg 27

<210> 561
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 561
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 562
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 562
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 563
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 563
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 564
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 564
ttcacctttg acacatatgc catgaat 27

<210> 565

<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 565
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 566
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 566
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 567
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 567
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 568
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 568
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 569
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 569
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 570
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 570
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 571
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 571
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 572
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 572
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 573
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 573
Gly Thr Asp Lys Arg Ala Pro

1 5

<210> 574
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 574
ggcacagaca agcgcgctcc t 21

<210> 575
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 575
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 576
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 576
gcgctgtggt acagtaacca ttgggtg 27

<210> 577
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 577
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 578
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 578
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 579
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 579
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1   5

<210> 580
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 580
ttcacctttg acacatatgc catgaat   27

<210> 581
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H2 amino acid sequence

<400> 581
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1   5   10   15

Val Lys Asp

<210> 582

<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 582
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 583
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 583
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 584
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 584
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 585
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 585
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 586
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 586
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 587
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 587
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 588
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 588
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 589
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 589
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 590
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 590
ggcacagaca agcgcgctcc t 21

<210> 591
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 591
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 592
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 592
gcgctgtggt acagtaacca ttgggtg 27

<210> 593
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 593
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 594
<211> 125

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 594
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
            20   25   30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
    50   55   60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65   70   75   80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85   90   95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
            100   105   110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 595
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 595
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1   5

<210> 596
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 596
ttcacctttg acacatatgc catgaat 27

<210> 597
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 597
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 598
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 598
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 599
<211> 16
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 599
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 600
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 600
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 601
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 601
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 602
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 602
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1   5   10   15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
            20   25   30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
        35   40   45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
    50   55   60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65   70   75   80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
                85   90   95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105

<210> 603
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 603
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1   5   10

<210> 604
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 604
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 605
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 605
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 606
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 606
ggcacagaca agcgcgctcc t 21

<210> 607
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 607
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 608
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 608
gcgctgtggt acagtaacca ttgggtg 27

<210> 609
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 609
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 610
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 610
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
    50   55   60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65   70   75   80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85   90   95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
            100   105   110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 611
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 611
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1   5

<210> 612
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 612
ttcacctttg acacatatgc catgaat   27

<210> 613
<211> 19
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 613
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 614
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 614
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 615
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 615
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 616
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 616

gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 617
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 617
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 618
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 618
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 619
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 619
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 620
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 620
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 621
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 621
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 622
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 622
ggcacagaca agcgcgctcc t 21

<210> 623
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 623
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 624
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 624
gcgctgtggt acagtaacca ttgggtg 27

<210> 625
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 625
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 626
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 626
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 627
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 627
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1   5

<210> 628
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 628
ttcacctttg acacatatgc catgaat   27

<210> 629
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H2 amino acid sequence

<400> 629
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1   5   10   15

Val Lys Asp

<210> 630
<211> 57
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 630
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 631
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 631
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 632
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 632
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 633
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 633
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 634
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 634
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 635
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 635
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 636
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 636
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 637
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 637
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 638
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 638
ggcacagaca agcgcgctcc t 21

<210> 639
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 639
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 640
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 640
gcgctgtggt acagtaacca ttgggtg 27

<210> 641
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 641
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactactcat actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 642
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 642
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ser Tyr
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 643
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 643
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 644
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 644
ttcacctttg acacatatgc catgaat 27

<210> 645
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 645
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ser Tyr Ser
1 5 10 15

Val Lys Asp

<210> 646
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 646
aggattagat ccaagtataa caattacgct acatactact catactccgt gaaggat 57

<210> 647
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 647
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 648
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 648
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 649
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 649
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 650
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 650

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Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1               5                   10                  15


Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
            20                  25                  30


Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
        35                  40                  45


Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65                  70                  75                  80


Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
                85                  90                  95


His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105


<210> 651
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 651
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1               5                   10


<210> 652
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 652
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ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 653
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 653
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 654
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 654
ggcacagaca agcgcgctcc t 21

<210> 655
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 655
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 656
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 656
gcgctgtggt acagtaacca ttgggtg 27

<210> 657
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 657
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 658
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 658
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 659
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 659
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 660
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 660
ttcacctttg acacatatgc catgaat 27

<210> 661
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 661
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 662
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 662
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 663
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 663
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 664
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 664
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 665
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 665
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 666
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 666
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 667
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 667
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 668
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 668
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 669
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 669
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 670

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 670
ggcacagaca agcgcgctcc t 21

<210> 671
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 671
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 672
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 672
gcgctgtggt acagtaacca ttgggtg 27

<210> 673
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 673
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 674
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 674

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5				10					15		

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Asp	Thr	Tyr
			20					25					30		

Ala	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			

Ala	Arg	Ile	Arg	Ser	Lys	Tyr	Asn	Asn	Tyr	Ala	Thr	Tyr	Tyr	Ala	Asp
	50					55					60				

Ser	Val	Lys	Asp	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	Ser	Thr
65					70				75					80	

Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr
				85					90					95	

Tyr	Cys	Val	Arg	His	Gly	Asn	Phe	Gly	Asn	Gly	Tyr	Val	Ser	Trp	Phe
			100					105					110		

Ala	His	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser			
		115					120					125			

<210> 675
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 675
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 676
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 676
ttcacctttg acacatatgc catgaat 27

<210> 677
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 677
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 678
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 678
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 679
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 679
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 680
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 680
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 681
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 681
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 682
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 682
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 683
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 683
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 684
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 684
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 685
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 685
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 686
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 686
ggcacagaca agcgcgctcc t 21

<210> 687
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 687
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 688
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 688
gcgctgtggt acagtaacca ttgggtg 27

<210> 689
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 689
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 690
<211> 125
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 690
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 691
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 691
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 692
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 692
ttcacctttg acacatatgc catgaat 27

<210> 693
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 693
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 694
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 694
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 695
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 695

Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 696
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 696
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 697
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 697
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 698
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 698
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
            20   25   30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
        35   40   45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
    50   55   60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65   70   75   80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
                85   90   95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105

<210> 699
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 699
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1   5   10

<210> 700
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 700
ggatcaagca ctggcgcagt cactactagt aactacgcca ac   42

<210> 701
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 701
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 702
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 702
ggcacagaca agcgcgctcc t 21

<210> 703
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 703
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 704
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 704

gcgctgtggt acagtaacca ttgggtg 27

<210> 705
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 705
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 706
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 706
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 707
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 707
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 708
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 708
ttcacctttg acacatatgc catgaat 27

<210> 709
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region CDR H2 amino acid sequence

<400> 709
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 710
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 710
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 711
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 711
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 712
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 712
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 713

<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 713
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 714
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 714
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 715
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 715
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 716
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 716
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 717
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 717
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 718
<211> 21
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 718
ggcacagaca agcgcgctcc t 21

<210> 719
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 719
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 720
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 720
gcgctgtggt acagtaacca ttgggtg 27

<210> 721
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 721
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 722
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 722
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 723
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 723
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 724
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 724
ttcacctttg acacatatgc catgaat 27

<210> 725
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 725
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 726
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region CDR H2 nucleic acid sequence

<400> 726
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 727
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 727
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 728
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 728
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 729
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 729
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 730
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 730
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 731
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 731

Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 732
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 732
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 733
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 733
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 734
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 734
ggcacagaca agcgcgctcc t 21

<210> 735
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 735
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 736
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 736
gcgctgtggt acagtaacca ttgggtg 27

<210> 737
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 737
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 738
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 738
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
            20   25   30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
    50   55   60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65   70   75   80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85   90   95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
            100   105   110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 739
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 739
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1   5

<210> 740
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 740
ttcacctttg acacatatgc catgaat 27

<210> 741
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 741
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 742
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 742
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 743
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 743
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 744
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 744
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 745
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 745
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgtt tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 746
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 746
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 747
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 747
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 748
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 748
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 749

<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 749
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 750
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 750
ggcacagaca agcgcgctcc t 21

<210> 751
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 751
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 752
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 752
gcgctgtggt acagtaacca ttgggtg 27

<210> 753
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 753
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 754
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 754
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 755
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 755
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 756
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 756
ttcacctttg acacatatgc catgaat 27

<210> 757
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 757
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 758
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 758
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 759
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 759
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 760
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 760
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 761
<211> 327
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 761
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 762
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 762
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 763
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 763
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 764
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 764
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 765
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 765
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 766
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 766
ggcacagaca agcgcgctcc t 21

<210> 767
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 767
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 768
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 768
gcgctgtggt acagtaacca ttgggtg 27

<210> 769
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 769
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 770
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 770
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 771
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 771
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 772
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 772
ttcacctttg acacatatgc catgaat 27

<210> 773
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 773
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 774
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 774
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 775
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 775
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 776
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 776
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 777
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 777
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 778
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 778
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 779
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 779
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 780
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 780
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 781
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 781
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 782
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 782
ggcacagaca agcgcgctcc t 21

<210> 783
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 783

Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 784
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 784
gcgctgtggt acagtaacca ttgggtg 27

<210> 785
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 785
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagt gtctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 786
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 786

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
            20                  25                  30


Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
        35                  40                  45


Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
    50                  55                  60


Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80


Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95


Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
            100                 105                 110


Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125


<210> 787
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 787
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1               5


<210> 788
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
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<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 788
ttcacctttg acacatatgc catgaat 27

<210> 789
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 789
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 790
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 790
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 791
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 791
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 792
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 792
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 793
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 793
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggctgtggga ccaagctgac cgtccta 327

<210> 794
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 794
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Cys Gly Thr Lys Leu Thr Val Leu
100 105

<210> 795
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 795
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 796
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 796
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 797
<211> 7
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 797
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 798
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 798
ggcacagaca agcgcgctcc t 21

<210> 799
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 799
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 800
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 800
gcgctgtggt acagtaacca ttgggtg 27

<210> 801

<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 801
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagt gtctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 802
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 802
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 803
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 803
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 804
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 804
ttcacctttg acacatatgc catgaat 27

<210> 805
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 805
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser

1 5 10 15

Val Lys Asp

<210> 806
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 806
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 807
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 807
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 808
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 808
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 809
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 809
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggctgtggga ccaagctgac cgtccta 327

<210> 810
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 810
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Cys Gly Thr Lys Leu Thr Val Leu
100 105

<210> 811
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 811
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 812
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 812
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 813
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 813
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 814
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region CDR L2 nucleic acid sequence

<400> 814
ggcacagaca agcgcgctcc t 21

<210> 815
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 815
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 816
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 816
gcgctgtggt acagtaacca ttgggtg 27

<210> 817
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 817
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagt gtctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 818
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 818
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 819
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 819
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 820
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 820
ttcacctttg acacatatgc catgaat 27

<210> 821
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 821
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 822
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 822
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 823
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 823
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 824
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 824
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 825
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 825
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggctgtggga ccaagctgac cgtccta 327

<210> 826
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 826
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Cys Gly Thr Lys Leu Thr Val Leu
100 105

<210> 827
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 827
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 828
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 828
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 829
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 829
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 830
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 830
ggcacagaca agcgcgctcc t 21

<210> 831
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 831
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 832
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 832
gcgctgtggt acagtaacca ttgggtg 27

<210> 833
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 833
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagt gtctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 834
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 834
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 835
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 835
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 836
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 836
ttcacctttg acacatatgc catgaat 27

<210> 837
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 837
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 838
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 838
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 839
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 839
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 840
<211> 48

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 840
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 841
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 841
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggctgtggga ccaagctgac cgtccta 327

<210> 842
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 842
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Cys Gly Thr Lys Leu Thr Val Leu
100 105

<210> 843
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 843
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 844
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 844
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 845
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 845
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 846
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 846
ggcacagaca agcgcgctcc t 21

<210> 847
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 847
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 848
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 848
gcgctgtggt acagtaacca ttgggtg 27

<210> 849
<211> 375
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 849
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagt gtctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 850
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 850
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 851
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 851
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 852
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 852
ttcacctttg acacatatgc catgaat 27

<210> 853
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 853
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 854
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 854
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 855
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 855
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 856
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 856
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 857
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region nucleic acid sequence

<400> 857
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggctgtggga ccaagctgac cgtccta 327

<210> 858
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 858
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Cys Gly Thr Lys Leu Thr Val Leu
100 105

<210> 859
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 859
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 860
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 860
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 861
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 861
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 862
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 862
ggcacagaca agcgcgctcc t 21

<210> 863
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 863
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 864
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 864
gcgctgtggt acagtaacca ttgggtg 27

<210> 865
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 865
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagt gtctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 866
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 866
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 867
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 867
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 868
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 868
ttcacctttg acacatatgc catgaat 27

<210> 869
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 869
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 870
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 870
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 871
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 871
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 872
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 872
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 873
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 873
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggctgtggga ccaagctgac cgtccta 327

<210> 874
<211> 109

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 874
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Cys Gly Thr Lys Leu Thr Val Leu
100 105

<210> 875
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 875
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 876
<211> 42

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 876
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 877
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 877
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 878
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 878
ggcacagaca agcgcgctcc t 21

<210> 879
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 879
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 880
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 880
gcgctgtggt acagtaacca ttgggtg 27

<210> 881
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 881
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagt gtctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 882
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 882
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
            20                  25                  30


Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
        35                  40                  45


Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
    50                  55                  60


Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80


Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95


Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
            100                 105                 110


Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125


<210> 883
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 883
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1               5


<210> 884
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 884
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ttcacctttg acacatatgc catgaat 27

<210> 885
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 885
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 886
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 886
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 887
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 887
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 888
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 888
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 889
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 889
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggctgtggga ccaagctgac cgtccta 327

<210> 890
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 890
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Cys Gly Thr Lys Leu Thr Val Leu
100 105

<210> 891
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 891
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 892
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 892
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 893
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region CDR L2 amino acid sequence

<400> 893
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 894
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 894
ggcacagaca agcgcgctcc t 21

<210> 895
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 895
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 896
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 896
gcgctgtggt acagtaacca ttgggtg 27

<210> 897
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 897
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagt gtctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 898
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 898
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 899
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 899
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 900
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 900
ttcacctttg acacatatgc catgaat 27

<210> 901
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 901
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 902
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 902
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 903
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 903
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 904
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 904
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 905
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 905
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggctgtggga ccaagctgac cgtccta 327

<210> 906
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 906
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Cys Gly Thr Lys Leu Thr Val Leu
100 105

<210> 907
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 907
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 908
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 908
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 909
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 909
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 910
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 910
ggcacagaca agcgcgctcc t 21

<210> 911
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 911
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 912
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 912
gcgctgtggt acagtaacca ttgggtg 27

<210> 913
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 913
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagt gtctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 914
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 914
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 915
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 915
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 916
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 916
ttcacctttg acacatatgc catgaat 27

<210> 917
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 917
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 918
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 918
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 919
<211> 16

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 919
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 920
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 920
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 921
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 921
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggctgtggga ccaagctgac cgtccta 327

<210> 922
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 922
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Cys Gly Thr Lys Leu Thr Val Leu
100 105

<210> 923
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 923
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 924
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 924
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 925
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 925
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 926
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 926
ggcacagaca agcgcgctcc t 21

<210> 927
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 927
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 928
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 928
gcgctgtggt acagtaacca ttgggtg 27

<210> 929
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 929
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagt gtctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 930
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 930
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 931
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 931
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 932
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 932
ttcacctttg acacatatgc catgaat 27

<210> 933
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 933
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 934
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 934
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 935
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 935
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 936
<211> 48
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 936
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 937
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 937
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggctgtggga ccaagctgac cgtccta 327

<210> 938
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 938
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Cys Gly Thr Lys Leu Thr Val Leu
100 105

<210> 939
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 939
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 940
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 940
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 941
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 941
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 942
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 942
ggcacagaca agcgcgctcc t 21

<210> 943
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 943
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 944
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 944
gcgctgtggt acagtaacca ttgggtg 27

<210> 945
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region nucleic acid sequence

<400> 945
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagt gtctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 946
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 946
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 947
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 947
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 948
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 948
ttcacctttg acacatatgc catgaat 27

<210> 949
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 949
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 950
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 950
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 951
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 951
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 952
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 952
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 953
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 953
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatctct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggctgtggga ccaagctgac cgtccta 327

<210> 954
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 954
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Leu Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Cys Gly Thr Lys Leu Thr Val Leu
100 105

<210> 955
<211> 14

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 955
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 956
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 956
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 957
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 957
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 958
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 958
ggcacagaca agcgcgctcc t 21

<210> 959
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 959
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 960
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 960
gcgctgtggt acagtaacca ttgggtg 27

<210> 961
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 961
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagt gtctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 962
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 962

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
            20                  25                  30


Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
        35                  40                  45


Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
    50                  55                  60


Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80


Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95


Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
            100                 105                 110


Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125
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<210> 963
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 963

Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 964
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 964
ttcacctttg acacatatgc catgaat 27

<210> 965
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 965
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 966
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 966
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 967
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 967
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 968
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 968
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 969
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 969
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggctgtggga ccaagctgac cgtccta 327

<210> 970
<211> 109
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 970
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Cys Gly Thr Lys Leu Thr Val Leu
100 105

<210> 971
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 971
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 972
<211> 42
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 972
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 973
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 973
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 974
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 974
ggcacagaca agcgcgctcc t 21

<210> 975
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 975
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 976
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 976
gcgctgtggt acagtaacca ttgggtg 27

<210> 977
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 977
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagt gtctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 978
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 978
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 979
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 979
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 980
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 980
ttcacctttg acacatatgc catgaat 27

<210> 981

<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 981
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 982
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 982
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 983
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 983
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 984
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 984
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 985
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 985
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggctgtggga ccaagctgac cgtccta 327

<210> 986
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 986
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Cys Gly Thr Lys Leu Thr Val Leu
100 105

<210> 987
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 987
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 988
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 988
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 989
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 989
Gly Thr Asp Lys Arg Ala Pro

1 5

<210> 990
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 990
ggcacagaca agcgcgctcc t 21

<210> 991
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 991
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 992
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 992
gcgctgtggt acagtaacca ttgggtg 27

<210> 993
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 993
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagt gtctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 994
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 994
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 995
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 995
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1   5

<210> 996
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 996
ttcacctttg acacatatgc catgaat   27

<210> 997
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H2 amino acid sequence

<400> 997
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1   5   10   15

Val Lys Asp

<210> 998

<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 998
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 999
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 999
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1000
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1000
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 1001
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1001
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggctgtggga ccaagctgac cgtccta 327

<210> 1002
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1002
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Cys Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1003
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1003
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1004
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1004
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1005
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1005
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1006
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1006
ggcacagaca agcgcgctcc t 21

<210> 1007
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1007
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 1008
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1008
gcgctgtggt acagtaacca ttgggtg 27

<210> 1009
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1009
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagt gtctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1010
<211> 125

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1010
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1011
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1011
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1012
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1012
ttcacctttg acacatatgc catgaat 27

<210> 1013
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1013
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1014
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1014
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 1015
<211> 16
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1015
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1016
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1016
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 1017
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1017
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggctgtggga ccaagctgac cgtccta 327

<210> 1018
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1018
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
            20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
        35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
    50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
                85 90 95

His Trp Val Phe Gly Cys Gly Thr Lys Leu Thr Val Leu
            100 105

<210> 1019
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 1019
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1020
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 1020
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1021
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1021
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1022
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1022
ggcacagaca agcgcgctcc t 21

<210> 1023
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1023
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 1024
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1024
gcgctgtggt acagtaacca ttgggtg 27

<210> 1025
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1025
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggggat gtctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1026
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1026
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Gly Cys Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
    50   55   60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65   70   75   80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85   90   95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
            100   105   110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 1027
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 1027
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1   5

<210> 1028
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1028
ttcacctttg acacatatgc catgaat   27

<210> 1029
<211> 19
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1029
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1030
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1030
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 1031
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1031
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1032
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1032

gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 1033
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1033
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggctgtggga ccaagctgac cgtccta 327

<210> 1034
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1034
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Cys Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1035
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1035
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1036
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1036
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1037
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1037
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1038
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1038
ggcacagaca agcgcgctcc t 21

<210> 1039
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1039
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 1040
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1040
gcgctgtggt acagtaacca ttgggtg 27

<210> 1041
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1041
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccaggggat gtctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1042
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1042
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Gly Cys Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 1043
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 1043
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1   5

<210> 1044
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1044
ttcacctttg acacatatgc catgaat   27

<210> 1045
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H2 amino acid sequence

<400> 1045
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1   5   10   15

Val Lys Asp

<210> 1046
<211> 57
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1046
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 1047
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1047
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1048
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1048
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 1049
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1049
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cttgatctct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggctgtggga ccaagctgac cgtccta 327

<210> 1050
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1050
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Leu Asp Leu Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Cys Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1051
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1051
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1052
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1052
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1053
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1053
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1054
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1054
ggcacagaca agcgcgctcc t 21

<210> 1055
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1055
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 1056
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1056
gcgctgtggt acagtaacca ttgggtg 27

<210> 1057
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1057
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tccagggtgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1058
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1058
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gln Gly Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1059
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1059
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1060
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1060
ttcacctttg acacatatgc catgaac 27

<210> 1061
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1061
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1062
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1062
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 1063
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1063
Val Arg His Gly Asn Phe Gln Gly Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1064
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1064
gtcaggcacg gtaacttcca gggtggttac gtatcctggt ttgctcat 48

<210> 1065
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1065
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1066
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1066

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Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1               5                   10                  15


Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
            20                  25                  30


Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
        35                  40                  45


Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65                  70                  75                  80


Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
                85                  90                  95


His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105


<210> 1067
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 1067
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1               5                   10


<210> 1068
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 1068
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ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1069
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1069
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1070
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1070
ggcacagaca agcgcgctcc t 21

<210> 1071
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1071
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 1072
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1072
gcgctgtggt acagtaacca ttgggtg 27

<210> 1073
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1073
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggggggg ttacgtatcc tggtttgctt ggtggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1074
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1074
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Gly Gly Tyr Val Ser Trp Phe
100 105 110

Ala Trp Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1075
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1075
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1076
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1076
ttcacctttg acacatatgc catgaac 27

<210> 1077
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1077
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1078
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1078
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 1079
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1079
Val Arg His Gly Asn Phe Gly Gly Gly Tyr Val Ser Trp Phe Ala Trp
1 5 10 15

<210> 1080
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1080
gtcaggcacg gtaacttcgg gggggttac gtatcctggt ttgcttgg 48

<210> 1081
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1081
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1082
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1082
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1083
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1083
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1084
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1084
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1085
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1085
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1086

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1086
ggcacagaca agcgcgctcc t 21

<210> 1087
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1087
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 1088
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1088
gcgctgtggt acagtaacca ttgggtg 27

<210> 1089
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1089
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacgcgaact tcggggcggg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1090
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1090
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Ala Asn Phe Gly Ala Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1091
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1091
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1092
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1092
ttcacctttg acacatatgc catgaac 27

<210> 1093
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1093
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1094
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1094
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 1095
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1095
Val Arg His Ala Asn Phe Gly Ala Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1096
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1096
gtcaggcacg cgaacttcgg ggcgggttac gtatcctggt ttgctcat 48

<210> 1097
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1097
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1098
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1098
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1099
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1099
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1100
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1100
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1101
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1101
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1102
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1102
ggcacagaca agcgcgctcc t 21

<210> 1103
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1103
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 1104
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1104
gcgctgtggt acagtaacca ttgggtg 27

<210> 1105
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1105
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcggggaagg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1106
<211> 125
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1106
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Glu Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1107
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1107
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1108
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1108
ttcacctttg acacatatgc catgaac 27

<210> 1109
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1109
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1110
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1110
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 1111
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1111

Val Arg His Gly Asn Phe Gly Glu Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1112
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1112
gtcaggcacg gtaacttcgg ggaaggttac gtatcctggt ttgctcat 48

<210> 1113
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1113
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1114
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1114
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
            20   25   30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
        35   40   45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
    50   55   60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65   70   75   80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
                85   90   95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105

<210> 1115
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 1115
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1   5   10

<210> 1116
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 1116
ggatcaagca ctggcgcagt cactactagt aactacgcca ac   42

<210> 1117
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1117
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1118
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1118
ggcacagaca agcgcgctcc t 21

<210> 1119
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1119
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 1120
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1120

gcgctgtggt acagtaacca ttgggtg 27

<210> 1121
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1121
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacgataact tcggggctgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1122
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1122
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Asp Asn Phe Gly Ala Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1123
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1123
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1124
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1124
ttcacctttg acacatatgc catgaac 27

<210> 1125
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region CDR H2 amino acid sequence

<400> 1125
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1126
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1126
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 1127
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1127
Val Arg His Asp Asn Phe Gly Ala Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1128
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1128
gtcaggcacg ataacttcgg ggctggttac gtatcctggt ttgctcat 48

<210> 1129

<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1129
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1130
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1130
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1131
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1131
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1132
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1132
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1133
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1133
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1134
<211> 21
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1134
ggcacagaca agcgcgctcc t 21

<210> 1135
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1135
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 1136
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1136
gcgctgtggt acagtaacca ttgggtg 27

<210> 1137
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1137
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcggggttgg ttacgtatcc tggtttgctt cttggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1138
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1138
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Val Gly Tyr Val Ser Trp Phe
100 105 110

Ala Ser Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1139
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1139
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1140
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1140
ttcacctttg acacatatgc catgaac 27

<210> 1141
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1141
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1142
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1142
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 1143
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1143
Val Arg His Gly Asn Phe Gly Val Gly Tyr Val Ser Trp Phe Ala Ser
1 5 10 15

<210> 1144
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1144
gtcaggcacg gtaacttcgg ggttggttac gtatcctggt ttgcttct 48

<210> 1145
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1145
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1146
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1146
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1147
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1147

Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1148
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1148
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1149
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1149
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1150
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1150
ggcacagaca agcgcgctcc t 21

<210> 1151
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1151
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 1152
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1152
gcgctgtggt acagtaacca ttgggtg 27

<210> 1153
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1153
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacga ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcggggaagg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1154
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1154
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
            20   25   30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ala Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp
    50   55   60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65   70   75   80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85   90   95

Tyr Cys Val Arg His Gly Asn Phe Gly Glu Gly Tyr Val Ser Trp Phe
            100   105   110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 1155
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 1155
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1   5

<210> 1156
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1156
ttcacctttg acacatatgc catgaac 27

<210> 1157
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1157
Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1158
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1158
aggattagat ccaagtataa cgattacgct acatactacg cagactccgt gaaggat 57

<210> 1159
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1159
Val Arg His Gly Asn Phe Gly Glu Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1160
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1160
gtcaggcacg gtaacttcgg ggaaggttac gtatcctggt ttgctcat 48

<210> 1161
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1161
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1162
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1162
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

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Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
            20                  25                  30


Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
        35                  40                  45


Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65                  70                  75                  80


Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
                85                  90                  95


His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105


<210> 1163
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 1163
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1               5                   10


<210> 1164
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 1164
ggatcaagca ctggcgcagt cactactagt aactacgcca ac                          42


<210> 1165
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<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1165
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1166
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1166
ggcacagaca agcgcgctcc t 21

<210> 1167
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1167
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 1168
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1168
gcgctgtggt acagtaacca ttgggtg 27

<210> 1169
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1169
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacga ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacgataact tcggggctgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1170
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1170
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Asp Asn Phe Gly Ala Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1171
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1171
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1172
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1172
ttcacctttg acacatatgc catgaac 27

<210> 1173
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1173
Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1174
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1174
aggattagat ccaagtataa cgattacgct acatactacg cagactccgt gaaggat 57

<210> 1175
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1175
Val Arg His Asp Asn Phe Gly Ala Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1176
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1176
gtcaggcacg ataacttcgg ggctggttac gtatcctggt ttgctcat 48

<210> 1177
<211> 327
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1177
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1178
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1178
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1179
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1179
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1180
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1180
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1181
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1181
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1182
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1182
ggcacagaca agcgcgctcc t 21

<210> 1183
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1183
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 1184
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1184
gcgctgtggt acagtaacca ttgggtg 27

<210> 1185
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1185
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacga ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcggggttgg ttacgtatcc tggtttgctt cttggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1186
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1186
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Val Gly Tyr Val Ser Trp Phe
100 105 110

Ala Ser Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1187
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1187
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1188
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1188
ttcacctttg acacatatgc catgaac 27

<210> 1189
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1189
Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1190
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1190
aggattagat ccaagtataa cgattacgct acatactacg cagactccgt gaaggat 57

<210> 1191
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1191
Val Arg His Gly Asn Phe Gly Val Gly Tyr Val Ser Trp Phe Ala Ser
1 5 10 15

<210> 1192
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1192
gtcaggcacg gtaacttcgg ggttggttac gtatcctggt ttgcttct 48

<210> 1193
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1193
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1194
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1194
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1195
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1195
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1196
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1196
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1197
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1197
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1198
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1198
ggcacagaca agcgcgctcc t 21

<210> 1199
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1199

Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 1200
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1200
gcgctgtggt acagtaacca ttgggtg 27

<210> 1201
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1201
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacga ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggggtgc ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1202
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1202

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
            20                  25                  30


Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ala Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp
    50                  55                  60


Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80


Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95


Tyr Cys Val Arg His Gly Asn Phe Gly Gly Ala Tyr Val Ser Trp Phe
            100                 105                 110


Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125


<210> 1203
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 1203
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1               5


<210> 1204
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
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<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1204
ttcacctttg acacatatgc catgaac 27

<210> 1205
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1205
Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1206
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1206
aggattagat ccaagtataa cgattacgct acatactacg cagactccgt gaaggat 57

<210> 1207
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1207
Val Arg His Gly Asn Phe Gly Gly Ala Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1208
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1208
gtcaggcacg gtaacttcgg gggtgcttac gtatcctggt ttgctcat 48

<210> 1209
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1209
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1210
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1210
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1211
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1211
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1212
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1212
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1213
<211> 7
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1213
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1214
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1214
ggcacagaca agcgcgctcc t 21

<210> 1215
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1215
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 1216
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1216
gcgctgtggt acagtaacca ttgggtg 27

<210> 1217

<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1217
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac gcttatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacga ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggggggg ttacgtatcc tggtttgggc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1218
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1218
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Ala Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Gly Gly Tyr Val Ser Trp Phe
100 105 110

Gly His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1219
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1219
Phe Thr Phe Asp Ala Tyr Ala Met Asn
1 5

<210> 1220
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1220
ttcacctttg acgcttatgc catgaac 27

<210> 1221
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1221
Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp Ser

1 5 10 15

Val Lys Asp

<210> 1222
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1222
aggattagat ccaagtataa cgattacgct acatactacg cagactccgt gaaggat 57

<210> 1223
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1223
Val Arg His Gly Asn Phe Gly Gly Gly Tyr Val Ser Trp Phe Gly His
1 5 10 15

<210> 1224
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1224
gtcaggcacg gtaacttcgg ggggggttac gtatcctggt ttgggcat 48

<210> 1225
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1225
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1226
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1226
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1227
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1227
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1228
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1228
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1229
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1229
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1230
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region CDR L2 nucleic acid sequence

<400> 1230
ggcacagaca agcgcgctcc t 21

<210> 1231
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1231
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 1232
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1232
gcgctgtggt acagtaacca ttgggtg 27

<210> 1233
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1233
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac gcttatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacga ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacta tgctgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1234
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1234
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Ala Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Tyr Ala Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1235
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1235
Phe Thr Phe Asp Ala Tyr Ala Met Asn
1 5

<210> 1236
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1236
ttcacctttg acgcttatgc catgaac 27

<210> 1237
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1237
Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1238
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1238
aggattagat ccaagtataa cgattacgct acatactacg cagactccgt gaaggat 57

<210> 1239
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1239
Val Arg His Gly Asn Phe Gly Asn Tyr Ala Val Ser Trp Phe Ala His
1 5 10 15

<210> 1240
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1240
gtcaggcacg gtaacttcgg gaactatgct gtatcctggt ttgctcat 48

<210> 1241
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1241
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1242
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1242
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1243
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1243
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1244
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1244
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1245
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1245
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1246
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1246
ggcacagaca agcgcgctcc t 21

<210> 1247
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1247
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 1248
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1248
gcgctgtggt acagtaacca ttgggtg 27

<210> 1249
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1249
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tccagggtgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1250
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1250
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gln Gly Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1251
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1251
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1252
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1252
ttcacctttg acacatatgc catgaac 27

<210> 1253
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1253
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1254
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1254
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 1255
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1255
Val Arg His Gly Asn Phe Gln Gly Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1256
<211> 48

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1256
gtcaggcacg gtaacttcca gggtggttac gtatcctggt ttgctcat 48

<210> 1257
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1257
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1258
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1258
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1259
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1259
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1260
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1260
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1261
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1261
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1262
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1262
ggcacagaca agcgcgctcc t 21

<210> 1263
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1263
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 1264
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1264
gcgctgtggt acagtaacct ttgggtg 27

<210> 1265
<211> 375
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1265
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacgcgaact tcggggcggg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1266
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1266
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Ala Asn Phe Gly Ala Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1267
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1267
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1268
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1268
ttcacctttg acacatatgc catgaac 27

<210> 1269
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1269
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1270
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1270
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 1271
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1271
Val Arg His Ala Asn Phe Gly Ala Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1272
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1272
gtcaggcacg cgaacttcgg ggcgggttac gtatcctggt ttgctcat 48

<210> 1273
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region nucleic acid sequence

<400> 1273
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1274
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1274
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1275
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1275
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1276
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1276
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1277
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1277
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1278
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1278
ggcacagaca agcgcgctcc t 21

<210> 1279
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1279
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 1280
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1280
gcgctgtggt acagtaacct ttgggtg 27

<210> 1281
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1281
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcggggaagg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1282
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1282
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Glu Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1283
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1283
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1284
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1284
ttcacctttg acacatatgc catgaac 27

<210> 1285
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1285
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1286
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1286
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 1287
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1287
Val Arg His Gly Asn Phe Gly Glu Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1288
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1288
gtcaggcacg gtaacttcgg ggaaggttac gtatcctggt ttgctcat 48

<210> 1289
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1289
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1290
<211> 109

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1290
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1291
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1291
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1292
<211> 42

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1292
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1293
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1293
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1294
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1294
ggcacagaca agcgcgctcc t 21

<210> 1295
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1295
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 1296
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1296
gcgctgtggt acagtaacct ttgggtg 27

<210> 1297
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1297
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacgataact tcggggctgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1298
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1298
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
            20                  25                  30


Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
    50                  55                  60


Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80


Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95


Tyr Cys Val Arg His Asp Asn Phe Gly Ala Gly Tyr Val Ser Trp Phe
            100                 105                 110


Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125


<210> 1299
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 1299
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1               5


<210> 1300
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1300
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ttcacctttg acacatatgc catgaac 27

<210> 1301
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1301
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1302
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1302
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 1303
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1303
Val Arg His Asp Asn Phe Gly Ala Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1304
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1304
gtcaggcacg ataacttcgg ggctggttac gtatcctggt ttgctcat 48

<210> 1305
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1305
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1306
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1306
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1307
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1307
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1308
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1308
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1309
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region CDR L2 amino acid sequence

<400> 1309
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1310
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1310
ggcacagaca agcgcgctcc t 21

<210> 1311
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1311
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 1312
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1312
gcgctgtggt acagtaacct ttgggtg 27

<210> 1313
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1313
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggggtgc ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1314
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1314
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Gly Ala Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1315
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1315
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1316
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1316
ttcacctttg acacatatgc catgaac 27

<210> 1317
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1317
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1318
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1318
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 1319
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1319
Val Arg His Gly Asn Phe Gly Gly Ala Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1320
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1320
gtcaggcacg gtaacttcgg gggtgcttac gtatcctggt ttgctcat 48

<210> 1321
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1321
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1322
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1322
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1323
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1323
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1324
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1324
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1325
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1325
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1326
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1326
ggcacagaca agcgcgctcc t 21

<210> 1327
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1327
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 1328
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1328
gcgctgtggt acagtaacct ttgggtg 27

<210> 1329
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1329
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacga ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

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gtcaccgtct cctca 375

<210> 1330
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1330
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Glu Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1331
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1331
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1332
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1332
ttcacctttg acacatatgc catgaac 27

<210> 1333
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1333
Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1334
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1334
aggattagat ccaagtataa cgattacgct acatactacg cagactccgt gaaggat 57

<210> 1335
<211> 16

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1335
Val Arg His Gly Asn Phe Gly Glu Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1336
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1336
gtcaggcacg gtaacttcgg ggaaggttac gtatcctggt ttgctcat 48

<210> 1337
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1337
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1338
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1338
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1339
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1339
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1340
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1340
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1341
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1341
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1342
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1342
ggcacagaca agcgcgctcc t 21

<210> 1343
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1343
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 1344
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1344
gcgctgtggt acagtaacct ttgggtg 27

<210> 1345
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1345
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacga ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacgataact tcggggctgg ttacgtatca tggtttgctc attggggcca aggaaccctg 360

gtcaccgtat cctca 375

<210> 1346
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1346
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Asp Asn Phe Gly Ala Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1347
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1347
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1348
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1348
ttcacctttg acacatatgc catgaac 27

<210> 1349
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1349
Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1350
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1350
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<210> 1351
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1351
Val Arg His Asp Asn Phe Gly Ala Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1352
<211> 48
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1352
gtcaggcacg ataacttcgg ggctggttac gtatcatggt ttgctcat 48

<210> 1353
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1353
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acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

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ggcggaggga ccaagctgac cgtccta 327

<210> 1354
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1354
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1355
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1355
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1356
<211> 42
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1356
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1357
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1357
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1358
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1358
ggcacagaca agcgcgctcc t 21

<210> 1359
<211> 9
<212> PRT
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<220>
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Light chain variable region CDR L3 amino acid sequence

<400> 1359
Ala Leu Trp Tyr Ser Asn Leu Trp Val
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<210> 1360
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1360
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<210> 1361
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region nucleic acid sequence

<400> 1361
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tcctgtgcag cctctggatt cacctttgac acatatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacga ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

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gtcaccgtct cctca 375

<210> 1362
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1362
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Val Gly Tyr Val Ser Trp Phe
100 105 110

Ala Ser Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1363
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1363
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1364
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1364
ttcacctttg acacatatgc catgaac 27

<210> 1365
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1365
Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1366
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1366
aggattagat ccaagtataa cgattacgct acatactacg cagactccgt gaaggat 57

<210> 1367
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1367
Val Arg His Gly Asn Phe Gly Val Gly Tyr Val Ser Trp Phe Ala Ser
1 5 10 15

<210> 1368
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1368
gtcaggcacg gtaacttcgg ggttggttac gtatcctggt ttgcttct 48

<210> 1369
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1369
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acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

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ggcggaggga ccaagctgac cgtccta 327

<210> 1370
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1370
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1371
<211> 14

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1371
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1372
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1372
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1373
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1373
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1374
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1374
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<210> 1375
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1375
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 1376
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1376
gcgctgtggt acagtaacct ttgggtg 27

<210> 1377
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1377
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tcctgtgcag cctctggatt cacctttgac acatatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacga ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

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gtcaccgtct cctca 375

<210> 1378
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1378

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
            20                  25                  30


Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ala Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp
    50                  55                  60


Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80


Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95


Tyr Cys Val Arg His Gly Asn Phe Gly Gly Ala Tyr Val Ser Trp Phe
            100                 105                 110


Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125
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<210> 1379
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1379

Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1380
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1380
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<210> 1381
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1381
Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1382
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1382
aggattagat ccaagtataa cgattacgct acatactacg cagactccgt gaaggat 57

<210> 1383
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1383
Val Arg His Gly Asn Phe Gly Gly Ala Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1384
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1384
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<210> 1385
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1385
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acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

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ggcggaggga ccaagctgac cgtccta 327

<210> 1386
<211> 109
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1386
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1387
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1387
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1388
<211> 42
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1388
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<210> 1389
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1389
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1390
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1390
ggcacagaca agcgcgctcc t 21

<210> 1391
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1391
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 1392
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1392
gcgctgtggt acagtaacct ttgggtg 27

<210> 1393
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

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tcctgtgcag cctctggatt cacctttgac gcttatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacga ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

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gtcaccgtct cctca 375

<210> 1394
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1394
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Ala Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Gly Gly Tyr Val Ser Trp Phe
100 105 110

Gly His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1395
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1395
Phe Thr Phe Asp Ala Tyr Ala Met Asn
1 5

<210> 1396
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1396
ttcacctttg acgcttatgc catgaac 27

<210> 1397

<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1397
Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1398
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1398
aggattagat ccaagtataa cgattacgct acatactacg cagactccgt gaaggat 57

<210> 1399
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1399
Val Arg His Gly Asn Phe Gly Gly Gly Tyr Val Ser Trp Phe Gly His
1 5 10 15

<210> 1400
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1400
gtcaggcacg gtaacttcgg ggggggttac gtatcctggt ttgggcat 48

<210> 1401
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1401
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accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

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ggcggaggga ccaagctgac cgtccta 327

<210> 1402
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1402
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1403
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1403
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1404
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1404
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1405
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1405
Gly Thr Asp Lys Arg Ala Pro

1 5

<210> 1406
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1406
ggcacagaca agcgcgctcc t 21

<210> 1407
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1407
Ala Leu Trp Tyr Ser Asn Leu Trp Val
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<210> 1408
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1408
gcgctgtggt acagtaacct ttgggtg 27

<210> 1409
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1409
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac gcttatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacga ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaacg tgggggGTGG ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1410
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1410
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Ala Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Val Gly Gly Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 1411
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 1411
Phe Thr Phe Asp Ala Tyr Ala Met Asn
1   5

<210> 1412
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1412
ttcacctttg acgcttatgc catgaac   27

<210> 1413
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H2 amino acid sequence

<400> 1413
Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp Ser
1   5   10   15

Val Lys Asp

<210> 1414

<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1414
aggattagat ccaagtataa cgattacgct acatactacg cagactccgt gaaggat 57

<210> 1415
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1415
Val Arg His Gly Asn Val Gly Gly Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1416
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1416
gtcaggcacg gtaacgtggg gggtggttac gtatcctggt ttgctcat 48

<210> 1417
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1417
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1418
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1418
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1419
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1419
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1420
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1420
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1421
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1421
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1422
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1422
ggcacagaca agcgcgctcc t 21

<210> 1423
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1423
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 1424
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1424
gcgctgtggt acagtaacct ttgggtg 27

<210> 1425
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1425
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac gcttatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacga ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacta tgctgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1426
<211> 125

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1426
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Ala Tyr
            20   25   30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ala Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp
    50   55   60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65   70   75   80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85   90   95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Tyr Ala Val Ser Trp Phe
            100   105   110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 1427
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1427
Phe Thr Phe Asp Ala Tyr Ala Met Asn
1   5

<210> 1428
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1428
ttcacctttg acgcttatgc catgaac 27

<210> 1429
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1429
Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1430
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1430
aggattagat ccaagtataa cgattacgct acatactacg cagactccgt gaaggat 57

<210> 1431
<211> 16
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1431
Val Arg His Gly Asn Phe Gly Asn Tyr Ala Val Ser Trp Phe Ala His
1 5 10 15

<210> 1432
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1432
gtcaggcacg gtaacttcgg gaactatgct gtatcctggt ttgctcat 48

<210> 1433
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1433
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1434
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1434
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
            20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
        35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
    50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
                85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100 105

<210> 1435
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 1435
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1436
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 1436
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1437
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1437
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1438
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1438
ggcacagaca agcgcgctcc t 21

<210> 1439
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1439
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 1440
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1440
gcgctgtggt acagtaacct ttgggtg 27

<210> 1441
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1441
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tccagggtgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1442
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1442
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
    50   55   60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65   70   75   80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85   90   95

Tyr Cys Val Arg His Gly Asn Phe Gln Gly Gly Tyr Val Ser Trp Phe
            100   105   110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 1443
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 1443
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1   5

<210> 1444
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1444
ttcacctttg acacatatgc catgaac   27

<210> 1445
<211> 19
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1445
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1446
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1446
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 1447
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1447
Val Arg His Gly Asn Phe Gln Gly Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1448
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1448

gtcaggcacg gtaacttcca gggtggttac gtatcctggt ttgctcat 48

<210> 1449
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1449
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtgatct gtgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1450
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1450
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asp
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1451
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1451
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1452
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1452
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1453
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1453
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1454
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1454
ggcacagaca agcgcgctcc t 21

<210> 1455
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1455
Ala Leu Trp Tyr Ser Asp Leu Trp Val
1 5

<210> 1456
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1456
gcgctgtggt acagtgatct gtgggtg 27

<210> 1457
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1457
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggggggg ttacgtatcc tggtttgctt ggtggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1458
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1458
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Gly Gly Tyr Val Ser Trp Phe
100 105 110

Ala Trp Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 1459
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 1459
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1   5

<210> 1460
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1460
ttcacctttg acacatatgc catgaac   27

<210> 1461
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H2 amino acid sequence

<400> 1461
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1   5   10   15

Val Lys Asp

<210> 1462
<211> 57
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1462
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 1463
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1463
Val Arg His Gly Asn Phe Gly Gly Gly Tyr Val Ser Trp Phe Ala Trp
1 5 10 15

<210> 1464
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1464
gtcaggcacg gtaacttcgg gggggttac gtatcctggt ttgcttgg 48

<210> 1465
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1465
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtgatct gtgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1466
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1466
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asp
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1467
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1467
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1468
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1468
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1469
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1469
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1470
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1470
ggcacagaca agcgcgctcc t 21

<210> 1471
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1471
Ala Leu Trp Tyr Ser Asp Leu Trp Val
1 5

<210> 1472
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1472
gcgctgtggt acagtgatct gtgggtg 27

<210> 1473
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1473
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacgcgaact tcggggcggg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1474
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1474
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Ala Asn Phe Gly Ala Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1475
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1475
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1476
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1476
ttcacctttg acacatatgc catgaac 27

<210> 1477
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1477
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1478
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1478
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 1479
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1479
Val Arg His Ala Asn Phe Gly Ala Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1480
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1480
gtcaggcacg cgaacttcgg ggcgggttac gtatcctggt ttgctcat 48

<210> 1481
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1481
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtgatct gtgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1482
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1482

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Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1               5                   10                  15


Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
            20                  25                  30


Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
        35                  40                  45


Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65                  70                  75                  80


Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asp
                85                  90                  95


Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105


<210> 1483
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 1483
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1               5                   10


<210> 1484
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 1484
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ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1485
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1485
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1486
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1486
ggcacagaca agcgcgctcc t 21

<210> 1487
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1487
Ala Leu Trp Tyr Ser Asp Leu Trp Val
1 5

<210> 1488
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1488
gcgctgtggt acagtgatct gtgggtg 27

<210> 1489
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1489
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcggggaagg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1490
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1490
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Glu Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1491
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1491
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1492
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1492
ttcacctttg acacatatgc catgaac 27

<210> 1493
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1493
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1494
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1494
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 1495
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1495
Val Arg His Gly Asn Phe Gly Glu Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1496
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1496
gtcaggcacg gtaacttcgg ggaaggttac gtatcctggt ttgctcat 48

<210> 1497
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1497
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtgatct gtgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1498
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1498
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asp
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1499
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1499
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1500
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1500
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1501
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1501
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1502

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1502
ggcacagaca agcgcgctcc t 21

<210> 1503
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1503
Ala Leu Trp Tyr Ser Asp Leu Trp Val
1 5

<210> 1504
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1504
gcgctgtggt acagtgatct gtgggtg 27

<210> 1505
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1505
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacgataact tcggggctgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1506
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1506
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Asp Asn Phe Gly Ala Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1507
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1507
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1508
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1508
ttcacctttg acacatatgc catgaac 27

<210> 1509
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1509
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1510
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1510
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 1511
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1511
Val Arg His Asp Asn Phe Gly Ala Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1512
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1512
gtcaggcacg ataacttcgg ggctggttac gtatcctggt ttgctcat 48

<210> 1513
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1513
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtgatct gtgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1514
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1514
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asp
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1515
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1515
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1516
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1516
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1517
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1517
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1518
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1518
ggcacagaca agcgcgctcc t 21

<210> 1519
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1519
Ala Leu Trp Tyr Ser Asp Leu Trp Val
1 5

<210> 1520
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1520
gcgctgtggt acagtgatct gtgggtg 27

<210> 1521
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1521
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcggggttgg ttacgtatcc tggtttgctt cttggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1522
<211> 125
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1522
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Val Gly Tyr Val Ser Trp Phe
100 105 110

Ala Ser Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1523
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1523
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1524
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1524
ttcacctttg acacatatgc catgaac 27

<210> 1525
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1525
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1526
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1526
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 1527
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1527

Val Arg His Gly Asn Phe Gly Val Gly Tyr Val Ser Trp Phe Ala Ser
1 5 10 15

<210> 1528
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1528
gtcaggcacg gtaacttcgg ggttggttac gtatcctggt ttgcttct 48

<210> 1529
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1529
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtgatct gtgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1530
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1530
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
            20   25   30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
        35   40   45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
    50   55   60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65   70   75   80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asp
                85   90   95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105

<210> 1531
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 1531
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1   5   10

<210> 1532
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 1532
ggatcaagca ctggcgcagt cactactagt aactacgcca ac   42

<210> 1533
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1533
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1534
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1534
ggcacagaca agcgcgctcc t 21

<210> 1535
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1535
Ala Leu Trp Tyr Ser Asp Leu Trp Val
1 5

<210> 1536
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1536

gcgctgtggt acagtgatct gtgggtg 27

<210> 1537
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1537
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggggtgc ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1538
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1538
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Gly Ala Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1539
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1539
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1540
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1540
ttcacctttg acacatatgc catgaac 27

<210> 1541
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region CDR H2 amino acid sequence

<400> 1541
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1542
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1542
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 1543
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1543
Val Arg His Gly Asn Phe Gly Gly Ala Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1544
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1544
gtcaggcacg gtaacttcgg gggtgcttac gtatcctggt ttgctcat 48

<210> 1545

<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1545
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtgatct gtgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1546
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1546
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asp
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1547
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1547
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1548
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1548
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1549
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1549
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1550
<211> 21
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1550
ggcacagaca agcgcgctcc t 21

<210> 1551
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1551
Ala Leu Trp Tyr Ser Asp Leu Trp Val
1 5

<210> 1552
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1552
gcgctgtggt acagtgatct gtgggtg 27

<210> 1553
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1553
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacga ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcggggaagg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1554
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1554
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Glu Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1555
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1555
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1556
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1556
ttcacctttg acacatatgc catgaac 27

<210> 1557
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1557
Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1558
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1558
aggattagat ccaagtataa cgattacgct acatactacg cagactccgt gaaggat 57

<210> 1559
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1559
Val Arg His Gly Asn Phe Gly Glu Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1560
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1560
gtcaggcacg gtaacttcgg ggaaggttac gtatcctggt ttgctcat 48

<210> 1561
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1561
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtgatct gtgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1562
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1562
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asp
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1563
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1563

Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1564
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1564
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1565
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1565
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1566
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1566
ggcacagaca agcgcgctcc t 21

<210> 1567
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1567
Ala Leu Trp Tyr Ser Asp Leu Trp Val
1 5

<210> 1568
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1568
gcgctgtggt acagtgatct gtgggtg 27

<210> 1569
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1569
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacga ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacgataact tcggggctgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1570
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1570
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Asp Asn Phe Gly Ala Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1571
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1571
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1572
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1572
ttcacctttg acacatatgc catgaac 27

<210> 1573
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1573
Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1574
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1574
aggattagat ccaagtataa cgattacgct acatactacg cagactccgt gaaggat 57

<210> 1575
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1575
Val Arg His Asp Asn Phe Gly Ala Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1576
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1576
gtcaggcacg ataacttcgg ggctggttac gtatcctggt ttgctcat 48

<210> 1577
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1577
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtgatct gtgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1578
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1578
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

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Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
            20                  25                  30


Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
        35                  40                  45


Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65                  70                  75                  80


Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asp
                85                  90                  95


Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105


<210> 1579
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 1579
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1               5                   10


<210> 1580
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 1580
ggatcaagca ctggcgcagt cactactagt aactacgcca ac                          42


<210> 1581
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<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1581
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1582
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1582
ggcacagaca agcgcgctcc t 21

<210> 1583
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1583
Ala Leu Trp Tyr Ser Asp Leu Trp Val
1 5

<210> 1584
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1584
gcgctgtggt acagtgatct gtgggtg 27

<210> 1585
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1585
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacga ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcggggttgg ttacgtatcc tggtttgctt cttggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1586
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1586
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Val Gly Tyr Val Ser Trp Phe
100 105 110

Ala Ser Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1587
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1587
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1588
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1588
ttcacctttg acacatatgc catgaac 27

<210> 1589
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1589
Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1590
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1590
aggattagat ccaagtataa cgattacgct acatactacg cagactccgt gaaggat 57

<210> 1591
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1591
Val Arg His Gly Asn Phe Gly Val Gly Tyr Val Ser Trp Phe Ala Ser
1 5 10 15

<210> 1592
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1592
gtcaggcacg gtaacttcgg ggttggttac gtatcctggt ttgcttct 48

<210> 1593
<211> 327
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1593
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtgatct gtgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1594
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1594
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asp
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1595
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1595
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1596
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1596
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1597
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1597
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1598
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1598
ggcacagaca agcgcgctcc t 21

<210> 1599
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1599
Ala Leu Trp Tyr Ser Asp Leu Trp Val
1 5

<210> 1600
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1600
gcgctgtggt acagtgatct gtgggtg 27

<210> 1601
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1601
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacga ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggggtgc ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1602
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1602
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Gly Ala Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1603
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1603
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1604
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1604
ttcacctttg acacatatgc catgaac 27

<210> 1605
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1605
Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1606
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1606
aggattagat ccaagtataa cgattacgct acatactacg cagactccgt gaaggat 57

<210> 1607
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1607
Val Arg His Gly Asn Phe Gly Gly Ala Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1608
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1608
gtcaggcacg gtaacttcgg gggtgcttac gtatcctggt ttgctcat 48

<210> 1609
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1609
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtgatct gtgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1610
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1610
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asp
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1611
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1611
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1612
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1612
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1613
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1613
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1614
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1614
ggcacagaca agcgcgctcc t 21

<210> 1615
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1615

Ala Leu Trp Tyr Ser Asp Leu Trp Val
1 5

<210> 1616
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1616
gcgctgtggt acagtgatct gtgggtg 27

<210> 1617
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1617
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac gcttatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacga ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggggggg ttacgtatcc tggtttgggc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1618
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1618

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Ala Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Gly Gly Tyr Val Ser Trp Phe
100 105 110

Gly His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1619
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1619
Phe Thr Phe Asp Ala Tyr Ala Met Asn
1 5

<210> 1620
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1620
ttcacctttg acgcttatgc catgaac 27

<210> 1621
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1621
Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1622
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1622
aggattagat ccaagtataa cgattacgct acatactacg cagactccgt gaaggat 57

<210> 1623
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1623
Val Arg His Gly Asn Phe Gly Gly Gly Tyr Val Ser Trp Phe Gly His
1 5 10 15

<210> 1624
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1624
gtcaggcacg gtaacttcgg gggggttac gtatcctggt ttgggcat 48

<210> 1625
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1625
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtgatct gtgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1626
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1626
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asp
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1627
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1627
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1628
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1628
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1629
<211> 7
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1629
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1630
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1630
ggcacagaca agcgcgctcc t 21

<210> 1631
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1631
Ala Leu Trp Tyr Ser Asp Leu Trp Val
1 5

<210> 1632
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1632
gcgctgtggt acagtgatct gtgggtg 27

<210> 1633

<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1633
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac gcttatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacga ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaacg tgggggtgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1634
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1634
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Ala Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Val Gly Gly Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1635
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1635
Phe Thr Phe Asp Ala Tyr Ala Met Asn
1 5

<210> 1636
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1636
ttcacctttg acgcttatgc catgaac 27

<210> 1637
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1637
Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp Ser

1 5 10 15

Val Lys Asp

<210> 1638
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1638
aggattagat ccaagtataa cgattacgct acatactacg cagactccgt gaaggat 57

<210> 1639
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1639
Val Arg His Gly Asn Val Gly Gly Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1640
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1640
gtcaggcacg gtaacgtggg gggtggttac gtatcctggt ttgctcat 48

<210> 1641
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1641
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtgatct gtgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1642
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1642
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asp
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1643
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1643
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1644
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1644
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1645
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1645
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1646
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region CDR L2 nucleic acid sequence

<400> 1646
ggcacagaca agcgcgctcc t 21

<210> 1647
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1647
Ala Leu Trp Tyr Ser Asp Leu Trp Val
1 5

<210> 1648
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1648
gcgctgtggt acagtgatct gtgggtg 27

<210> 1649
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1649
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac gcttatgcca tgaactgggt gcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacga ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacta tgctgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1650
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1650
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Ala Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Tyr Ala Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1651
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1651
Phe Thr Phe Asp Ala Tyr Ala Met Asn
1 5

<210> 1652
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1652
ttcacctttg acgcttatgc catgaac 27

<210> 1653
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1653
Arg Ile Arg Ser Lys Tyr Asn Asp Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1654
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1654
aggattagat ccaagtataa cgattacgct acatactacg cagactccgt gaaggat 57

<210> 1655
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1655
Val Arg His Gly Asn Phe Gly Asn Tyr Ala Val Ser Trp Phe Ala His
1 5 10 15

<210> 1656
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1656
gtcaggcacg gtaacttcgg gaactatgct gtatcctggt ttgctcat 48

<210> 1657
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1657
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtgatct gtgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1658
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1658
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asp
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1659
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1659
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1660
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1660
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1661
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1661
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1662
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1662
ggcacagaca agcgcgctcc t 21

<210> 1663
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1663
Ala Leu Trp Tyr Ser Asp Leu Trp Val
1 5

<210> 1664
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1664
gcgctgtggt acagtgatct gtgggtg 27

<210> 1665
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1665
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1666
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1666
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1667
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1667
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1668
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1668
ttcacctttg acacatatgc catgaat 27

<210> 1669
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1669
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1670
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1670
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 1671
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1671
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1672
<211> 48

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1672
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 1673
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1673
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcatcat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1674
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1674
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Ile Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1675
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1675
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1676
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1676
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1677
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1677
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1678
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1678
ggcacagaca agcgcgctcc t 21

<210> 1679
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1679
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 1680
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1680
gcgctgtggt acagtaacct ttgggtg 27

<210> 1681
<211> 375
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1681
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1682
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1682
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1683
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1683
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1684
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1684
ttcacctttg acacatatgc catgaat 27

<210> 1685
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1685
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1686
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1686
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 1687
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1687
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1688
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1688
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 1689
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region nucleic acid sequence

<400> 1689
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcatcat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1690
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1690
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Ile Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1691
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1691
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1692
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1692
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1693
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1693
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1694
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1694
ggcacagaca agcgcgctcc t 21

<210> 1695
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1695
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 1696
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1696
gcgctgtggt acagtaacct ttgggtg 27

<210> 1697
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1697
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1698
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1698
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1699
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1699
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1700
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1700
ttcacctttg acacatatgc catgaat 27

<210> 1701
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1701
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1702
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1702
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 1703
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1703
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1704
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1704
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 1705
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1705
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcatcat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gtgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1706
<211> 109

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1706
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Ile Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1707
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1707
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1708
<211> 42

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1708
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1709
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1709
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1710
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1710
ggcacagaca agcgcgctcc t 21

<210> 1711
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1711
Val Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 1712
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1712
gtgctgtggt acagtaacct ttgggtg 27

<210> 1713
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1713
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1714
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1714
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
            20                  25                  30


Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
    50                  55                  60


Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80


Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95


Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
            100                 105                 110


Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125


<210> 1715
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 1715
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1               5


<210> 1716
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1716
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ttcacctttg acacatatgc catgaat 27

<210> 1717
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1717
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1718
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1718
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 1719
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1719
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1720
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1720
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 1721
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1721
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggtc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1722
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1722
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Val
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1723
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1723
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1724
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1724
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1725
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region CDR L2 amino acid sequence

<400> 1725
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1726
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1726
ggcacagaca agcgcgctcc t 21

<210> 1727
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1727
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 1728
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1728
gcgctgtggt acagtaacct ttgggtg 27

<210> 1729
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1729
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1730
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1730
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1731
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1731
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1732
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1732
ttcacctttg acacatatgc catgaat 27

<210> 1733
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1733
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1734
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1734
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 1735
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1735
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1736
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1736
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 1737
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1737
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcgctgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccacg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggtc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1738
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1738
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Ala Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Val
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1739
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1739
Gly Ser Ser Ala Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1740
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1740
ggatcaagcg ctggcgcagt cactactagt aactacgcca ac 42

<210> 1741
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1741
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1742
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1742
ggcacagaca agcgcgctcc t 21

<210> 1743
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1743
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 1744
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1744
gcgctgtggt acagtaacct ttgggtg 27

<210> 1745
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1745
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1746
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1746
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1747
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1747
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1748
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1748
ttcacctttg acacatatgc catgaat 27

<210> 1749
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1749
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1750
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1750
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 1751
<211> 16

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1751
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1752
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1752
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 1753
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1753
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggtc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1754
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1754
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Val
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1755
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1755
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1756
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1756
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1757
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1757
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1758
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1758
ggcacagaca agcgcgctcc t 21

<210> 1759
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1759
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 1760
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1760
gcgctgtggt acagtaacct ttgggtg 27

<210> 1761
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1761
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1762
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1762
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1763
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1763
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1764
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1764
ttcacctttg acacatatgc catgaat 27

<210> 1765
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1765
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1766
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1766
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 1767
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1767
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1768
<211> 48
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1768
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 1769
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1769
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggtc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acaataacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1770
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1770
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Val
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Asn Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1771
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1771
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1772
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1772
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1773
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1773
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1774
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1774
ggcacagaca agcgcgctcc t 21

<210> 1775
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1775
Ala Leu Trp Tyr Asn Asn Leu Trp Val
1 5

<210> 1776
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1776
gcgctgtggt acaataacct ttgggtg 27

<210> 1777
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region nucleic acid sequence

<400> 1777
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1778
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1778
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1779
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1779
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1780
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1780
ttcacctttg acacatatgc catgaat 27

<210> 1781
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1781
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1782
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1782
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 1783
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1783
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1784
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1784
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 1785
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1785
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggtc 240

caggcagatg atgaagctga ttattactgt gtgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1786
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1786
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Val
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1787
<211> 14

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1787
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1788
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1788
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1789
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1789
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1790
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1790
ggcacagaca agcgcgctcc t 21

<210> 1791
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1791
Val Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 1792
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1792
gtgctgtggt acagtaacct ttgggtg 27

<210> 1793
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1793
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1794
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1794
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1795
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1795

Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1796
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1796
ttcacctttg acacatatgc catgaat 27

<210> 1797
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1797
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1798
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1798
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 1799
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1799
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1800
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1800
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 1801
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1801
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcgctgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccacg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1802
<211> 109
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1802
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Ala Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1803
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1803
Gly Ser Ser Ala Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1804
<211> 42
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1804
ggatcaagcg ctggcgcagt cactactagt aactacgcca ac 42

<210> 1805
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1805
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1806
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1806
ggcacagaca agcgcgctcc t 21

<210> 1807
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1807
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 1808
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1808
gcgctgtggt acagtaacct ttgggtg 27

<210> 1809
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1809
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1810
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1810
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1811
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1811
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1812
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1812
ttcacctttg acacatatgc catgaat 27

<210> 1813

<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1813
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 1814
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1814
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 1815
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1815
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1816
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1816
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 1817
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1817
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acaataacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1818
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1818
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Asn Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1819
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1819
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1820
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1820
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1821
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1821
Gly Thr Asp Lys Arg Ala Pro

1 5

<210> 1822
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1822
ggcacagaca agcgcgctcc t 21

<210> 1823
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1823
Ala Leu Trp Tyr Asn Asn Leu Trp Val
1 5

<210> 1824
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1824
gcgctgtggt acaataacct ttgggtg 27

<210> 1825
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1825
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1826
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1826
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 1827
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 1827
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1   5

<210> 1828
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1828
ttcacctttg acacatatgc catgaat   27

<210> 1829
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H2 amino acid sequence

<400> 1829
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1   5   10   15

Val Lys Asp

<210> 1830

<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1830
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 1831
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1831
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1832
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1832
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 1833
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1833
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gtgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1834
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1834
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1835
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1835
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1836
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1836
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1837
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1837
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1838
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1838
ggcacagaca agcgcgctcc t 21

<210> 1839
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1839
Val Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 1840
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1840
gtgctgtggt acagtaacct ttgggtg 27

<210> 1841
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1841
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa gggtcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aagtgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1842
<211> 125

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1842
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
            20   25   30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
    50   55   60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65   70   75   80

Leu Tyr Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85   90   95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
            100   105   110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 1843
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1843
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1   5

<210> 1844
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1844
ttcacctttg acacatatgc catgaat 27

<210> 1845
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1845
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Gly

<210> 1846
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1846
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaagggt 57

<210> 1847
<211> 16
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1847
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1848
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1848
gtcaggcacg gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 1849
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1849
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcatcat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1850
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1850
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
            20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
        35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
    50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Ile Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
                85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100 105

<210> 1851
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 1851
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1852
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 1852
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1853
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1853
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1854
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1854
ggcacagaca agcgcgctcc t 21

<210> 1855
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1855
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 1856
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1856
gcgctgtggt acagtaacct ttgggtg 27

<210> 1857
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1857
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa gggtcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aagtgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1858
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1858
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
    50   55   60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65   70   75   80

Leu Tyr Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85   90   95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
            100   105   110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 1859
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 1859
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1   5

<210> 1860
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1860
ttcacctttg acacatatgc catgaat   27

<210> 1861
<211> 19
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1861
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Gly

<210> 1862
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1862
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaagggt 57

<210> 1863
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1863
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1864
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1864

gtcaggcacg gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 1865
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1865
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcatcat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1866
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1866
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Ile Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1867
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1867
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1868
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1868
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1869
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1869
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1870
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1870
ggcacagaca agcgcgctcc t 21

<210> 1871
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1871
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 1872
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1872
gcgctgtggt acagtaacct ttgggtg 27

<210> 1873
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1873
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa gggtcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aagtgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1874
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1874
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 1875
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 1875
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1   5

<210> 1876
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1876
ttcacctttg acacatatgc catgaat   27

<210> 1877
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H2 amino acid sequence

<400> 1877
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1   5   10   15

Val Lys Gly

<210> 1878
<211> 57
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1878
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaagggt 57

<210> 1879
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1879
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1880
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1880
gtcaggcacg gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 1881
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1881
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcatcat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gtgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1882
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1882
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Ile Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1883
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1883
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1884
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1884
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1885
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1885
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1886
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1886
ggcacagaca agcgcgctcc t 21

<210> 1887
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1887
Val Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 1888
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1888
gtgctgtggt acagtaacct ttgggtg 27

<210> 1889
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1889
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa gggtcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aagtgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1890
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1890
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1891
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1891
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1892
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1892
ttcacctttg acacatatgc catgaat 27

<210> 1893
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1893
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Gly

<210> 1894
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1894
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaagggt 57

<210> 1895
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1895
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1896
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1896
gtcaggcacg gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 1897
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1897
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcatcat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1898
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1898

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Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1               5                   10                  15


Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
            20                  25                  30


Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
        35                  40                  45


Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Ile Ile Thr Gly Ala
65                  70                  75                  80


Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
                85                  90                  95


His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105


<210> 1899
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 1899
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1               5                   10


<210> 1900
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 1900
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ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1901
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1901
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1902
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1902
ggcacagaca agcgcgctcc t 21

<210> 1903
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1903
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 1904
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1904
gcgctgtggt acagtaacca ttgggtg 27

<210> 1905
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1905
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa gggtcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aagtgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1906
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1906
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1907
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1907
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1908
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1908
ttcacctttg acacatatgc catgaat 27

<210> 1909
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1909
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Gly

<210> 1910
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1910
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaagggt 57

<210> 1911
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1911
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1912
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1912
gtcaggcacg gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 1913
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1913
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggtc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1914
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1914
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Val
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1915
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1915
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1916
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1916
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1917
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1917
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1918

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1918
ggcacagaca agcgcgctcc t 21

<210> 1919
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1919
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 1920
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1920
gcgctgtggt acagtaacct ttgggtg 27

<210> 1921
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1921
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa gggtcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aagtgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1922
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1922
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1923
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1923
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1924
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1924
ttcacctttg acacatatgc catgaat 27

<210> 1925
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1925
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Gly

<210> 1926
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1926
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaagggt 57

<210> 1927
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1927
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1928
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1928
gtcaggcacg gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 1929
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1929
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggtc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1930
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1930
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Val
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1931
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1931
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1932
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1932
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1933
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1933
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1934
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1934
ggcacagaca agcgcgctcc t 21

<210> 1935
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1935
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 1936
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1936
gcgctgtggt acagtaacct ttgggtg 27

<210> 1937
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1937
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa gggtcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aagtgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1938
<211> 125
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1938
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1939
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1939
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1940
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1940
ttcacctttg acacatatgc catgaat 27

<210> 1941
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1941
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Gly

<210> 1942
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1942
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaagggt 57

<210> 1943
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1943

Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1944
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1944
gtcaggcacg gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 1945
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1945
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggtc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acaataacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1946
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1946
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

```
Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
            20                  25                  30


Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
        35                  40                  45


Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Val
65                  70                  75                  80


Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Asn Asn
                85                  90                  95


Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105


<210> 1947
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 1947
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1               5                   10


<210> 1948
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 1948
ggatcaagca ctggcgcagt cactactagt aactacgcca ac                          42
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<210> 1949
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1949
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1950
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1950
ggcacagaca agcgcgctcc t 21

<210> 1951
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1951
Ala Leu Trp Tyr Asn Asn Leu Trp Val
1 5

<210> 1952
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1952

gcgctgtggt acaataacct ttgggtg 27

<210> 1953
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1953
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa gggtcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aagtgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1954
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1954
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1955
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1955
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1956
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1956
ttcacctttg acacatatgc catgaat 27

<210> 1957
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region CDR H2 amino acid sequence

<400> 1957
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Gly

<210> 1958
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1958
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaagggt 57

<210> 1959
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1959
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1960
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1960
gtcaggcacg gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 1961

<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1961
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggtc 240

caggcagatg atgaagctga ttattactgt gtgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1962
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1962
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Val
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1963
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1963
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1964
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1964
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1965
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1965
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1966
<211> 21
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1966
ggcacagaca agcgcgctcc t 21

<210> 1967
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1967
Val Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 1968
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1968
gtgctgtggt acagtaacct ttgggtg 27

<210> 1969
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1969
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa gggtcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aagtgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1970
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1970
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 1971
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 1971
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 1972
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1972
ttcacctttg acacatatgc catgaat 27

<210> 1973
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1973
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Gly

<210> 1974
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1974
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaagggt 57

<210> 1975
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1975
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1976
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1976
gtcaggcacg gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 1977
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1977
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggtc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1978
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1978
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Val
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1979
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1979

Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1980
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1980
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 1981
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1981
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1982
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1982
ggcacagaca agcgcgctcc t 21

<210> 1983
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1983
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 1984
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 1984
gcgctgtggt acagtaacca ttgggtg 27

<210> 1985
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 1985
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa gggtcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aagtgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 1986
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 1986
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
            20   25   30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
    50   55   60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65   70   75   80

Leu Tyr Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85   90   95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
            100   105   110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 1987
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 1987
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1   5

<210> 1988
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 1988
ttcacctttg acacatatgc catgaat 27

<210> 1989
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 1989
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Gly

<210> 1990
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 1990
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaagggt 57

<210> 1991
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 1991
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 1992
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 1992
gtcaggcacg gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 1993
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 1993
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcgctgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccacg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 1994
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 1994
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Ala Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 1995
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 1995
Gly Ser Ser Ala Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 1996
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 1996
ggatcaagcg ctggcgcagt cactactagt aactacgcca ac 42

<210> 1997

<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 1997
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 1998
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 1998
ggcacagaca agcgcgctcc t 21

<210> 1999
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 1999
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 2000
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2000
gcgctgtggt acagtaacct ttgggtg 27

<210> 2001
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2001
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa gggtcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aagtgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2002
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2002
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2003
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2003
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2004
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2004
ttcacctttg acacatatgc catgaat 27

<210> 2005
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2005
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Gly

<210> 2006
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2006
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaagggt 57

<210> 2007
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2007
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2008
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2008
gtcaggcacg gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2009
<211> 327
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2009
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcgctgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccacg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gtgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2010
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2010
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Ala Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2011
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2011
Gly Ser Ser Ala Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2012
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2012
ggatcaagcg ctggcgcagt cactactagt aactacgcca ac 42

<210> 2013
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2013
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2014
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2014
ggcacagaca agcgcgctcc t 21

<210> 2015
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2015
Val Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 2016
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2016
gtgctgtggt acagtaacct ttgggtg 27

<210> 2017
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2017
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa gggtcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aagtgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2018
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2018
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2019
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2019
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2020
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2020
ttcacctttg acacatatgc catgaat 27

<210> 2021
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2021
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Gly

<210> 2022
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2022
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaagggt 57

<210> 2023
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2023
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2024
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2024
gtcaggcacg gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2025
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2025
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcgctgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccacg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2026
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2026
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Ala Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2027
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2027
Gly Ser Ser Ala Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2028
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2028
ggatcaagcg ctggcgcagt cactactagt aactacgcca ac 42

<210> 2029
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2029
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2030
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2030
ggcacagaca agcgcgctcc t 21

<210> 2031
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2031

Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 2032
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2032
gcgctgtggt acagtaacca ttgggtg 27

<210> 2033
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2033
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa gggtcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aagtgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2034
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2034

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
            20                  25                  30


Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
    50                  55                  60


Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80


Leu Tyr Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95


Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
            100                 105                 110


Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125


<210> 2035
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 2035
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1               5


<210> 2036
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
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<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2036
ttcacctttg acacatatgc catgaat 27

<210> 2037
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2037
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Gly

<210> 2038
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2038
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaagggt 57

<210> 2039
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2039
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2040
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2040
gtcaggcacg gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2041
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2041
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acaataacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2042
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2042
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Asn Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2043
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2043
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2044
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2044
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2045
<211> 7
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2045
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2046
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2046
ggcacagaca agcgcgctcc t 21

<210> 2047
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2047
Ala Leu Trp Tyr Asn Asn Leu Trp Val
1 5

<210> 2048
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2048
gcgctgtggt acaataacct ttgggtg 27

<210> 2049

<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2049
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa gggtcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aagtgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2050
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2050
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2051
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2051
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2052
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2052
ttcacctttg acacatatgc catgaat 27

<210> 2053
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2053
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser

1 5 10 15

Val Lys Gly

<210> 2054
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2054
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaagggt 57

<210> 2055
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2055
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2056
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2056
gtcaggcacg gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2057
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2057
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gtgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2058
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2058
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2059
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2059
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2060
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2060
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2061
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2061
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2062
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region CDR L2 nucleic acid sequence

<400> 2062
ggcacagaca agcgcgctcc t 21

<210> 2063
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2063
Val Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 2064
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2064
gtgctgtggt acagtaacct ttgggtg 27

<210> 2065
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2065
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc gccatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacagtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2066
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2066
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Ala Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2067
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2067
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2068
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2068
ttcacctttg acacatatgc catgaat 27

<210> 2069
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2069
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 2070
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2070
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 2071
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2071
Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2072
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2072
gtcaggcaca gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2073
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2073
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcatcat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2074
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2074
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Ile Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2075
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2075
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2076
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2076
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2077
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2077
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2078
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2078
ggcacagaca agcgcgctcc t 21

<210> 2079
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2079
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 2080
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2080
gcgctgtggt acagtaacct ttgggtg 27

<210> 2081
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2081
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc gccatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacagtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2082
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2082
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Ala Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2083
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2083
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2084
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2084
ttcacctttg acacatatgc catgaat 27

<210> 2085
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2085
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 2086
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2086
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 2087
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2087
Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2088
<211> 48

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2088
gtcaggcaca gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2089
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2089
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcatcat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2090
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2090
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Ile Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2091
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2091
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2092
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2092
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2093
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2093
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2094
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2094
ggcacagaca agcgcgctcc t 21

<210> 2095
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2095
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 2096
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2096
gcgctgtggt acagtaacct ttgggtg 27

<210> 2097
<211> 375
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2097
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc gccatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacagtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2098
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2098
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Ala Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2099
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2099
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2100
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2100
ttcacctttg acacatatgc catgaat 27

<210> 2101
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2101
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 2102
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2102
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 2103
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2103
Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2104
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2104
gtcaggcaca gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2105
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region nucleic acid sequence

<400> 2105
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcatcat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gtgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2106
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2106
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Ile Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2107
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2107
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2108
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2108
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2109
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2109
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2110
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2110
ggcacagaca agcgcgctcc t 21

<210> 2111
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2111
Val Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 2112
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2112
gtgctgtggt acagtaacct ttgggtg 27

<210> 2113
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2113
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc gccatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacagtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2114
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2114
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Ala Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2115
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2115
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2116
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2116
ttcacctttg acacatatgc catgaat 27

<210> 2117
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2117
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 2118
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2118
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 2119
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2119
Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2120
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2120
gtcaggcaca gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2121
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2121
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcatcat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2122
<211> 109

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2122
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Ile Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2123
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2123
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2124
<211> 42

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2124
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2125
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2125
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2126
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2126
ggcacagaca agcgcgctcc t 21

<210> 2127
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2127
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 2128
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2128
gcgctgtggt acagtaacca ttgggtg 27

<210> 2129
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2129
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc gccatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacagtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2130
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2130
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
            20                  25                  30


Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
    50                  55                  60


Ser Val Lys Asp Arg Phe Ala Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80


Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95


Tyr Cys Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
            100                 105                 110


Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125


<210> 2131
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 2131
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1               5


<210> 2132
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2132
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ttcacctttg acacatatgc catgaat 27

<210> 2133
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2133
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 2134
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2134
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 2135
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2135
Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2136
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2136
gtcaggcaca gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2137
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2137
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggtc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2138
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2138
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Val
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2139
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2139
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2140
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2140
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2141
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region CDR L2 amino acid sequence

<400> 2141
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2142
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2142
ggcacagaca agcgcgctcc t 21

<210> 2143
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2143
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 2144
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2144
gcgctgtggt acagtaacct ttgggtg 27

<210> 2145
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2145
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc gccatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacagtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2146
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2146
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Ala Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2147
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2147
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2148
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2148
ttcacctttg acacatatgc catgaat 27

<210> 2149
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2149
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 2150
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2150
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 2151
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2151
Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2152
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2152
gtcaggcaca gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2153
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2153
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcgctgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccacg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggtc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2154
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2154
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Ala Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Val
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2155
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2155
Gly Ser Ser Ala Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2156
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2156
ggatcaagcg ctggcgcagt cactactagt aactacgcca ac 42

<210> 2157
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2157
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2158
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2158
ggcacagaca agcgcgctcc t 21

<210> 2159
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2159
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 2160
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2160
gcgctgtggt acagtaacct ttgggtg 27

<210> 2161
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2161
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc gccatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacagtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2162
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2162
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Ala Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2163
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2163
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2164
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2164
ttcacctttg acacatatgc catgaat 27

<210> 2165
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2165
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 2166
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2166
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 2167
<211> 16

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2167
Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2168
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2168
gtcaggcaca gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2169
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2169
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggtc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2170
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2170
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Val
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2171
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2171
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2172
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2172
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2173
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2173
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2174
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2174
ggcacagaca agcgcgctcc t 21

<210> 2175
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2175
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 2176
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2176
gcgctgtggt acagtaacct ttgggtg 27

<210> 2177
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2177
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc gccatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacagtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2178
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2178
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Ala Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2179
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2179
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2180
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2180
ttcacctttg acacatatgc catgaat 27

<210> 2181
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2181
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 2182
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2182
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 2183
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2183
Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2184
<211> 48
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2184
gtcaggcaca gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2185
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2185
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggtc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acaataacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2186
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2186
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Val
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Asn Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2187
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2187
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2188
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2188
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2189
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2189
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2190
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2190
ggcacagaca agcgcgctcc t 21

<210> 2191
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2191
Ala Leu Trp Tyr Asn Asn Leu Trp Val
1 5

<210> 2192
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2192
gcgctgtggt acaataacct ttgggtg 27

<210> 2193
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region nucleic acid sequence

<400> 2193
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc gccatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacagtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2194
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2194
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Ala Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2195
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2195
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2196
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2196
ttcacctttg acacatatgc catgaat 27

<210> 2197
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2197
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 2198
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2198
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 2199
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2199
Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2200
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2200
gtcaggcaca gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2201
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2201
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggtc 240

caggcagatg atgaagctga ttattactgt gtgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2202
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2202
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Val
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2203
<211> 14

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2203
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2204
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2204
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2205
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2205
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2206
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2206
ggcacagaca agcgcgctcc t 21

<210> 2207
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2207
Val Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 2208
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2208
gtgctgtggt acagtaacct ttgggtg 27

<210> 2209
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2209
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc gccatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacagtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2210
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2210
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Ala Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2211
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2211

Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2212
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2212
ttcacctttg acacatatgc catgaat 27

<210> 2213
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2213
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 2214
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2214
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 2215
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2215
Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2216
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2216
gtcaggcaca gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2217
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2217
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggtc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2218
<211> 109
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2218
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Val
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2219
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2219
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2220
<211> 42
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2220
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2221
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2221
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2222
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2222
ggcacagaca agcgcgctcc t 21

<210> 2223
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2223
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 2224
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2224
gcgctgtggt acagtaacca ttgggtg 27

<210> 2225
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2225
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc gccatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacagtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2226
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2226
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Ala Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2227
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2227
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2228
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2228
ttcacctttg acacatatgc catgaat 27

<210> 2229

<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2229
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 2230
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2230
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 2231
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2231
Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2232
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2232
gtcaggcaca gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2233
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2233
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcgctgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccacg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2234
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2234
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Ala Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2235
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2235
Gly Ser Ser Ala Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2236
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2236
ggatcaagcg ctggcgcagt cactactagt aactacgcca ac 42

<210> 2237
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2237
Gly Thr Asp Lys Arg Ala Pro

1 5

<210> 2238
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2238
ggcacagaca agcgcgctcc t 21

<210> 2239
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2239
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 2240
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2240
gcgctgtggt acagtaacct ttgggtg 27

<210> 2241
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2241
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc gccatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacagtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2242
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2242
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Ala Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 2243
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 2243
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1   5

<210> 2244
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2244
ttcacctttg acacatatgc catgaat   27

<210> 2245
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H2 amino acid sequence

<400> 2245
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1   5   10   15

Val Lys Asp

<210> 2246

<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2246
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 2247
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2247
Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2248
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2248
gtcaggcaca gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2249
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2249
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acaataacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2250
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2250
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Asn Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2251
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2251
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2252
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2252
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2253
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2253
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2254
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2254
ggcacagaca agcgcgctcc t 21

<210> 2255
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2255
Ala Leu Trp Tyr Asn Asn Leu Trp Val
1 5

<210> 2256
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2256
gcgctgtggt acaataacct ttgggtg 27

<210> 2257
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2257
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc gccatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacagtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2258
<211> 125

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2258
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
            20   25   30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
    50   55   60

Ser Val Lys Asp Arg Phe Ala Ile Ser Arg Asp Asp Ser Lys Ser Thr
65   70   75   80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85   90   95

Tyr Cys Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
            100   105   110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 2259
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2259
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1   5

<210> 2260
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2260
ttcacctttg acacatatgc catgaat 27

<210> 2261
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2261
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 2262
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2262
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 2263
<211> 16
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2263
Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2264
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2264
gtcaggcaca gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2265
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2265
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gtgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2266
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2266
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
            20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
        35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
    50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
                85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100 105

<210> 2267
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 2267
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2268
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 2268
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2269
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2269
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2270
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2270
ggcacagaca agcgcgctcc t 21

<210> 2271
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2271
Val Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 2272
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2272
gtgctgtggt acagtaacct ttgggtg 27

<210> 2273
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2273
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc gccatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacagtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2274
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2274
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
    50   55   60

Ser Val Lys Asp Arg Phe Ala Ile Ser Arg Asp Asp Ser Lys Ser Thr
65   70   75   80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85   90   95

Tyr Cys Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
            100   105   110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 2275
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 2275
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1   5

<210> 2276
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2276
ttcacctttg acacatatgc catgaat   27

<210> 2277
<211> 19
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2277
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 2278
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2278
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 2279
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2279
Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2280
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2280

gtcaggcaca gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2281
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2281
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2282
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2282
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2283
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2283
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2284
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2284
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2285
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2285
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2286
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2286
ggcacagaca agcgcgctcc t 21

<210> 2287
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2287
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 2288
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2288
gcgctgtggt acagtaacca ttgggtg 27

<210> 2289
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2289
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2290
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2290
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2291
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2291
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2292
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2292
ttcacctttg acacatatgc catgaat 27

<210> 2293
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2293
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 2294
<211> 57
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2294
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 2295
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2295
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2296
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2296
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 2297
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2297
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcatcat cacgggggtc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2298
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2298
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Ile Ile Thr Gly Val
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2299
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2299
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2300
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2300
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2301
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2301
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2302
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2302
ggcacagaca agcgcgctcc t 21

<210> 2303
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2303
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 2304
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2304
gcgctgtggt acagtaacct ttgggtg 27

<210> 2305
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2305
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2306
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2306
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2307
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2307
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2308
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2308
ttcacctttg acacatatgc catgaat 27

<210> 2309
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2309
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 2310
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2310
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 2311
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2311
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2312
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2312
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 2313
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2313
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcatcat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acaataacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2314
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2314

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Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1               5                   10                  15


Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
            20                  25                  30


Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
        35                  40                  45


Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Ile Ile Thr Gly Ala
65                  70                  75                  80


Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Asn Asn
                85                  90                  95


Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105


<210> 2315
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 2315
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1               5                   10


<210> 2316
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 2316
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ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2317
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2317
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2318
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2318
ggcacagaca agcgcgctcc t 21

<210> 2319
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2319
Ala Leu Trp Tyr Asn Asn Leu Trp Val
1 5

<210> 2320
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2320
gcgctgtggt acaataacct ttgggtg 27

<210> 2321
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2321
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2322
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2322
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2323
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2323
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2324
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2324
ttcacctttg acacatatgc catgaat 27

<210> 2325
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2325
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 2326
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2326
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 2327
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2327
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2328
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2328
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 2329
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2329
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gtgctgtggt acaataacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2330
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2330
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Val Leu Trp Tyr Asn Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2331
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2331
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2332
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2332
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2333
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2333
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2334

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2334
ggcacagaca agcgcgctcc t 21

<210> 2335
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2335
Val Leu Trp Tyr Asn Asn Leu Trp Val
1 5

<210> 2336
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2336
gtgctgtggt acaataacct ttgggtg 27

<210> 2337
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2337
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa gggtcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aagtgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2338
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2338
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2339
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2339
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2340
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2340
ttcacctttg acacatatgc catgaat 27

<210> 2341
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2341
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Gly

<210> 2342
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2342
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaagggt 57

<210> 2343
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2343
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2344
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2344
gtcaggcacg gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2345
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2345
agacatgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcccag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcatcat cacgggggtc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2346
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2346
Arg His Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Pro Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Ile Ile Thr Gly Val
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2347
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2347
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2348
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2348
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2349
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2349
Gly Pro Asp Lys Arg Ala Pro
1 5

<210> 2350
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2350
ggcccagaca agcgcgctcc t 21

<210> 2351
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2351
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 2352
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2352
gcgctgtggt acagtaacct ttgggtg 27

<210> 2353
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2353
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc gccatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacagtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2354
<211> 125
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2354
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Ala Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2355
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2355
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2356
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2356
ttcacctttg acacatatgc catgaat 27

<210> 2357
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2357
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 2358
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2358
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 2359
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2359

Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2360
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2360
gtcaggcaca gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2361
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2361
agaactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gtgctgtggt acaataacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2362
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2362
Arg Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
            20   25   30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
        35   40   45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
    50   55   60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65   70   75   80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Val Leu Trp Tyr Asn Asn
                85   90   95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105

<210> 2363
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 2363
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1   5   10

<210> 2364
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 2364
ggatcaagca ctggcgcagt cactactagt aactacgcca ac   42

<210> 2365
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2365
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2366
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2366
ggcacagaca agcgcgctcc t 21

<210> 2367
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2367
Val Leu Trp Tyr Asn Asn Leu Trp Val
1 5

<210> 2368
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2368

gtgctgtggt acaataacct ttgggtg 27

<210> 2369
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2369
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa gggtcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aagtgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2370
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2370
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2371
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2371
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2372
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2372
ttcacctttg acacatatgc catgaat 27

<210> 2373
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region CDR H2 amino acid sequence

<400> 2373
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Gly

<210> 2374
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2374
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaagggt 57

<210> 2375
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2375
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2376
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2376
gtcaggcacg gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2377

<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2377
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcgctgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccacg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggtc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2378
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2378
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Ala Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Val
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2379
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2379
Gly Ser Ser Ala Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2380
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2380
ggatcaagcg ctggcgcagt cactactagt aactacgcca ac 42

<210> 2381
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2381
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2382
<211> 21
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2382
ggcacagaca agcgcgctcc t 21

<210> 2383
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2383
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 2384
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2384
gcgctgtggt acagtaacct ttgggtg 27

<210> 2385
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2385
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2386
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2386
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2387
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2387
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2388
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2388
ttcacctttg acacatatgc catgaat 27

<210> 2389
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2389
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 2390
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2390
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 2391
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2391
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2392
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2392
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 2393
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2393
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2394
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2394
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2395
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2395

Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2396
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2396
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2397
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2397
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2398
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2398
ggcacagaca agcgcgctcc t 21

<210> 2399
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2399
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 2400
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2400
gcgctgtggt acagtaacct ttgggtg 27

<210> 2401
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2401
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2402
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2402
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
            20   25   30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
    50   55   60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65   70   75   80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85   90   95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
            100   105   110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 2403
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 2403
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1   5

<210> 2404
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2404
ttcacctttg acacatatgc catgaat 27

<210> 2405
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2405
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 2406
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2406
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 2407
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2407
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2408
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2408
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 2409
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2409
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acaataacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2410
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2410
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

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Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
            20                  25                  30


Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
        35                  40                  45


Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65                  70                  75                  80


Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Asn Asn
                85                  90                  95


Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105


<210> 2411
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 2411
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1               5                   10


<210> 2412
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 2412
ggatcaagca ctggcgcagt cactactagt aactacgcca ac                          42


<210> 2413
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<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2413
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2414
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2414
ggcacagaca agcgcgctcc t 21

<210> 2415
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2415
Ala Leu Trp Tyr Asn Asn Leu Trp Val
1 5

<210> 2416
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2416
gcgctgtggt acaataacct ttgggtg 27

<210> 2417
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2417
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2418
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2418
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2419
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2419
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2420
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2420
ttcacctttg acacatatgc catgaat 27

<210> 2421
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2421
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 2422
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2422
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 2423
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2423
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2424
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2424
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 2425
<211> 327
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2425
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gtgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2426
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2426
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2427
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2427
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2428
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2428
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2429
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2429
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2430
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2430
ggcacagaca agcgcgctcc t 21

<210> 2431
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2431
Val Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 2432
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2432
gtgctgtggt acagtaacca ttgggtg 27

<210> 2433
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2433
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2434
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2434
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2435
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2435
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2436
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2436
ttcacctttg acacatatgc catgaat 27

<210> 2437
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2437
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 2438
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2438
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 2439
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2439
Val Arg His Gly Asn Phe Gly Asn Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2440
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2440
gtcaggcacg gtaacttcgg gaacggttac gtatcctggt ttgctcat 48

<210> 2441
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2441
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2442
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2442
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2443
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2443
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2444
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2444
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2445
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2445
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2446
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2446
ggcacagaca agcgcgctcc t 21

<210> 2447
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2447

Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 2448
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2448
gcgctgtggt acagtaacca ttgggtg 27

<210> 2449
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2449
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa gggtcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aagtgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2450
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2450

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
            20                  25                  30


Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
    50                  55                  60


Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80


Leu Tyr Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95


Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
            100                 105                 110


Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125


<210> 2451
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 2451
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1               5


<210> 2452
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
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<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2452
ttcacctttg acacatatgc catgaat 27

<210> 2453
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2453
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Gly

<210> 2454
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2454
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaagggt 57

<210> 2455
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2455
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2456
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2456
gtcaggcacg gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2457
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2457
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acaataacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2458
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2458
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Asn Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2459
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2459
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2460
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2460
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2461
<211> 7
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2461
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2462
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2462
ggcacagaca agcgcgctcc t 21

<210> 2463
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2463
Ala Leu Trp Tyr Asn Asn His Trp Val
1 5

<210> 2464
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2464
gcgctgtggt acaataacca ttgggtg 27

<210> 2465

<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2465
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa gggtcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aagtgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2466
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2466
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2467
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2467
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2468
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2468
ttcacctttg acacatatgc catgaat 27

<210> 2469
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2469
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser

1 5 10 15

Val Lys Gly

<210> 2470
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2470
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaagggt 57

<210> 2471
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2471
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2472
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2472
gtcaggcacg gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2473
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2473
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcgctgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccacg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcatcat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2474
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2474
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Ala Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Ile Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2475
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2475
Gly Ser Ser Ala Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2476
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2476
ggatcaagcg ctggcgcagt cactactagt aactacgcca ac 42

<210> 2477
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2477
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2478
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region CDR L2 nucleic acid sequence

<400> 2478
ggcacagaca agcgcgctcc t 21

<210> 2479
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2479
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 2480
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2480
gcgctgtggt acagtaacct ttgggtg 27

<210> 2481
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2481
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa gggtcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aagtgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2482
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2482
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2483
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2483
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2484
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2484
ttcacctttg acacatatgc catgaat 27

<210> 2485
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2485
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Gly

<210> 2486
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2486
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaagggt 57

<210> 2487
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2487
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2488
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2488
gtcaggcacg gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2489
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2489
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcatcat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acaataacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2490
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2490
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Ile Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Asn Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2491
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2491
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2492
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2492
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2493
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2493
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2494
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2494
ggcacagaca agcgcgctcc t 21

<210> 2495
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2495
Ala Leu Trp Tyr Asn Asn Leu Trp Val
1 5

<210> 2496
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2496
gcgctgtggt acaataacct ttgggtg 27

<210> 2497
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2497
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa gggtcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aagtgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2498
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2498
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2499
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2499
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2500
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2500
ttcacctttg acacatatgc catgaat 27

<210> 2501
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2501
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Gly

<210> 2502
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2502
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaagggt 57

<210> 2503
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2503
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2504
<211> 48

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2504
gtcaggcacg gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2505
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2505
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcgctgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccacg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2506
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2506
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Ala Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2507
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2507
Gly Ser Ser Ala Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2508
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2508
ggatcaagcg ctggcgcagt cactactagt aactacgcca ac 42

<210> 2509
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2509
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2510
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2510
ggcacagaca agcgcgctcc t 21

<210> 2511
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2511
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 2512
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2512
gcgctgtggt acagtaacct ttgggtg 27

<210> 2513
<211> 375
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2513
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa gggtcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aagtgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2514
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2514
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2515
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2515
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2516
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2516
ttcacctttg acacatatgc catgaat 27

<210> 2517
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2517
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Gly

<210> 2518
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2518
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaagggt 57

<210> 2519
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2519
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2520
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2520
gtcaggcacg gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2521
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region nucleic acid sequence

<400> 2521
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcgctgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccacg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acaataacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2522
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2522
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Ala Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Asn Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2523
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2523
Gly Ser Ser Ala Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2524
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2524
ggatcaagcg ctggcgcagt cactactagt aactacgcca ac 42

<210> 2525
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2525
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2526
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2526
ggcacagaca agcgcgctcc t 21

<210> 2527
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2527
Ala Leu Trp Tyr Asn Asn Leu Trp Val
1 5

<210> 2528
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2528
gcgctgtggt acaataacct ttgggtg 27

<210> 2529
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2529
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa gggtcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aagtgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2530
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2530
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2531
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2531
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2532
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2532
ttcacctttg acacatatgc catgaat 27

<210> 2533
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2533
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Gly

<210> 2534
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2534
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaagggt 57

<210> 2535
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2535
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2536
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2536
gtcaggcacg gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2537
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2537
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2538
<211> 109

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2538
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2539
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2539
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2540
<211> 42

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2540
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2541
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2541
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2542
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2542
ggcacagaca agcgcgctcc t 21

<210> 2543
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2543
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 2544
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2544
gcgctgtggt acagtaacct ttgggtg 27

<210> 2545
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2545
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa gggtcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aagtgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2546
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2546
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
            20                  25                  30


Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
    50                  55                  60


Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80


Leu Tyr Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95


Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
            100                 105                 110


Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125


<210> 2547
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 2547
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1               5


<210> 2548
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2548
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ttcacctttg acacatatgc catgaat 27

<210> 2549
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2549
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Gly

<210> 2550
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2550
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaagggt 57

<210> 2551
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2551
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2552
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2552
gtcaggcacg gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2553
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2553
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gtgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2554
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2554
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2555
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2555
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2556
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2556
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2557
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region CDR L2 amino acid sequence

<400> 2557
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2558
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2558
ggcacagaca agcgcgctcc t 21

<210> 2559
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2559
Val Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 2560
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2560
gtgctgtggt acagtaacct ttgggtg 27

<210> 2561
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2561
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa gggtcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aagtgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2562
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2562
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2563
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2563
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2564
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2564
ttcacctttg acacatatgc catgaat 27

<210> 2565
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2565
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Gly

<210> 2566
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2566
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaagggt 57

<210> 2567
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2567
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2568
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2568
gtcaggcacg gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2569
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2569
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2570
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2570
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2571
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2571
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2572
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2572
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2573
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2573
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2574
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2574
ggcacagaca agcgcgctcc t 21

<210> 2575
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2575
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 2576
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2576
gcgctgtggt acagtaacca ttgggtg 27

<210> 2577
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2577
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa gggtcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aagtgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2578
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2578
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2579
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2579
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2580
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2580
ttcacctttg acacatatgc catgaat 27

<210> 2581
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2581
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Gly

<210> 2582
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2582
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaagggt 57

<210> 2583
<211> 16

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2583
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2584
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2584
gtcaggcacg gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2585
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2585
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gtgctgtggt acaataacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2586
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2586
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Val Leu Trp Tyr Asn Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2587
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2587
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2588
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2588
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2589
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2589
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2590
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2590
ggcacagaca agcgcgctcc t 21

<210> 2591
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2591
Val Leu Trp Tyr Asn Asn Leu Trp Val
1 5

<210> 2592
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2592
gtgctgtggt acaataacct ttgggtg 27

<210> 2593
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2593
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa gggtcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aagtgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2594
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2594
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2595
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2595
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2596
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2596
ttcacctttg acacatatgc catgaat 27

<210> 2597
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2597
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Gly

<210> 2598
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2598
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaagggt 57

<210> 2599
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2599
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2600
<211> 48
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2600
gtcaggcacg gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2601
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2601
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gtgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2602
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2602
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2603
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2603
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2604
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2604
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2605
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2605
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2606
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2606
ggcacagaca agcgcgctcc t 21

<210> 2607
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2607
Val Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 2608
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2608
gtgctgtggt acagtaacca ttgggtg 27

<210> 2609
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region nucleic acid sequence

<400> 2609
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa gggtcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aagtgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2610
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2610
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Val Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2611
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2611
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2612
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2612
ttcacctttg acacatatgc catgaat 27

<210> 2613
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2613
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Gly

<210> 2614
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2614
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaagggt 57

<210> 2615
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2615
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2616
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2616
gtcaggcacg gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2617
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2617
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2618
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2618
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2619
<211> 14

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2619
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2620
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2620
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2621
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2621
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2622
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2622
ggcacagaca agcgcgctcc t 21

<210> 2623
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2623
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 2624
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2624
gcgctgtggt acagtaacca ttgggtg 27

<210> 2625
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2625
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc gccatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacagtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2626
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2626
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Ala Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2627
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2627

Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2628
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2628
ttcacctttg acacatatgc catgaat 27

<210> 2629
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2629
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 2630
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2630
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 2631
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2631
Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2632
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2632
gtcaggcaca gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2633
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2633
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcatcat cacgggggtc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2634
<211> 109
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2634
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Ile Ile Thr Gly Val
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2635
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2635
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2636
<211> 42
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2636
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2637
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2637
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2638
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2638
ggcacagaca agcgcgctcc t 21

<210> 2639
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2639
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 2640
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2640
gcgctgtggt acagtaacct ttgggtg 27

<210> 2641
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2641
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc gccatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacagtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2642
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2642
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Ala Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2643
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2643
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2644
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2644
ttcacctttg acacatatgc catgaat 27

<210> 2645

<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2645
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 2646
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2646
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 2647
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2647
Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2648
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2648
gtcaggcaca gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2649
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2649
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcatcat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acaataacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2650
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2650
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Ile Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Asn Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2651
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2651
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2652
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2652
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2653
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2653
Gly Thr Asp Lys Arg Ala Pro

1 5

<210> 2654
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2654
ggcacagaca agcgcgctcc t 21

<210> 2655
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2655
Ala Leu Trp Tyr Asn Asn Leu Trp Val
1 5

<210> 2656
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2656
gcgctgtggt acaataacct ttgggtg 27

<210> 2657
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2657
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc gccatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacagtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2658
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2658
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Ala Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 2659
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 2659
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1   5

<210> 2660
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2660
ttcacctttg acacatatgc catgaat   27

<210> 2661
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H2 amino acid sequence

<400> 2661
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1   5   10   15

Val Lys Asp

<210> 2662

<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2662
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 2663
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2663
Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2664
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2664
gtcaggcaca gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2665
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2665
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcgctgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccacg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2666
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2666
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Ala Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2667
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2667
Gly Ser Ser Ala Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2668
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2668
ggatcaagcg ctggcgcagt cactactagt aactacgcca ac 42

<210> 2669
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2669
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2670
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2670
ggcacagaca agcgcgctcc t 21

<210> 2671
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2671
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 2672
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2672
gcgctgtggt acagtaacct ttgggtg 27

<210> 2673
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2673
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc gccatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacagtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2674
<211> 125

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2674
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
            20   25   30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
    50   55   60

Ser Val Lys Asp Arg Phe Ala Ile Ser Arg Asp Asp Ser Lys Ser Thr
65   70   75   80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85   90   95

Tyr Cys Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
            100   105   110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 2675
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2675
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1   5

<210> 2676
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2676
ttcacctttg acacatatgc catgaat 27

<210> 2677
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2677
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 2678
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2678
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 2679
<211> 16
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2679
Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2680
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2680
gtcaggcaca gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2681
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2681
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2682
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2682
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
            20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
        35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
    50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
                85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100 105

<210> 2683
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 2683
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2684
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 2684
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2685
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2685
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2686
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2686
ggcacagaca agcgcgctcc t 21

<210> 2687
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2687
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 2688
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2688
gcgctgtggt acagtaacct ttgggtg 27

<210> 2689
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2689
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc gccatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacagtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2690
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2690
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
    50   55   60

Ser Val Lys Asp Arg Phe Ala Ile Ser Arg Asp Asp Ser Lys Ser Thr
65   70   75   80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85   90   95

Tyr Cys Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
            100   105   110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 2691
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 2691
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1   5

<210> 2692
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2692
ttcacctttg acacatatgc catgaat   27

<210> 2693
<211> 19
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2693
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 2694
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2694
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 2695
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2695
Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2696
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2696

gtcaggcaca gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2697
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2697
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acaataacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2698
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2698
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Asn Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2699
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2699
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2700
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2700
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2701
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2701
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2702
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2702
ggcacagaca agcgcgctcc t 21

<210> 2703
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2703
Ala Leu Trp Tyr Asn Asn Leu Trp Val
1 5

<210> 2704
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2704
gcgctgtggt acaataacct ttgggtg 27

<210> 2705
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2705
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc gccatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacagtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2706
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2706
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Ala Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2707
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2707
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2708
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2708
ttcacctttg acacatatgc catgaat 27

<210> 2709
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2709
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 2710
<211> 57
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2710
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 2711
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2711
Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2712
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2712
gtcaggcaca gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2713
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2713
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gtgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2714
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2714
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2715
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2715
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2716
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2716
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2717
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2717
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2718
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2718
ggcacagaca agcgcgctcc t 21

<210> 2719
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2719
Val Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 2720
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2720
gtgctgtggt acagtaacct ttgggtg 27

<210> 2721
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2721
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc gccatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacagtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2722
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2722
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Ala Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2723
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2723
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2724
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2724
ttcacctttg acacatatgc catgaat 27

<210> 2725
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2725
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 2726
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2726
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 2727
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2727
Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2728
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2728
gtcaggcaca gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2729
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2729
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2730
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2730

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Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1               5                   10                  15


Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
            20                  25                  30


Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
        35                  40                  45


Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65                  70                  75                  80


Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
                85                  90                  95


His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105


<210> 2731
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 2731
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1               5                   10


<210> 2732
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 2732
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ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2733
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2733
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2734
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2734
ggcacagaca agcgcgctcc t 21

<210> 2735
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2735
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 2736
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2736
gcgctgtggt acagtaacca ttgggtg 27

<210> 2737
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2737
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc gccatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacagtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 2738
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2738
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Ala Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 2739
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2739
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 2740
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2740
ttcacctttg acacatatgc catgaat 27

<210> 2741
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2741
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 2742
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2742
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 2743
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2743
Val Arg His Ser Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 2744
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2744
gtcaggcaca gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 2745
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2745
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gtgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 2746
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2746
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 2747
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2747
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 2748
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2748
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 2749
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2749
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 2750

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2750
ggcacagaca agcgcgctcc t 21

<210> 2751
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2751
Val Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 2752
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2752
gtgctgtggt acagtaacca ttgggtg 27

<210> 2753
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2753
caggtacagc tgcagcagtc aggacctgag ctggtgaagc ctggggcttc agtgaggata 60

tcctgcaagg cttctggcta caccttcata agctactata tacactgggt gaagcagagg 120

cctggacagg gacttgagtg gattggatgg atttatcctg gaaatgttaa tactaagtac 180

aatgagaagt tcaaggccaa ggccacactg actgcagaca aatcctccag cacagcctac 240

atgcagctca gcagtctgac ctctgaggac tctgcggtct atttctgtgc aagagatgat 300

aactactcct ttgcttactg gggccaaggc aaccacggtc accgtctcct c 351

<210> 2754
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2754
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Arg Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ile Ser Tyr
20 25 30

Tyr Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Ala Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Asp Asp Asn Tyr Ser Phe Ala Tyr Trp Gly Gln Gly Asn His
100 105 110

Gly His Arg Leu Leu
115

<210> 2755
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2755
Tyr Thr Phe Ile Ser Tyr Tyr Ile His
1 5

<210> 2756
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2756
tacaccttca taagctacta tatacac 27

<210> 2757
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2757
Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Ala

<210> 2758
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2758
tggatttatc ctggaaatgt taatactaag tacaatgaga agttcaaggc c 51

<210> 2759
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2759
Ala Arg Asp Asp Asn Tyr Ser Phe Ala Tyr
1 5 10

<210> 2760
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2760
gcaagagatg ataactactc ctttgcttac 30

<210> 2761
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2761
gacatcgtga tgatccagtc tccatcctcc ctggctgtgt cagcaggaga gaaggtcact 60

atgagctgca aatccagtca gagtctgctc aacagtagaa cccgaaagaa ctacttggct 120

tggtaccagc agaaaccagg gcagtctcct aaactgctga tctactgggc atccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg ggacagattt cactctcacc 240

atcagcagtg tgcaggctga agacctggca gtttattact gcaagcaatc ttataatctt 300

cggacgttcg gtggagggac caagctggaa ataaaa 336

<210> 2762
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2762
Asp Ile Val Met Ile Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 2763
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2763

Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 2764
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2764
aaatccagtc agagtctgct caacagtaga acccgaaaga actacttggc t 51

<210> 2765
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2765
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 2766
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2766
tgggcatcca ctagggaatc t 21

<210> 2767
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2767
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 2768
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2768
aagcaatctt ataatcttcg gacg 24

<210> 2769
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2769
gaagtacagc tgcagcagtc tggacctgac ctggtgaagc ctggggcttc agtgaagatg 60

tcctgcaagg cttctggcta cgccttcaca agctactata tacactgggt gaagcagagg 120

cctggacagg gacttgagtg gattggatgg atttatcttg gagatggtag tactaactac 180

aatgagaagt tcaagggcaa gaccacactg actgcagaca aatcctccag cacagcctac 240

atgttgctca gcagcctgac ctctgaggac tctgcgacct atttctgtgc aagggatgat 300

tcgtactact ttgactactg gggccaaggc accacggtca ccgtctcctc a 351

<210> 2770
<211> 117
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2770
Glu Val Gln Leu Gln Gln Ser Gly Pro Asp Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Leu Gly Asp Gly Ser Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Leu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Thr Tyr Phe Cys
85 90 95

Ala Arg Asp Asp Ser Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

<210> 2771
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2771
Tyr Ala Phe Thr Ser Tyr Tyr Ile His
1 5

<210> 2772
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2772
tacgccttca caagctacta tatacac 27

<210> 2773
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2773
Trp Ile Tyr Leu Gly Asp Gly Ser Thr Asn Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 2774
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2774
tggatttatc ttggagatgg tagtactaac tacaatgaga agttcaaggg c 51

<210> 2775
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2775

Ala Arg Asp Asp Ser Tyr Tyr Phe Asp Tyr
1 5 10

<210> 2776
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2776
gcaagggatg attcgtacta ctttgactac 30

<210> 2777
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2777
gacattcagc tcactcagtc tccatcctcc ctggctgtgt cagcaggaga gaaggtcact 60

atgagctgca aatccagtca gagtctgctc aacagtagaa cccgaaagaa ctacttggct 120

tggtaccaac agaaaccagg gcagtctcct aaactgctga tctactgggc atccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg ggacagattt cactctcacc 240

atcagcagtg tgcaggctga agacctggca gtttattact gcaagcaatc ttatagtctt 300

cggacgttcg gtggagggac caagctggaa atcaaa 336

<210> 2778
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2778
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
            20   25   30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Lys Gln
                85   90   95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105   110

<210> 2779
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 2779
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1   5   10   15

Ala

<210> 2780
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 2780
aaatccagtc agagtctgct caacagtaga acccgaaaga actacttggc t 51

<210> 2781
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2781
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 2782
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2782
tgggcatcca ctagggaatc t 21

<210> 2783
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2783
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 2784
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2784
aagcaatctt atagtcttcg gacg 24

<210> 2785
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2785
caggtgaagc tggaggagtc aggacctgag ctggtgaagc ctggggcttc agtgaggata 60

tcctgcaagg cttctggcta caccttcaca cgctactata tacactgggt gaagcagagg 120

cctggacagg gacttgagtg gattggatgg atttatcctg gaaatgttaa tactaaatac 180

aatgagaagt tcaagggcaa ggccacactg tctgcagaca aatcctccag cacagcctac 240

atgcagctca gcagcctgac ctctgaggac tctgcggtct atttctgtgc aagagatggt 300

gattactact ttgactactg gggccaaggc accacggtca ccgtctcctc a 351

<210> 2786
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2786
Gln Val Lys Leu Glu Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Arg Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
20 25 30

Tyr Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Ser Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Asp Gly Asp Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

<210> 2787
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2787
Tyr Thr Phe Thr Arg Tyr Tyr Ile His
1 5

<210> 2788
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2788
tacaccttca cacgctacta tatacac 27

<210> 2789
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2789
Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 2790
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2790
tggatttatc ctggaaatgt taatactaaa tacaatgaga agttcaaggg c 51

<210> 2791
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2791
Ala Arg Asp Gly Asp Tyr Tyr Phe Asp Tyr
1 5 10

<210> 2792
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2792
gcaagagatg gtgattacta ctttgactac 30

<210> 2793
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2793
gacattcagc tcactcagtc tccatcctcc ctggctgtgt cagcaggaga gaaggtcact 60

atgagctgca aatccagtca gagtctgctc aacagtagaa cccgaaagaa ctacttggct 120

tggtaccagc agaaaccagg gcagtctcct aaactgctga tctactgggc atccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg ggacagattt cactctcacc 240

atcagcagtg tgcaggctga agacctggca gtttattact gcaagcaatc ttataatctt 300

cggacgttcg gtggaggcac caagctggaa atcaaa 336

<210> 2794
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2794
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 2795
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2795
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 2796
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2796
aaatccagtc agagtctgct caacagtaga acccgaaaga actacttggc t 51

<210> 2797
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2797
Trp Ala Ser Thr Arg Glu Ser

1 5

<210> 2798
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2798
tgggcatcca ctagggaatc t 21

<210> 2799
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2799
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 2800
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2800
aagcaatctt ataatcttcg gacg 24

<210> 2801
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2801
gaggtgcagc tgcaggagtc tggacctgag ctggtgaaac ctggggcttc agtgaggata 60

tcctgcaagg cttctggcta caccttcaca agctactata tacactgggt gaagcagagg 120

cctggacagg gacttgagtg gattggatgg atttatcctg gaaatgttaa tactaagtac 180

aatgagaagt tcaagggcaa ggccacactg actgcagaca aatcctccag cacagcctac 240

atgcagctca gcagcctgac ctctgaggac tctgcggtct atttctgtgc aagagatggt 300

gattactact ttgactactg gggccaaggc accacggtca ccgtctcctc a 351

<210> 2802
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2802
Glu Val Gln Leu Gln Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Arg Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Asp Gly Asp Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
        115

<210> 2803
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 2803
Tyr Thr Phe Thr Ser Tyr Tyr Ile His
1   5

<210> 2804
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2804
tacaccttca caagctacta tatacac   27

<210> 2805
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H2 amino acid sequence

<400> 2805
Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe Lys
1   5   10   15

Gly

<210> 2806
<211> 51
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2806
tggatttatc ctggaaatgt taatactaag tacaatgaga agttcaaggg c 51

<210> 2807
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2807
Ala Arg Asp Gly Asp Tyr Tyr Phe Asp Tyr
1 5 10

<210> 2808
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2808
gcaagagatg gtgattacta ctttgactac 30

<210> 2809
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2809
gacattcagc tgacccagtc tccatcctcc ctggctgtgt cagcaggaga gaaggtcact 60

atgagctgca aatccagtca gagtctgctc aacagtagaa cccgaaagaa ctacttggct 120

tggtaccagc agaaaccagg gcagtctcct aaactgctga tctactgggc atccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg ggacagattt cactctcacc 240

atcagcagtg tgcaggctga agacctggca gtttattact gcaagcaatc ttataatctt 300

cggacgttcg gtggagggac caagctggag ctgaaa 336

<210> 2810
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2810
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys
100 105 110

<210> 2811
<211> 17
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2811
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 2812
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2812
aaatccagtc agagtctgct caacagtaga acccgaaaga actacttggc t 51

<210> 2813
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2813
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 2814
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2814
tgggcatcca ctagggaatc t 21

<210> 2815
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2815
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 2816
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2816
aagcaatctt ataatcttcg gacg 24

<210> 2817
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2817
gaggtcaagc tggaggagtc aggacctgag ctggcgaagc ctggggcttc agtgaggata 60

tcctgcaagg cttctggcta caccttcaca agctactata tacactgggt gaagcagagg 120

cctggacagg gacttgagtg gattggatgg atttatcctg gaaatgttaa tactaagtac 180

aatgagaagt tcaagggcaa ggccacactg actgcagaca catcctccag cacagcctac 240

atgcagctca gcagcctgac ctctgaggac tctgcggtct atttctgtgc aagagatggt 300

aactacttct tcgatgtctg gggccaaggc accacggtca ccgtctcctc a 351

<210> 2818
<211> 117

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2818
Glu Val Lys Leu Glu Glu Ser Gly Pro Glu Leu Ala Lys Pro Gly Ala
1 5 10 15

Ser Val Arg Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Asp Gly Asn Tyr Phe Phe Asp Val Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

<210> 2819
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2819
Tyr Thr Phe Thr Ser Tyr Tyr Ile His
1 5

<210> 2820
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2820
tacaccttca caagctacta tatacac 27

<210> 2821
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2821
Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 2822
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2822
tggatttatc ctggaaatgt taatactaag tacaatgaga agttcaaggg c 51

<210> 2823
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2823
Ala Arg Asp Gly Asn Tyr Phe Phe Asp Val
1 5 10

<210> 2824
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2824
gcaagagatg gtaactactt cttcgatgtc 30

<210> 2825
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2825
gacatccagc tgactcagtc tccatcctcc ctggctgtgt cagcaggaga gaaggtcact 60

atgagctgca aatccagtca gagtctgctc aacagtagaa cccgaaagaa ctacctggct 120

tggtaccagc agaaaccagg gcagtctcct aaactgctga tctactgggc atccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg ggacagattt cactctcacc 240

atcagcagtg tgcaggctga agacctggca gtttattact gcaagcaatc ttataacctt 300

cggacgttcg gtggagggac caagctggag ctgaaa 336

<210> 2826
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2826
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys
100 105 110

<210> 2827
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2827
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 2828
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2828
aaatccagtc agagtctgct caacagtaga acccgaaaga actacctggc t 51

<210> 2829
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2829
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 2830
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2830
tgggcatcca ctagggaatc t 21

<210> 2831
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2831
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 2832
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2832
aagcaatctt ataaccttcg gacg 24

<210> 2833
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2833
gaggttcagc tggaggagtc tggacctgaa ctggtgaagc ctggggcttc agtgaggata 60

tcctgcaagg cttctggcta caccttcaca agctactata tacactgggt gaagcagagg 120

cctggacagg gacttgagtg gattggatgg atttatcctg gaaatgttaa tactaagtac 180

aatgagaagt tcaagggcaa ggccacactg actgcagaca aatcctccag cacagcctac 240

atgcagctca gcagcctgac ctctgaggac tctgcaatct atttctgtgc aagagatggt 300

aactacttct tcgatgtctg gggccaaggc accacggtca ccgtctcctc a 351

<210> 2834
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2834
Glu Val Gln Leu Glu Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Arg Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Ile Tyr Phe Cys
85 90 95

Ala Arg Asp Gly Asn Tyr Phe Phe Asp Val Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

<210> 2835
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2835
Tyr Thr Phe Thr Ser Tyr Tyr Ile His
1 5

<210> 2836
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2836
tacaccttca caagctacta tatacac 27

<210> 2837

<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2837
Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 2838
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2838
tggatttatc ctggaaatgt taatactaag tacaatgaga agttcaaggg c 51

<210> 2839
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2839
Ala Arg Asp Gly Asn Tyr Phe Phe Asp Val
1 5 10

<210> 2840
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2840
gcaagagatg gtaactactt cttcgatgtc 30

<210> 2841
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2841
gatatcgagc tgattcagtc tccatcctcc ctggctgtgt cagcaggaga gaaggtcact 60

atgagctgca aatccagtca gaatctgctc aacagtagaa cccgaaagaa ctacttggct 120

tggtaccggc agaaaccagg gcagtctcct aaactgctga tctactgggc atccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg ggacagattt cactctcacc 240

atcagcagtg tgcaggctga agacctggca gtatattact gcaagcaatc ttataatctt 300

cggacgttcg gtggagggac caagctggag ctgaaa 336

<210> 2842
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2842
Asp Ile Glu Leu Ile Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Asn Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Arg Gln Lys Pro Gly Gln
35 40 45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys
100 105 110

<210> 2843
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2843
Lys Ser Ser Gln Asn Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 2844
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2844
aaatccagtc agaatctgct caacagtaga acccgaaaga actacttggc t 51

<210> 2845
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region CDR L2 amino acid sequence

<400> 2845
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 2846
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2846
tgggcatcca ctagggaatc t 21

<210> 2847
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2847
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 2848
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2848
aagcaatctt ataatcttcg gacg 24

<210> 2849
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2849
caggtaaagc tgcagcagtc tggacctgag ctggtgaagc ctggggcttc agtgaggata 60

tcctgcaagg cttctggcaa caccttcaca agctcctata tacactgggt gaagcagagg 120

cctggacagg gacttgagtg gattggatgg atttatcctg gaaatgttaa tactaagtac 180

aatgagaagt tcaagggcaa ggccacactg actgcagaca aatcctccag cacagtctac 240

atgcagctca gcagcctgac ctctgaggac tctgcggtct atttctgtgc aagagacggt 300

agtagctact actttgacta ctggggccaa ggcaccacgg tcaccgtctc ctca 354

<210> 2850
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2850
Gln Val Lys Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Arg Ile Ser Cys Lys Ala Ser Gly Asn Thr Phe Thr Ser Ser
20 25 30

Tyr Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Val Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Asp Gly Ser Ser Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Thr Val Thr Val Ser Ser
115

<210> 2851
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2851
Asn Thr Phe Thr Ser Ser Tyr Ile His
1 5

<210> 2852
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2852
aacaccttca caagctccta tatacac 27

<210> 2853
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2853
Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 2854
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2854
tggatttatc ctggaaatgt taatactaag tacaatgaga agttcaaggg c 51

<210> 2855
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2855
Ala Arg Asp Gly Ser Ser Tyr Tyr Phe Asp Tyr
1 5 10

<210> 2856
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2856
gcaagagacg gtagtagcta ctactttgac tac 33

<210> 2857
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2857
gacatccagc tgactcagtc tccatcctcc ctggctgtgt cagcaggaga gaaggtcact 60

atgagctgca aatccagtca gagtctgctc aacagtagaa cccgaaagaa ctacttggct 120

tggtaccagc agaaaccagg gcagtctcct aaactgctga tctactgggc atccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg ggacagattt cactctcacc 240

atcagcagtg tgcaggctga agacctggca gtttattact gcaagcaatc ttataatctt 300

cggacgttcg gtggagggac caagctggag ctgaaa 336

<210> 2858
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2858
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys
100 105 110

<210> 2859
<211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2859
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 2860
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2860
aaatccagtc agagtctgct caacagtaga acccgaaaga actacttggc t 51

<210> 2861
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2861
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 2862
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2862
tgggcatcca ctagggaatc t 21

<210> 2863
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2863
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 2864
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2864
aagcaatctt ataatcttcg gacg 24

<210> 2865
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2865
gaagtgcagc tggagcagtc aggacctgag ctggtgaagc ctggggcttc agtgaagatg 60

tcctgcaagg cttctggcta caccttcaca agctactata tacactgggt gaagcagagg 120

cctggacagg gacttgagtg gattggatgg atttatcctg gagatggtag tactaagtac 180

aatgagaagt tcaagggcaa gaccacactg actgcagaca aatcctccag cacagcctac 240

atgttgctca gcagcctgac ctctgaggac tctgcgatct atttctgtgc aagggatggt 300

tcgtactact ttgactactg gggccaaggc accacggtca ccgtctcctc a 351

<210> 2866
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2866
Glu Val Gln Leu Glu Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Leu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Ile Tyr Phe Cys
85 90 95

Ala Arg Asp Gly Ser Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

<210> 2867
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2867
Tyr Thr Phe Thr Ser Tyr Tyr Ile His
1 5

<210> 2868
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2868
tacaccttca caagctacta tatacac 27

<210> 2869
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2869
Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 2870
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2870
tggatttatc ctggagatgg tagtactaag tacaatgaga agttcaaggg c 51

<210> 2871
<211> 10

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2871
Ala Arg Asp Gly Ser Tyr Tyr Phe Asp Tyr
1 5 10

<210> 2872
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2872
gcaagggatg gttcgtacta ctttgactac 30

<210> 2873
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2873
gacattcagc tcacccagtc tccatcctcc ctggctgtgt cagcaggaga gaaggtcact 60

atgagctgca aatccagtca gagtctgctc aacagtagaa cccgaaagaa ctacttggct 120

tggtaccaac agaaaccagg gcagtctcct aaactgctga tctactgggc atccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg ggacagattt cactctcacc 240

atcagcagtg tgcaggctga agacctggca gtttattact gcaagcaatc ttatagtctt 300

cggacgttcg gtggagggac caagctggag ctgaaa 336

<210> 2874
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2874
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys
100 105 110

<210> 2875
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2875
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 2876
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2876
aaatccagtc agagtctgct caacagtaga acccgaaaga actacttggc t 51

<210> 2877
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2877
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 2878
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2878
tgggcatcca ctagggaatc t 21

<210> 2879
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2879
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 2880
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2880
aagcaatctt atagtcttcg gacg 24

<210> 2881
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2881
gaggtgaagc tggaggagtc tggacctgag ctggtgaagc ctggggcttc agtgaagatg 60

tcctgcaagg cttctggcta caccttcaca agctactata tacactgggt gaagcagagg 120

cctggacagg gacttgagtg gattggatgg atttatcctg gagatggtag tactaagtac 180

aatgagaagt tcaagggcaa gaccacactg actgcagaca aatcctccag cacagcctac 240

atgttgctca gcagcctgac ctctgaggac tctgcgatct atttctgtgc aagggatggt 300

tcgtactact ttgactactg gggccaaggc accacggtca ccgtctcctc a 351

<210> 2882
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2882
Glu Val Lys Leu Glu Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Leu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Ile Tyr Phe Cys
85 90 95

Ala Arg Asp Gly Ser Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

<210> 2883
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2883
Tyr Thr Phe Thr Ser Tyr Tyr Ile His
1 5

<210> 2884
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2884

tacaccttca caagctacta tatacac 27

<210> 2885
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2885
Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 2886
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2886
tggatttatc ctggagatgg tagtactaag tacaatgaga agttcaaggg c 51

<210> 2887
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2887
Ala Arg Asp Gly Ser Tyr Tyr Phe Asp Tyr
1 5 10

<210> 2888
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2888
gcaagggatg gttcgtacta ctttgactac 30

<210> 2889
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2889
gacatccagc tgacccagtc tccatcctcc ctggctgtgt cagcaggaga gaaggtcact 60

atgagctgca aatccagtca gagtctgctc aacagtagaa cccgaaagaa ctacttggct 120

tggtaccaac agaaaccagg gcagtctcct aaactgctga tctactgggc atccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg ggacagattt cactctcacc 240

atcagcagtg tgcaggctga agacctggca gtttattact gcaagcaatc ttatagtctt 300

cggacgttcg gtggagggac caagctggag ctgaaa 336

<210> 2890
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2890
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys
100 105 110

<210> 2891
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2891
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 2892
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2892
aaatccagtc agagtctgct caacagtaga acccgaaaga actacttggc t 51

<210> 2893
<211> 7
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2893
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 2894
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2894
tgggcatcca ctagggaatc t 21

<210> 2895
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2895
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 2896
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2896
aagcaatctt atagtcttcg gacg 24

<210> 2897

<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2897
gaagtcaagc tgcaggagtc tggacctgag ctggtgaagc ctggggcttc agtgaagatg 60

tcctgcaagg cttctggcta caccttcaca agctactata tacactgggt gaagcagagg 120

cctggacagg gacttgagtg gattggatgg atttatcctg gagatggtag tactaagtac 180

aatgagaagt tcaagggcaa gaccacactg actgcagaca aatcctccag cacagcctac 240

atgttgctca gcagcctgac ctctgaggac tctgcgatct atttctgtgc aagggactac 300

gggtactact ttgactactg gggccaaggc accacggtca ccgtctcctc a 351

<210> 2898
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2898
Glu Val Lys Leu Gln Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Leu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Ile Tyr Phe Cys
85 90 95

Ala Arg Asp Tyr Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

<210> 2899
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2899
Tyr Thr Phe Thr Ser Tyr Tyr Ile His
1 5

<210> 2900
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2900
tacaccttca caagctacta tatacac 27

<210> 2901
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2901
Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 2902
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2902
tggatttatc ctggagatgg tagtactaag tacaatgaga agttcaaggg c 51

<210> 2903
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2903
Ala Arg Asp Tyr Gly Tyr Tyr Phe Asp Tyr
1 5 10

<210> 2904
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2904
gcaagggact acgggtacta ctttgactac 30

<210> 2905
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region nucleic acid sequence

<400> 2905
gacattcagc tgacccagtc tccatcctcc ctggctgtgt cagcaggaga gaaggtcact 60

atgagctgca aatccagtca gagtctgctc aacagtagaa cccgaaagaa ctacttggct 120

tggtaccagc agaaaccagg gcagtctcct aaactgctga tctactgggc atccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg ggacagattt cactctcacc 240

atcagcagtg tgcaggctga agacctggca gtttattact gcaagcaatc ttataatctt 300

cggacgttcg gtggagggac caagctggag ctgaaa 336

<210> 2906
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2906
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys
100 105 110

<210> 2907
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2907
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 2908
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2908
aaatccagtc agagtctgct caacagtaga acccgaaaga actacttggc t 51

<210> 2909
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2909
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 2910
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2910
tgggcatcca ctagggaatc t 21

<210> 2911
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2911
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 2912
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2912
aagcaatctt ataatcttcg gacg 24

<210> 2913
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2913
gaggttaagc tggaggagtc aggacctgag ctggtgaagc ctggggcttc agtgaggata 60

tcctgcaagg cttctggcta caccttcaca agctactata tacactgggt gaagcagagg 120

cctggacagg gacttgagtg gattggatgg atttatcctg gaaatgttaa tactaagtac 180

aatgagaagt tcaagggcaa ggccacactg actgcagaca aatcctccag cacagtttat 240

atgcagctca gcagcctgac ctctgaggac tctgcggtct atttctgtgc aagagactat 300

ggttactact ttgactattg gggccaaggc accacggtca ccgtctcctc a 351

<210> 2914
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2914
Glu Val Lys Leu Glu Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Arg Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Val Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Asp Tyr Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

<210> 2915
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2915
Tyr Thr Phe Thr Ser Tyr Tyr Ile His
1 5

<210> 2916
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2916
tacaccttca caagctacta tatacac 27

<210> 2917
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2917
Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 2918
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2918
tggatttatc ctggaaatgt taatactaag tacaatgaga agttcaaggg c 51

<210> 2919
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2919
Ala Arg Asp Tyr Gly Tyr Tyr Phe Asp Tyr
1 5 10

<210> 2920
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2920
gcaagagact atggttacta ctttgactat 30

<210> 2921
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2921
gacattgtgc tgacccagtc tccatcctcc ctggctgtgt cagcaggaga gaaggtcacc 60

atgagctgca aatccagtca gagtctgctc aacagtagaa cccgaaagaa ctacttggct 120

tggtaccagc agaaaccagg gcagtctcct aaactgctga tctactgggc atccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg ggacagattt cactctcacc 240

atcagcagtg tgcaggctga agacctggca gtttattact gcaagcaatc ttataatctt 300

cggacgttcg gtggagggac caagctggag ctgaaa 336

<210> 2922
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2922
Asp Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys
100 105 110

<210> 2923
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2923
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 2924
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2924
aaatccagtc agagtctgct caacagtaga acccgaaaga actacttggc t 51

<210> 2925
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2925
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 2926
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2926
tgggcatcca ctagggaatc t 21

<210> 2927
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2927
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 2928
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2928
aagcaatctt ataatcttcg gacg 24

<210> 2929
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2929
gaggtgcagc tggaggagtc aggacctgag ctggtgaggc ctggggcttc agtgaggata 60

tcctgcaagg cttctggcta caccttcaca agctcctata tacactgggt gaagcagagg 120

cctggacagg gacttgagtg gattggatgg atttatcctg gaaatgttaa tactaagtac 180

aatgagaagt tcaagggcaa ggccacactg actgcagaca aatcctccag cacagcctac 240

atgcacctca gcagcctgac ctctgaggac tctgcggtct atttctgtgc aagagactat 300

ggttactact ttgactactg gggccaaggc accacggtca ccgtctcctc a 351

<210> 2930
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2930

Glu Val Gln Leu Glu Glu Ser Gly Pro Glu Leu Val Arg Pro Gly Ala
1 5 10 15

Ser Val Arg Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Ser
20 25 30

Tyr Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met His Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Asp Tyr Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

<210> 2931
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2931
Tyr Thr Phe Thr Ser Ser Tyr Ile His
1 5

<210> 2932
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2932
tacaccttca caagctccta tatacac 27

<210> 2933
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2933
Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 2934
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2934
tggatttatc ctggaaatgt taatactaag tacaatgaga agttcaaggg c 51

<210> 2935
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2935
Ala Arg Asp Tyr Gly Tyr Tyr Phe Asp Tyr
1 5 10

<210> 2936
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2936
gcaagagact atggttacta ctttgactac 30

<210> 2937
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2937
gacattgtgc tgacccaatc tccatcctcc ctggctgtgt cagcaggaga gaaggtcact 60

atgagctgca aatccagtca gagtctgctc aacagtagaa cccgaaagaa ctacttggct 120

tggtaccagc agaaagcagg gcagtctcct aaactgctga tctactgggc atccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg ggacagattt cactctcacc 240

atcagcagtg tgcaggctga agacctggca gtttattact gcaagcaatc ttataatctt 300

cggacgttcg gtggagggac caagctggag ctgaaa 336

<210> 2938
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2938
Asp Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Ala Gly Gln
35 40 45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys
100 105 110

<210> 2939
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2939
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 2940
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2940
aaatccagtc agagtctgct caacagtaga acccgaaaga actacttggc t 51

<210> 2941
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2941
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 2942
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2942
tgggcatcca ctagggaatc t 21

<210> 2943
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2943
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 2944
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2944

aagcaatctt ataatcttcg gacg 24

<210> 2945
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2945
gaggttcagc tggagcagtc aggacctgag ctggtgaagc ctggggcttc agtgaggata 60

tcctgcaagt cttctggcta caccttcaca agctactata tacactgggt gaagcagagg 120

cctggacagg gacttgagtg gattggatgg atttatcctg gaaatgttaa tactaaatac 180

aatgagaagt tcaagggcaa ggccacactg actgcagaca aatcctccag cacagcctac 240

atgcagctca gcagcctgac ctctgaggac tctgcggtct atttctgtgc aagagactat 300

ggttactact ttggctcctg gggccaaggc accacggtca ccgtctcctc a 351

<210> 2946
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2946
Glu Val Gln Leu Glu Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Arg Ile Ser Cys Lys Ser Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Asp Tyr Gly Tyr Tyr Phe Gly Ser Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

<210> 2947
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2947
Tyr Thr Phe Thr Ser Tyr Tyr Ile His
1 5

<210> 2948
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2948
tacaccttca caagctacta tatacac 27

<210> 2949
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2949
Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 2950
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2950
tggatttatc ctggaaatgt taatactaaa tacaatgaga agttcaaggg c 51

<210> 2951
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2951
Ala Arg Asp Tyr Gly Tyr Tyr Phe Gly Ser
1 5 10

<210> 2952
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2952
gcaagagact atggttacta ctttggctcc 30

<210> 2953
<211> 336
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2953
gacatccagc tcacccagtc tccatcctcc ctggctgtgt cagcaggaga gaaggtcact 60

atgaactgca aatccagtca gagtctgctc aacagtagaa cccgaaagaa ctacttggct 120

tggtaccagc agaaaccagg gcagtctcct aaattgctga tctactgggc atccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg ggacagattt cactctcacc 240

atcagcagtg tgcaggctga agacctggca gtttattact gtaagcaatc ttataatctt 300

cggacgttcg gtggaggcac aaagctggaa atcaaa 336

<210> 2954
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2954
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
1 5 10 15

Glu Lys Val Thr Met Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 2955
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2955
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 2956
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2956
aaatccagtc agagtctgct caacagtaga acccgaaaga actacttggc t 51

<210> 2957
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2957
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 2958

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2958
tgggcatcca ctagggaatc t 21

<210> 2959
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2959
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 2960
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2960
aagcaatctt ataatcttcg gacg 24

<210> 2961
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2961
gaagtccagc tgcagcagtc tggacctgag ctggtgaagc ctggggcttc agtgaggata 60

tcctgcaagg cttctggtta caccttcaca agctactata tacactgggt gaagcagagg 120

cctggacagg gacttgagtg gattggatgg atttatcctg gaaatgttaa tactaagtac 180

aatgagaagt tcaagggcaa ggccacactg actgcagaca aatcctccag cacagtctac 240

atgcagctca gcagcctgac ctctgaggac tctgcggtct atttctgtgg aagagattac 300

tacggctcgt actactttga caactggggc caaggcacca cggtcaccgt ctcctca 357

<210> 2962
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2962
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Arg Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Val Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Gly Arg Asp Tyr Tyr Gly Ser Tyr Tyr Phe Asp Asn Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 2963
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2963
Tyr Thr Phe Thr Ser Tyr Tyr Ile His
1 5

<210> 2964
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2964
tacaccttca caagctacta tatacac 27

<210> 2965
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2965
Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 2966
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2966
tggatttatc ctggaaatgt taatactaag tacaatgaga agttcaaggg c 51

<210> 2967
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2967
Gly Arg Asp Tyr Tyr Gly Ser Tyr Tyr Phe Asp Asn
1 5 10

<210> 2968
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2968
ggaagagatt actacggctc gtactacttt gacaac 36

<210> 2969
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2969
gacatccagc tgactcagtc tccatcctcc ctggctgtgt cagcaggaga gaaggtcact 60

atgagctgca aatccagtca gagtctgctc aacagtagaa cccgaaagaa ctacttggct 120

tggtaccagc agaaaccagg gcagcctcct aaactgctga tctactgggc atccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg ggacagattt cactctcacc 240

atcagcagtg tgcaggctga ggacctggca gtttattact gcaagcaatc ttataatctt 300

cggacgttcg gtggaggcac aaagttggaa ataaaa 336

<210> 2970
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2970
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 2971
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 2971

Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 2972
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 2972
aaatccagtc agagtctgct caacagtaga acccgaaaga actacttggc t 51

<210> 2973
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2973
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 2974
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2974
tgggcatcca ctagggaatc t 21

<210> 2975
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2975
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 2976
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2976
aagcaatctt ataatcttcg gacg 24

<210> 2977
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2977
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcacc agctactata tacactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atctaccctg gtgatggtag cacaaagtac 180

aacgagaagt tcaagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc tagggatggc 300

tcctactact ttgactactg gggccaagga accctggtca ccgtctcctc a 351

<210> 2978
<211> 117
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2978
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Ser Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 2979
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2979
Tyr Thr Phe Thr Ser Tyr Tyr Ile His
1 5

<210> 2980
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2980
tacaccttca ccagctacta tatacac 27

<210> 2981
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2981
Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 2982
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2982
tggatctacc ctggtgatgg tagcacaaag tacaacgaga agttcaaggg c 51

<210> 2983
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2983

Ala Arg Asp Gly Ser Tyr Tyr Phe Asp Tyr
1 5 10

<210> 2984
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 2984
gctagggatg gctcctacta ctttgactac 30

<210> 2985
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 2985
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 2986
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 2986
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
            20   25   30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
                85   90   95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 2987
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 2987
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1   5   10   15

Ala

<210> 2988
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 2988
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 2989
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 2989
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 2990
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 2990
tgggcatcta cccgggaatc c 21

<210> 2991
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 2991
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 2992
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 2992
aagcaatctt attctctgag aact 24

<210> 2993
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 2993
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcacc agctactata tacactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atctaccctg gtgatggtag cacaaagtac 180

aacgagaagt tcaagggcag agtcaccata accgcggaca agtccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc gagggatgga 300

agctattact ttgactactg gggccaagga accctggtca ccgtctcctc a 351

<210> 2994
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 2994
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Ser Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 2995
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 2995
Tyr Thr Phe Thr Ser Tyr Tyr Ile His
1 5

<210> 2996
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 2996
tacaccttca ccagctacta tatacac 27

<210> 2997
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 2997
Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 2998
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 2998
tggatctacc ctggtgatgg tagcacaaag tacaacgaga agttcaaggg c 51

<210> 2999
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 2999
Ala Arg Asp Gly Ser Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3000
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3000
gcgagggatg gaagctatta ctttgactac 30

<210> 3001
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3001
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3002
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3002
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3003
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3003
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3004
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3004
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3005
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3005
Trp Ala Ser Thr Arg Glu Ser

1 5

<210> 3006
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3006
tgggcatcta cccgggaatc c 21

<210> 3007
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3007
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 3008
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3008
aagcaatctt attctctgag aact 24

<210> 3009
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3009
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcacc agctactata tacactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gataggatgg atctaccctg gtgatggtag cacaaagtac 180

aacgagaagt tcaagggcag agtcaccatg accgcggaca agtccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc cagggatggt 300

tcctattact ttgactactg gggccaagga accctggtca ccgtctcctc a 351

<210> 3010
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3010
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Val Thr Met Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Ser Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
        115

<210> 3011
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 3011
Tyr Thr Phe Thr Ser Tyr Tyr Ile His
1   5

<210> 3012
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3012
tacaccttca ccagctacta tatacac   27

<210> 3013
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H2 amino acid sequence

<400> 3013
Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe Lys
1   5   10   15

Gly

<210> 3014
<211> 51
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3014
tggatctacc ctggtgatgg tagcacaaag tacaacgaga agttcaaggg c 51

<210> 3015
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3015
Ala Arg Asp Gly Ser Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3016
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3016
gccagggatg gttcctatta ctttgactac 30

<210> 3017
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3017
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3018
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3018
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3019
<211> 17
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3019
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3020
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3020
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3021
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3021
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3022
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3022
tgggcatcta cccgggaatc c 21

<210> 3023
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3023
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 3024
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3024
aagcaatctt attctctgag aact 24

<210> 3025
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3025
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcacc agctactata tacactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atctaccctg gtgatggtag cacaaagtac 180

aacgagaagt tcaagggcag agtcaccatg accgcggaca agtccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc tagagatggc 300

tcatattact ttgactactg gggccaagga accctggtca ccgtctcctc a 351

<210> 3026
<211> 117

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3026
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20   25   30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe
    50   55   60

Lys Gly Arg Val Thr Met Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65   70   75   80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Asp Gly Ser Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100   105   110

Val Thr Val Ser Ser
        115

<210> 3027
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3027
Tyr Thr Phe Thr Ser Tyr Tyr Ile His
1   5

<210> 3028
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3028
tacaccttca ccagctacta tatacac 27

<210> 3029
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3029
Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 3030
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3030
tggatctacc ctggtgatgg tagcacaaag tacaacgaga agttcaaggg c 51

<210> 3031
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3031
Ala Arg Asp Gly Ser Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3032
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3032
gctagagatg gctcatatta ctttgactac 30

<210> 3033
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3033
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3034
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3034
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3035
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3035
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3036
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3036
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3037
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3037
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3038
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3038
tgggcatcta cccgggaatc c 21

<210> 3039
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3039
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 3040
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3040
aagcaatctt attctctgag aact 24

<210> 3041
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3041
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcacc agctactata tacactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gataggatgg atctaccctg gtgatggtag cacaaagtac 180

aacgagaagt tcaagggcag aaccaccctg accgcggaca agtccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc tagagacgga 300

tcttattact ttgactactg gggccaagga accctggtca ccgtctcctc a 351

<210> 3042
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3042
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Thr Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Ser Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 3043
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3043
Tyr Thr Phe Thr Ser Tyr Tyr Ile His
1 5

<210> 3044
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3044
tacaccttca ccagctacta tatacac 27

<210> 3045

<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3045
Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 3046
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3046
tggatctacc ctggtgatgg tagcacaaag tacaacgaga agttcaaggg c 51

<210> 3047
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3047
Ala Arg Asp Gly Ser Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3048
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3048
gctagagacg gatcttatta ctttgactac 30

<210> 3049
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3049
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3050
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3050
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3051
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3051
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3052
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3052
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3053
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region CDR L2 amino acid sequence

<400> 3053
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3054
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3054
tgggcatcta cccgggaatc c 21

<210> 3055
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3055
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 3056
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3056
aagcaatctt attctctgag aact 24

<210> 3057
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3057
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcacc agctactata tacactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gataggatgg atctaccctg gtgatggtag cacaaagtac 180

aacgagaagt tcaagggcag aaccaccctg accgcggaca agtccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc gagagatggt 300

agctactact ttgactactg gggccaagga accctggtca ccgtctcctc a 351

<210> 3058
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3058
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Thr Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Ser Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 3059
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3059
Tyr Thr Phe Thr Ser Tyr Tyr Ile His
1 5

<210> 3060
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3060
tacaccttca ccagctacta tatacac 27

<210> 3061
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3061
Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 3062
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3062
tggatctacc ctggtgatgg tagcacaaag tacaacgaga agttcaaggg c 51

<210> 3063
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3063
Ala Arg Asp Gly Ser Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3064
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3064
gcgagagatg gtagctacta ctttgactac 30

<210> 3065
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3065
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctt 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3066
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3066
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3067
<211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3067
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3068
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3068
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3069
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3069
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3070
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3070
tgggcatcta cccgggaatc c 21

<210> 3071
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3071
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 3072
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3072
aagcaatctt attctcttag aact 24

<210> 3073
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3073
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcacc agctactata tacactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atctaccctg gtgatggtag cacaaagtac 180

aacgagaagt tcaagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc tagggatggc 300

tcctactact ttgactactg gggccaagga accctggtca ccgtctcctc a 351

<210> 3074
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3074
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Ser Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 3075
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3075
Tyr Thr Phe Thr Ser Tyr Tyr Ile His
1 5

<210> 3076
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3076
tacaccttca ccagctacta tatacac 27

<210> 3077
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3077
Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 3078
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3078
tggatctacc ctggtgatgg tagcacaaag tacaacgaga agttcaaggg c 51

<210> 3079
<211> 10

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3079
Ala Arg Asp Gly Ser Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3080
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3080
gctagggatg gctcctacta ctttgactac 30

<210> 3081
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3081
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcagag ttacaatttg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3082
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3082
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3083
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3083
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3084
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3084
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3085
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3085
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3086
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3086
tgggcatcta cccgggaatc c 21

<210> 3087
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3087
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 3088
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3088
aagcagagtt acaatttgag aact 24

<210> 3089
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3089
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcacc agctactata tacactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atctaccctg gtgatggtag cacaaagtac 180

aacgagaagt tcaagggcag agtcaccata accgcggaca agtccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc gagggatgga 300

agctattact ttgactactg gggccaagga accctggtca ccgtctcctc a 351

<210> 3090
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3090
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30


Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Gly Ser Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser
        115


<210> 3091
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 3091
Tyr Thr Phe Thr Ser Tyr Tyr Ile His
1               5


<210> 3092
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3092
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tacaccttca ccagctacta tatacac 27

<210> 3093
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3093
Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 3094
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3094
tggatctacc ctggtgatgg tagcacaaag tacaacgaga agttcaaggg c 51

<210> 3095
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3095
Ala Arg Asp Gly Ser Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3096
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3096
gcgagggatg gaagctatta ctttgactac 30

<210> 3097
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3097
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcagag ttacaatttg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3098
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3098
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
                85   90   95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 3099
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 3099
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1   5   10   15

Ala

<210> 3100
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 3100
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t   51

<210> 3101
<211> 7
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3101
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3102
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3102
tgggcatcta cccgggaatc c 21

<210> 3103
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3103
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 3104
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3104
aagcagagtt acaatttgag aact 24

<210> 3105

<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3105
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcacc agctactata tacactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gataggatgg atctaccctg gtgatggtag cacaaagtac 180

aacgagaagt tcaagggcag agtcaccatg accgcggaca agtccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc cagggatggt 300

tcctattact ttgactactg gggccaagga accctggtca ccgtctcctc a 351

<210> 3106
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3106
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Val Thr Met Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Ser Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 3107
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3107
Tyr Thr Phe Thr Ser Tyr Tyr Ile His
1 5

<210> 3108
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3108
tacaccttca ccagctacta tatacac 27

<210> 3109
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3109
Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 3110
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3110
tggatctacc ctggtgatgg tagcacaaag tacaacgaga agttcaaggg c 51

<210> 3111
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3111
Ala Arg Asp Gly Ser Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3112
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3112
gccagggatg gttcctatta ctttgactac 30

<210> 3113
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region nucleic acid sequence

<400> 3113
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcagag ttacaatttg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3114
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3114
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3115
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3115
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3116
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3116
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3117
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3117
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3118
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3118
tgggcatcta cccgggaatc c 21

<210> 3119
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3119
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 3120
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3120
aagcagagtt acaatttgag aact 24

<210> 3121
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3121
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcacc agctactata tacactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atctaccctg gtgatggtag cacaaagtac 180

aacgagaagt tcaagggcag agtcaccatg accgcggaca agtccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc tagagatggc 300

tcatattact ttgactactg gggccaagga accctggtca ccgtctcctc a 351

<210> 3122
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3122
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Val Thr Met Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Ser Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 3123
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3123
Tyr Thr Phe Thr Ser Tyr Tyr Ile His
1 5

<210> 3124
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3124
tacaccttca ccagctacta tatacac 27

<210> 3125
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3125
Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 3126
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3126
tggatctacc ctggtgatgg tagcacaaag tacaacgaga agttcaaggg c 51

<210> 3127
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3127
Ala Arg Asp Gly Ser Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3128
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3128
gctagagatg gctcatatta ctttgactac 30

<210> 3129
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3129
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcagag ttacaatttg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3130
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3130
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3131
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3131
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3132
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3132
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3133
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3133
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3134
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3134
tgggcatcta cccgggaatc c 21

<210> 3135
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3135
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 3136
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3136
aagcagagtt acaatttgag aact 24

<210> 3137
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3137
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcacc agctactata tacactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gataggatgg atctaccctg gtgatggtag cacaaagtac 180

aacgagaagt tcaagggcag aaccaccctg accgcggaca agtccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc tagagacgga 300

tcttattact ttgactactg gggccaagga accctggtca ccgtctcctc a 351

<210> 3138
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3138

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30


Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Gly Arg Thr Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Gly Ser Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser
        115


<210> 3139
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 3139
Tyr Thr Phe Thr Ser Tyr Tyr Ile His
1               5


<210> 3140
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
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<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3140
tacaccttca ccagctacta tatacac 27

<210> 3141
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3141
Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 3142
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3142
tggatctacc ctggtgatgg tagcacaaag tacaacgaga agttcaaggg c 51

<210> 3143
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3143
Ala Arg Asp Gly Ser Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3144
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3144
gctagagacg gatcttatta ctttgactac 30

<210> 3145
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3145
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcagag ttacaatttg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3146
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3146
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3147
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3147
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3148
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3148
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3149
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3149
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3150
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3150
tgggcatcta cccgggaatc c 21

<210> 3151
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3151
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 3152
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3152

aagcagagtt acaatttgag aact 24

<210> 3153
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3153
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcacc agctactata tacactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gataggatgg atctaccctg gtgatggtag cacaaagtac 180

aacgagaagt tcaagggcag aaccaccctg accgcggaca agtccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc gagagatggt 300

agctactact ttgactactg gggccaagga accctggtca ccgtctcctc a 351

<210> 3154
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3154
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Thr Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Ser Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 3155
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3155
Tyr Thr Phe Thr Ser Tyr Tyr Ile His
1 5

<210> 3156
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3156
tacaccttca ccagctacta tatacac 27

<210> 3157
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3157
Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 3158
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3158
tggatctacc ctggtgatgg tagcacaaag tacaacgaga agttcaaggg c 51

<210> 3159
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3159
Ala Arg Asp Gly Ser Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3160
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3160
gcgagagatg gtagctacta ctttgactac 30

<210> 3161
<211> 336
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3161
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcagag ttacaatttg 300

agaactttcg gcggagggac caagctggag atcaaa 336

<210> 3162
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3162
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 3163
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3163
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3164
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3164
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3165
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3165
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3166

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3166
tgggcatcta cccgggaatc c 21

<210> 3167
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3167
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 3168
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3168
aagcagagtt acaatttgag aact 24

<210> 3169
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3169
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcacc agctcctata tacactgggt gcgacaggcc 120

cctggacaaa ggcttgagtg gatgggatgg atctaccctg gtaatgttaa cacaaagtac 180

aacgagaagt tcaagggcag agtcaccata accagggaca cgtccgcgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc tagggattat 300

ggctactact ttgactactg gggccaagga accctggtca ccgtctcctc a 351

<210> 3170
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3170

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala
1				5					10					15	

Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Ser
		20					25					30			

Tyr	Ile	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Arg	Leu	Glu	Trp	Met
	35					40					45				

Gly	Trp	Ile	Tyr	Pro	Gly	Asn	Val	Asn	Thr	Lys	Tyr	Asn	Glu	Lys	Phe
	50					55					60				

Lys	Gly	Arg	Val	Thr	Ile	Thr	Arg	Asp	Thr	Ser	Ala	Ser	Thr	Ala	Tyr
65				70					75					80	

Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	

Ala	Arg	Asp	Tyr	Gly	Tyr	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu
		100					105					110			

Val	Thr	Val	Ser	Ser	
	115				

<210> 3171
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3171
Tyr Thr Phe Thr Ser Ser Tyr Ile His
1 5

<210> 3172
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3172
tacaccttca ccagctccta tatacac 27

<210> 3173
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3173
Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 3174
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3174
tggatctacc ctggtaatgt taacacaaag tacaacgaga agttcaaggg c 51

<210> 3175
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3175
Ala Arg Asp Tyr Gly Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3176
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3176
gctagggatt atggctacta ctttgactac 30

<210> 3177
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3177
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3178
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3178
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3179
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3179

Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3180
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3180
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3181
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3181
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3182
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3182
tgggcatcta cccgggaatc c 21

<210> 3183
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3183
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 3184
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3184
aagcaatctt attctctgag aact 24

<210> 3185
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3185
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcacc agctcctata tacactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gataggatgg atctaccctg gtaatgttaa cacaaagtac 180

aacgagaagt tcaagggcag agccaccctg accgcggaca agtccgcgag cacagcctac 240

atgcacctga gcagcctgag atctgaggac acggcggtgt actactgcgc gagagactac 300

ggctactact ttgactactg gggccaagga accctggtca ccgtctcctc a 351

<210> 3186
<211> 117
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3186
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Ser
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Ala Thr Leu Thr Ala Asp Lys Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met His Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Tyr Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 3187
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3187
Tyr Thr Phe Thr Ser Ser Tyr Ile His
1 5

<210> 3188
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3188
tacaccttca ccagctccta tatacac 27

<210> 3189
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3189
Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 3190
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3190
tggatctacc ctggtaatgt taacacaaag tacaacgaga agttcaaggg c 51

<210> 3191
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3191

Ala Arg Asp Tyr Gly Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3192
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3192
gcgagagact acggctacta ctttgactac 30

<210> 3193
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3193
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3194
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3194
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
            20   25   30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
                85   90   95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 3195
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 3195
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1   5   10   15

Ala

<210> 3196
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 3196
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3197
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3197
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3198
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3198
tgggcatcta cccgggaatc c 21

<210> 3199
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3199
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 3200
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3200
aagcaatctt attctctgag aact 24

<210> 3201
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3201
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcacc agctcctata tacactgggt gcgacaggcc 120

cctggacaaa ggcttgagtg gataggatgg atctaccctg gtaatgttaa cacaaagtac 180

aacgagaagt tcaagggcag agtcaccata accgcggaca agtccgcgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc gagggattac 300

ggatactact ttgactactg gggccaagga accctggtca ccgtctcctc a 351

<210> 3202
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3202
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Ser
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Tyr Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 3203
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3203
Tyr Thr Phe Thr Ser Ser Tyr Ile His
1 5

<210> 3204
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3204
tacaccttca ccagctccta tatacac 27

<210> 3205
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3205
Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 3206
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3206
tggatctacc ctggtaatgt taacacaaag tacaacgaga agttcaaggg c 51

<210> 3207
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3207
Ala Arg Asp Tyr Gly Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3208
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3208
gcgagggatt acggatacta ctttgactac 30

<210> 3209
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3209
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3210
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3210
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3211
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3211
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3212
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3212
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3213
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3213
Trp Ala Ser Thr Arg Glu Ser

1 5

<210> 3214
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3214
tgggcatcta cccgggaatc c 21

<210> 3215
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3215
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 3216
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3216
aagcaatctt attctctgag aact 24

<210> 3217
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3217
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcacc agctcctata tacactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atctaccctg gtaatgttaa cacaaagtac 180

aacgagaagt tcaagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc tagggactat 300

ggttactact ttgactactg gggccaagga accctggtca ccgtctcctc a 351

<210> 3218
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3218
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Ser
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Tyr Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
        115

<210> 3219
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 3219
Tyr Thr Phe Thr Ser Ser Tyr Ile His
1   5

<210> 3220
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3220
tacaccttca ccagctccta tatacac   27

<210> 3221
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H2 amino acid sequence

<400> 3221
Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe Lys
1   5   10   15

Gly

<210> 3222
<211> 51
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3222
tggatctacc ctggtaatgt taacacaaag tacaacgaga agttcaaggg c 51

<210> 3223
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3223
Ala Arg Asp Tyr Gly Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3224
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3224
gctagggact atggttacta ctttgactac 30

<210> 3225
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3225
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3226
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3226
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3227
<211> 17
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3227
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3228
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3228
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3229
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3229
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3230
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3230
tgggcatcta cccgggaatc c 21

<210> 3231
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3231
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 3232
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3232
aagcaatctt attctctgag aact 24

<210> 3233
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3233
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcacc agctcctata tacactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gataggatgg atctaccctg gtaatgttaa cacaaagtac 180

aacgagaagt tcaagggcag agtcaccatg accgcggaca agtccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc tagggactac 300

ggttattact ttgactactg gggccaagga accctggtca ccgtctcctc a 351

<210> 3234
<211> 117

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3234
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Ser
            20   25   30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
    50   55   60

Lys Gly Arg Val Thr Met Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65   70   75   80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Asp Tyr Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100   105   110

Val Thr Val Ser Ser
        115

<210> 3235
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3235
Tyr Thr Phe Thr Ser Ser Tyr Ile His
1   5

<210> 3236
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3236
tacaccttca ccagctccta tatacac 27

<210> 3237
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3237
Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 3238
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3238
tggatctacc ctggtaatgt taacacaaag tacaacgaga agttcaaggg c 51

<210> 3239
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3239
Ala Arg Asp Tyr Gly Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3240
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3240
gctagggact acggttatta ctttgactac 30

<210> 3241
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3241
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3242
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3242
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3243
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3243
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3244
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3244
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3245
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3245
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3246
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3246
tgggcatcta cccgggaatc c 21

<210> 3247
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3247
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 3248
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3248
aagcaatctt attctctgag aact 24

<210> 3249
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3249
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcacc agctcctata tacactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gataggatgg atctaccctg gtaatgttaa cacaaagtac 180

aacgagaagt tcaagggcag agccaccctg accgcggaca agtccacgag cacagcctac 240

atgcacctga gcagcctgag atctgaggac acggcggtgt actactgcgc gagggactat 300

ggctactact ttgactactg gggccaagga accctggtca ccgtctcctc a 351

<210> 3250
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3250
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Ser
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Ala Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met His Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Tyr Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 3251
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3251
Tyr Thr Phe Thr Ser Ser Tyr Ile His
1 5

<210> 3252
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3252
tacaccttca ccagctccta tatacac 27

<210> 3253

<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3253
Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 3254
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3254
tggatctacc ctggtaatgt taacacaaag tacaacgaga agttcaaggg c 51

<210> 3255
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3255
Ala Arg Asp Tyr Gly Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3256
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3256
gcgagggact atggctacta ctttgactac 30

<210> 3257
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3257
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3258
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3258
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3259
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3259
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3260
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3260
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3261
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region CDR L2 amino acid sequence

<400> 3261
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3262
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3262
tgggcatcta cccgggaatc c 21

<210> 3263
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3263
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 3264
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3264
aagcaatctt attctctgag aact 24

<210> 3265
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3265
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcacc agctcctata tacactgggt gcgacaggcc 120

cctggacaaa ggcttgagtg gatgggatgg atctaccctg gtaatgttaa cacaaagtac 180

aacgagaagt tcaagggcag agtcaccata accagggaca cgtccgcgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc tagggattat 300

ggctactact ttgactactg gggccaagga accctggtca ccgtctcctc a 351

<210> 3266
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3266
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Ser
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Tyr Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 3267
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3267
Tyr Thr Phe Thr Ser Ser Tyr Ile His
1 5

<210> 3268
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3268
tacaccttca ccagctccta tatacac 27

<210> 3269
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3269
Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 3270
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3270
tggatctacc ctggtaatgt taacacaaag tacaacgaga agttcaaggg c 51

<210> 3271
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3271
Ala Arg Asp Tyr Gly Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3272
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3272
gctagggatt atggctacta ctttgactac 30

<210> 3273
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3273
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcagag ttacaatttg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3274
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3274
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3275
<211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3275
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3276
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3276
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3277
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3277
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3278
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3278
tgggcatcta cccgggaatc c 21

<210> 3279
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3279
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 3280
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3280
aagcagagtt acaatttgag aact 24

<210> 3281
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3281
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcacc agctcctata tacactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gataggatgg atctaccctg gtaatgttaa cacaaagtac 180

aacgagaagt tcaagggcag agccaccctg accgcggaca agtccgcgag cacagcctac 240

atgcacctga gcagcctgag atctgaggac acggcggtgt actactgcgc gagagactac 300

ggctactact ttgactactg gggccaagga accctggtca ccgtctcctc a 351

<210> 3282
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3282
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Ser
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Ala Thr Leu Thr Ala Asp Lys Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met His Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Tyr Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 3283
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3283
Tyr Thr Phe Thr Ser Ser Tyr Ile His
1 5

<210> 3284
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3284
tacaccttca ccagctccta tatacac 27

<210> 3285
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3285
Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 3286
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3286
tggatctacc ctggtaatgt taacacaaag tacaacgaga agttcaaggg c 51

<210> 3287
<211> 10

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3287
Ala Arg Asp Tyr Gly Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3288
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3288
gcgagagact acggctacta ctttgactac 30

<210> 3289
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3289
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcagag ttacaatttg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3290
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3290
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3291
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3291
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3292
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3292
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3293
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3293
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3294
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3294
tgggcatcta cccgggaatc c 21

<210> 3295
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3295
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 3296
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3296
aagcagagtt acaatttgag aact 24

<210> 3297
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3297
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcacc agctcctata tacactgggt gcgacaggcc 120

cctggacaaa ggcttgagtg gataggatgg atctaccctg gtaatgttaa cacaaagtac 180

aacgagaagt tcaagggcag agtcaccata accgcggaca agtccgcgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc gagggattac 300

ggatactact ttgactactg gggccaagga accctggtca ccgtctcctc a 351

<210> 3298
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3298
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

```
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Ser
            20                  25                  30


Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Ile
        35                  40                  45


Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Ala Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Tyr Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser
        115


<210> 3299
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 3299
Tyr Thr Phe Thr Ser Ser Tyr Ile His
1               5


<210> 3300
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3300
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tacaccttca ccagctccta tatacac 27

<210> 3301
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3301
Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 3302
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3302
tggatctacc ctggtaatgt taacacaaag tacaacgaga agttcaaggg c 51

<210> 3303
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3303
Ala Arg Asp Tyr Gly Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3304
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3304
gcgagggatt acggatacta ctttgactac 30

<210> 3305
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3305
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcagag ttacaatttg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3306
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3306
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
                85   90   95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 3307
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 3307
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1   5   10   15

Ala

<210> 3308
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 3308
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t   51

<210> 3309
<211> 7
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3309
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3310
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3310
tgggcatcta cccgggaatc c 21

<210> 3311
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3311
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 3312
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3312
aagcagagtt acaatttgag aact 24

<210> 3313

<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3313
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcacc agctcctata tacactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atctaccctg gtaatgttaa cacaaagtac 180

aacgagaagt tcaagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc tagggactat 300

ggttactact ttgactactg gggccaagga accctggtca ccgtctcctc a 351

<210> 3314
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3314
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Ser
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Tyr Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 3315
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3315
Tyr Thr Phe Thr Ser Ser Tyr Ile His
1 5

<210> 3316
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3316
tacaccttca ccagctccta tatacac 27

<210> 3317
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3317
Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 3318
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3318
tggatctacc ctggtaatgt taacacaaag tacaacgaga agttcaaggg c 51

<210> 3319
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3319
Ala Arg Asp Tyr Gly Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3320
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3320
gctagggact atggttacta ctttgactac 30

<210> 3321
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region nucleic acid sequence

<400> 3321
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcagag ttacaatttg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3322
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3322
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3323
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3323
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3324
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3324
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3325
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3325
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3326
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3326
tgggcatcta cccgggaatc c 21

<210> 3327
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3327
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 3328
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3328
aagcagagtt acaatttgag aact 24

<210> 3329
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3329
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcacc agctcctata tacactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gataggatgg atctaccctg gtaatgttaa cacaaagtac 180

aacgagaagt tcaagggcag agtcaccatg accgcggaca agtccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc tagggactac 300

ggttattact ttgactactg gggccaagga accctggtca ccgtctcctc a 351

<210> 3330
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3330
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Ser
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Val Thr Met Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Tyr Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 3331
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3331
Tyr Thr Phe Thr Ser Ser Tyr Ile His
1 5

<210> 3332
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3332
tacaccttca ccagctccta tatacac 27

<210> 3333
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3333
Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 3334
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3334
tggatctacc ctggtaatgt taacacaaag tacaacgaga agttcaaggg c 51

<210> 3335
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3335
Ala Arg Asp Tyr Gly Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3336
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3336
gctagggact acggttatta ctttgactac 30

<210> 3337
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3337
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctaggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcagag ttacaatttg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3338
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3338
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3339
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3339
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3340
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3340
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3341
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3341
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3342
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3342
tgggcatcta cccgggaatc c 21

<210> 3343
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3343
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 3344
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3344
aagcagagtt acaatttgag aact 24

<210> 3345
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3345
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcacc agctcctata tacactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gataggatgg atctaccctg gtaatgttaa cacaaagtac 180

aacgagaagt tcaagggcag agccaccctg accgcggaca agtccacgag cacagcctac 240

atgcacctga gcagcctgag atctgaggac acggcggtgt actactgcgc gagggactat 300

ggctactact ttgactactg gggccaagga accctggtca ccgtctcctc a 351

<210> 3346
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3346

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Ser
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Ala Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met His Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Tyr Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 3347
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3347
Tyr Thr Phe Thr Ser Ser Tyr Ile His
1 5

<210> 3348
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3348
tacaccttca ccagctccta tatacac 27

<210> 3349
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3349
Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 3350
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3350
tggatctacc ctggtaatgt taacacaaag tacaacgaga agttcaaggg c 51

<210> 3351
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3351
Ala Arg Asp Tyr Gly Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3352
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3352
gcgagggact atggctacta ctttgactac 30

<210> 3353
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3353
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcagag ttacaatttg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3354
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3354
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
                85   90   95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 3355
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 3355
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1   5   10   15

Ala

<210> 3356
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 3356
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t   51

<210> 3357
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3357
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3358
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3358
tgggcatcta cccgggaatc c 21

<210> 3359
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3359
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 3360
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3360

aagcagagtt acaatttgag aact 24

<210> 3361
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3361
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggatt caacatcaag gactactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atcgaccctg aaaatggtaa cacaatctac 180

gacccgaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc tagagacgga 300

tatgcaaggt attactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3362
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3362
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 3363
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3363
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 3364
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3364
ttcaacatca aggactacta tatgcac 27

<210> 3365
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3365
Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 3366
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3366
tggatcgacc ctgaaaatgg taacacaatc tacgacccga agttccaggg c 51

<210> 3367
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3367
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3368
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3368
gctagagacg gatatgcaag gtattacttt gactac 36

<210> 3369
<211> 336
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3369
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3370
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3370
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3371
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3371
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3372
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3372
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3373
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3373
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3374

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3374
tgggcatcta cccgggaatc c 21

<210> 3375
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3375
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 3376
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3376
aagcaatctt attctctgag aact 24

<210> 3377
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3377
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggatt caacatcaag gactactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gataggatgg atcgaccctg aaaatggtaa cacaatctac 180

gacccgaagt tccagggcag agtcaccatg accgcggaca cgtccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc gagggacggt 300

tatgctagat attactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3378
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3378
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 3379
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3379
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 3380
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3380
ttcaacatca aggactacta tatgcac 27

<210> 3381
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3381
Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 3382
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3382
tggatcgacc ctgaaaatgg taacacaatc tacgacccga agttccaggg c 51

<210> 3383
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3383
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3384
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3384
gcgagggacg gttatgctag atattacttt gactac 36

<210> 3385
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3385
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3386
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3386
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3387
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3387

Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3388
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3388
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3389
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3389
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3390
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3390
tgggcatcta cccgggaatc c 21

<210> 3391
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3391
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 3392
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3392
aagcaatctt attctctgag aact 24

<210> 3393
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3393
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggatt caacatcaag gactactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gataggatgg atcgaccctg aaaatggtaa cacaatctac 180

gacccgaagt tccagggcag agccaccata accgcggaca cgtccacgaa cacagcctac 240

atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc cagagatggt 300

tatgccagat actactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3394
<211> 119
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3394
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Ala Thr Ile Thr Ala Asp Thr Ser Thr Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 3395
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3395
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 3396
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3396
ttcaacatca aggactacta tatgcac 27

<210> 3397
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3397
Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 3398
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3398
tggatcgacc ctgaaaatgg taacacaatc tacgacccga agttccaggg c 51

<210> 3399
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3399

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3400
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3400
gccagagatg gttatgccag atactacttt gactac 36

<210> 3401
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3401
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3402
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3402
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
            20   25   30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
                85   90   95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 3403
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 3403
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1   5   10   15

Ala

<210> 3404
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 3404
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3405
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3405
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3406
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3406
tgggcatcta cccgggaatc c 21

<210> 3407
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3407
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 3408
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3408
aagcaatctt attctctgag aact 24

<210> 3409
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3409
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggcc 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccctg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgctagat attactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3410
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3410
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 3411
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3411
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 3412
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3412
ttcaacatca aggactacta tatgcac 27

<210> 3413
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3413
Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 3414
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3414
tggatcgacc ctgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 3415
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3415
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3416
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3416
gcgagagatg gatacgctag atattacttt gactac 36

<210> 3417
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3417
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3418
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3418
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3419
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3419
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3420
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3420
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3421
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3421
Trp Ala Ser Thr Arg Glu Ser

1 5

<210> 3422
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3422
tgggcatcta cccgggaatc c 21

<210> 3423
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3423
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 3424
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3424
aagcaatctt attctctgag aact 24

<210> 3425
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3425
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggcc 120

cctggacaaa ggcttgagtg gataggatgg atcgaccctg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accgcggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc tagagacggt 300

tacgccagat attactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3426
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3426
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
        115

<210> 3427
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 3427
Phe Asn Ile Lys Asp Tyr Tyr Met His
1   5

<210> 3428
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3428
ttcaacatca aggactacta tatgcac   27

<210> 3429
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H2 amino acid sequence

<400> 3429
Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1   5   10   15

Gly

<210> 3430
<211> 51
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3430
tggatcgacc ctgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 3431
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3431
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3432
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3432
gctagagacg gttacgccag atattacttt gactac 36

<210> 3433
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3433
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3434
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3434
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3435
<211> 17
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3435
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3436
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3436
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3437
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3437
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3438
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3438
tgggcatcta cccgggaatc c 21

<210> 3439
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3439
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 3440
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3440
aagcaatctt attctctgag aact 24

<210> 3441
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3441
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggcc 120

cctggacaaa ggcttgagtg gataggatgg atcgaccctg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggccaccata accgcggaca cgtccgccaa cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagacgga 300

tacgcgagat actactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3442
<211> 119

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3442
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
            20   25   30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Ile
        35   40   45

Gly Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
    50   55   60

Gln Gly Arg Ala Thr Ile Thr Ala Asp Thr Ser Ala Asn Thr Ala Tyr
65   70   75   80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Leu Val Thr Val Ser Ser
        115

<210> 3443
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3443
Phe Asn Ile Lys Asp Tyr Tyr Met His
1   5

<210> 3444
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3444
ttcaacatca aggactacta tatgcac 27

<210> 3445
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3445
Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 3446
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3446
tggatcgacc ctgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 3447
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3447
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3448
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3448
gcgagagacg gatacgcgag atactacttt gactac 36

<210> 3449
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3449
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3450
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3450
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3451
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3451
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3452
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3452
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3453
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3453
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3454
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3454
tgggcatcta cccgggaatc c 21

<210> 3455
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3455
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 3456
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3456
aagcaatctt attctctgag aact 24

<210> 3457
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3457
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggatt caacatcaag gactactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atcgaccctg aaaatggtaa cacaatctac 180

gacccgaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc tagagacgga 300

tatgcaaggt attactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3458
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3458
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 3459
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3459
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 3460
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3460
ttcaacatca aggactacta tatgcac 27

<210> 3461

<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3461
Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 3462
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3462
tggatcgacc ctgaaaatgg taacacaatc tacgacccga agttccaggg c 51

<210> 3463
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3463
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3464
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3464
gctagagacg gatatgcaag gtattacttt gactac 36

<210> 3465
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3465
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcagag ttacaatttg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3466
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3466
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3467
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3467
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3468
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3468
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3469
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region CDR L2 amino acid sequence

<400> 3469
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3470
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3470
tgggcatcta cccgggaatc c 21

<210> 3471
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3471
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 3472
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3472
aagcagagtt acaatttgag aact 24

<210> 3473
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3473
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggatt caacatcaag gactactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gataggatgg atcgaccctg aaaatggtaa cacaatctac 180

gacccgaagt tccagggcag agccaccata accgcggaca cgtccacgaa cacagcctac 240

atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc cagagatggt 300

tatgccagat actactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3474
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3474
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Ala Thr Ile Thr Ala Asp Thr Ser Thr Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 3475
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3475
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 3476
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3476
ttcaacatca aggactacta tatgcac 27

<210> 3477
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3477
Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 3478
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3478
tggatcgacc ctgaaaatgg taacacaatc tacgacccga agttccaggg c 51

<210> 3479
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3479
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3480
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3480
gccagagatg gttatgccag atactacttt gactac 36

<210> 3481
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3481
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcagag ttacaatttg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3482
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3482
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3483
<211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3483
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3484
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3484
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3485
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3485
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3486
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3486
tgggcatcta cccgggaatc c 21

<210> 3487
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3487
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 3488
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3488
aagcagagtt acaatttgag aact 24

<210> 3489
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3489
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggcc 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccctg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgctagat attactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3490
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3490
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 3491
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3491
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 3492
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3492
ttcaacatca aggactacta tatgcac 27

<210> 3493
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3493
Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 3494
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3494
tggatcgacc ctgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 3495
<211> 12

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3495
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3496
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3496
gcgagagatg gatacgctag atattacttt gactac 36

<210> 3497
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3497
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agtgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcagag ttacaatttg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3498
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3498
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3499
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3499
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3500
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3500
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3501
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3501
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3502
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3502
tgggcatcta cccgggaatc c 21

<210> 3503
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3503
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 3504
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3504
aagcagagtt acaatttgag aact 24

<210> 3505
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3505
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggcc 120

cctggacaaa ggcttgagtg gataggatgg atcgaccctg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accgcggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc tagagacggt 300

tacgccagat attactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3506
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3506
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Ile
        35                  40                  45


Gly Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Ala Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 3507
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 3507
Phe Asn Ile Lys Asp Tyr Tyr Met His
1               5


<210> 3508
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3508
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ttcaacatca aggactacta tatgcac 27

<210> 3509
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3509
Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 3510
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3510
tggatcgacc ctgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 3511
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3511
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3512
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3512
gctagagacg gttacgccag atattacttt gactac 36

<210> 3513
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3513
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcagag ttacaatttg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3514
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3514
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
                85   90   95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 3515
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 3515
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1   5   10   15

Ala

<210> 3516
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 3516
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t   51

<210> 3517
<211> 7
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3517
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3518
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3518
tgggcatcta cccgggaatc c 21

<210> 3519
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3519
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 3520
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3520
aagcagagtt acaatttgag aact 24

<210> 3521

<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3521
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggcc 120

cctggacaaa ggcttgagtg gataggatgg atcgaccctg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggccaccata accgcggaca cgtccgccaa cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagacgga 300

tacgcgagat actactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3522
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3522
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Ala Thr Ile Thr Ala Asp Thr Ser Ala Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 3523
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3523
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 3524
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3524
ttcaacatca aggactacta tatgcac 27

<210> 3525
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3525
Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 3526
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3526
tggatcgacc ctgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 3527
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3527
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3528
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3528
gcgagagacg gatacgcgag atactacttt gactac 36

<210> 3529
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region nucleic acid sequence

<400> 3529
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcagag ttacaatttg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3530
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3530
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3531
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3531
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3532
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3532
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3533
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3533
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3534
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3534
tgggcatcta cccgggaatc c 21

<210> 3535
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3535
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 3536
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3536
aagcagagtt acaatttgag aact 24

<210> 3537
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3537
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggatt caacatcaag gactactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gataggatgg atcgaccctg aaaatggtaa cacaatctac 180

gacccgaagt tccagggcag agtcaccatg accgcggaca cgtccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc gagggacggt 300

tatgctagat attactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3538
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3538
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 3539
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3539
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 3540
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3540
ttcaacatca aggactacta tatgcac 27

<210> 3541
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3541
Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 3542
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3542
tggatcgacc ctgaaaatgg taacacaatc tacgacccga agttccaggg c 51

<210> 3543
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3543
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3544
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3544
gcgagggacg gttatgctag atattacttt gactac 36

<210> 3545
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3545
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcagag ttacaatttg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3546
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3546
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3547
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3547
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3548
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3548
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3549
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3549
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3550
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3550
tgggcatcta cccgggaatc c 21

<210> 3551
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3551
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 3552
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3552
aagcagagtt acaatttgag aact 24

<210> 3553
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3553
caggtccagc ttgtacagtc tggggctgag gtgaagaagc ctggggcctc agtgaagatt 60

tcctgcaagg cttcgggata ccccttcagt tcctatccta tgcattgggt gcgccaggcc 120

cccggacaaa ggcttgagtg gatgggatgg atcaacgttg acaatgagaa cacaaaatat 180

tcatggaagt tccggggcag agtcaccatt accagggaca catccgcgag cacagtttac 240

atggagctga gcagtctgat atctgaagac acggctgtgt attactgtgg gagagactgg 300

gacggggcga tccgtgtctt ggactactgg ggccagggaa ccctggtcac cgtctcctca 360

<210> 3554
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3554

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Pro Phe Ser Ser Tyr
            20                  25                  30


Pro Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Asn Val Asp Asn Glu Asn Thr Lys Tyr Ser Trp Lys Phe
    50                  55                  60


Arg Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Val Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Ile Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Gly Arg Asp Trp Asp Gly Ala Ile Arg Val Leu Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 3555
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 3555
Tyr Pro Phe Ser Ser Tyr Pro Met His
1               5


<210> 3556
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
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<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3556
tacccttca gttcctatcc tatgcat 27

<210> 3557
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3557
Trp Ile Asn Val Asp Asn Glu Asn Thr Lys Tyr Ser Trp Lys Phe Arg
1 5 10 15

Gly

<210> 3558
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3558
tggatcaacg ttgacaatga gaacacaaaa tattcatgga agttccgggg c 51

<210> 3559
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3559
Gly Arg Asp Trp Asp Gly Ala Ile Arg Val Leu Asp Tyr
1 5 10

<210> 3560
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3560
gggagagact gggacggggc gatccgtgtc ttggactac 39

<210> 3561
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3561
gatattgtga tgactcagac tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcacctgca agtccagcca gagtgtttta ttcagctccg acaataagaa ctacttagct 120

tggtaccagc agaaaccggg acagcctcct aaattgctca tttactgggc atctatccgg 180

gaatccgggg tccctgaccg attcggtggc agcgggtctg ggacacattt cactctcacc 240

atcaccagcg tgcaggctgc agatgtggca gtttattact gtcagcaata ttatggtaat 300

ttccccacct tcggccaagg gacacgactg gagattaaa 339

<210> 3562
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3562
Asp Ile Val Met Thr Gln Thr Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Thr Cys Lys Ser Ser Gln Ser Val Leu Phe Ser
20 25 30

Ser Asp Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ile Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Gly Gly Ser Gly Ser Gly Thr His Phe Thr Leu Thr
65 70 75 80

Ile Thr Ser Val Gln Ala Ala Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Gly Asn Phe Pro Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile
100 105 110

Lys

<210> 3563
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3563
Lys Ser Ser Gln Ser Val Leu Phe Ser Ser Asp Asn Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3564
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3564
aagtccagcc agagtgtttt attcagctcc gacaataaga actacttagc t 51

<210> 3565
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3565
Trp Ala Ser Ile Arg Glu Ser
1 5

<210> 3566
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3566
tgggcatcta tccgggaatc c 21

<210> 3567
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3567
Gln Gln Tyr Tyr Gly Asn Phe Pro Thr
1 5

<210> 3568
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3568
cagcaatatt atggtaattt ccccacc 27

<210> 3569
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3569
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgctagat attactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3570
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3570
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 3571
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3571
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 3572
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3572
ttcaacatca aggactacta tatgcac 27

<210> 3573
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3573
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 3574
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3574
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 3575
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3575
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3576
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3576
gcgagagatg gatacgctag atattacttt gactac 36

<210> 3577
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3577
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattttcgg 300

agagctttcg gcggagggac caaggttgag atcaaa 336

<210> 3578
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3578
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Phe Arg Arg Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3579
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3579
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3580
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3580
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3581
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3581
Trp Ala Ser Thr Arg Glu Ser

1 5

<210> 3582
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3582
tgggcatcta cccgggaatc c 21

<210> 3583
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3583
Lys Gln Ser Tyr Phe Arg Arg Ala
1 5

<210> 3584
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3584
aagcaatctt attttcggag agct 24

<210> 3585
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3585
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ccggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacaccaag gactactata tgcactgggt gcgacaggcc 120

cccgggcaaa ggcttgagtg gatgggatgg atcggccctg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag gtctgaagac acggcggtgt actactgcgc gagggatgga 300

tacgctagat attactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3586
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3586
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Thr Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Gly Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 3587
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3587
Phe Asn Thr Lys Asp Tyr Tyr Met His
1 5

<210> 3588
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3588
ttcaacacca aggactacta tatgcac 27

<210> 3589
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3589
Trp Ile Gly Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 3590
<211> 51
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3590
tggatcggcc ctgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 3591
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3591
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3592
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3592
gcgagggatg gatacgctag atattacttt gactac 36

<210> 3593
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3593
gacatcgtaa tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca ggtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggttgag atcaaa 336

<210> 3594
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3594
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Arg Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3595
<211> 17
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3595
Arg Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3596
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3596
aggtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3597
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3597
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3598
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3598
tgggcatcta cccgggaatc c 21

<210> 3599
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3599
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 3600
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3600
aagcaatctt attctcggag aact 24

<210> 3601
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3601
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggcc 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaaat ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atccgaagac acggcggtgt actactgcgc gagagatgga 300

tacgctagat attactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3602
<211> 119

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3602
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
            20   25   30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35   40   45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
    50   55   60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65   70   75   80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Leu Val Thr Val Ser Ser
        115

<210> 3603
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3603
Phe Asn Ile Lys Asp Tyr Tyr Met His
1   5

<210> 3604
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3604
ttcaacatca aggactacta tatgcac 27

<210> 3605
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3605
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 3606
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3606
tggatcgacc ttgaaaatgg taacacaatc tatgacccga aatttcaggg c 51

<210> 3607
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3607
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3608
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3608
gcgagagatg gatacgctag atattacttt gactac 36

<210> 3609
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3609
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacggcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggactg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggttgag atcaaa 336

<210> 3610
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3610
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Gly
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Thr Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3611
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3611
Lys Ser Ser Gln Ser Leu Leu Asn Gly Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3612
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3612
aagtccagcc agagtctttt aaacggcaga accagaaaga actacttagc t 51

<210> 3613
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3613
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3614
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3614
tgggcatcta cccgggaatc c 21

<210> 3615
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3615
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 3616
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3616
aagcaatctt attctcggag aact 24

<210> 3617
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3617
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaag ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgctagat attactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3618
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3618
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

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Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 3619
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 3619
Phe Asn Ile Lys Asp Tyr Tyr Met His
1               5


<210> 3620
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3620
ttcaacatca aggactacta tatgcac                                          27


<210> 3621
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<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3621
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 3622
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3622
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 3623
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3623
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3624
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3624
gcgagagatg gatacgctag atattacttt gactac 36

<210> 3625
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3625
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattttcgg 300

agagctttcg gcggagggac caaggttgag atcaaa 336

<210> 3626
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3626
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Phe Arg Arg Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3627
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3627
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3628
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3628
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3629
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region CDR L2 amino acid sequence

<400> 3629
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3630
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3630
tgggcatcta cccgggaatc c 21

<210> 3631
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3631
Lys Gln Ser Tyr Phe Arg Arg Ala
1 5

<210> 3632
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3632
aagcaatctt attttcggag agct 24

<210> 3633
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3633
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggcc 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgctagat attactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3634
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3634
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 3635
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3635
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 3636
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3636
ttcaacatca aggactacta tatgcac 27

<210> 3637
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3637
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 3638
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3638
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 3639
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3639
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3640
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3640
gcgagagatg gatacgctag atattacttt gactac 36

<210> 3641
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3641
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggttgag atcaaa 336

<210> 3642
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3642
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3643
<211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3643
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3644
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3644
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3645
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3645
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3646
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3646
tgggcatcta cccgggaatc c 21

<210> 3647
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3647
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 3648
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3648
aagcaatctt attctcggag aact 24

<210> 3649
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3649
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggcc 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaaat ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgctagat attactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3650
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3650
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 3651
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3651
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 3652
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3652
ttcaacatca aggactacta tatgcac 27

<210> 3653
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3653
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 3654
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3654
tggatcgacc ttgaaaatgg taacacaatc tatgacccga aatttcaggg c 51

<210> 3655
<211> 12

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3655
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3656
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3656
gcgagagatg gatacgctag atattacttt gactac 36

<210> 3657
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3657
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcgg gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 3658
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3658
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gly Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3659
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3659
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3660
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3660
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3661
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3661
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3662
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3662
tgggcatcta cccgggaatc c 21

<210> 3663
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3663
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 3664
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3664
aagcaatctt attctcggag aact 24

<210> 3665
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3665
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ccggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacaccaag gactactata tgcactgggt gcgacaggcc 120

cccgggcaaa ggcttgagtg gatgggatgg atcggccctg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag gtctgaagac acggcggtgt actactgcgc gagggatgga 300

tacgctagat attactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3666
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3666
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Thr Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Gly Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 3667
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3667
Phe Asn Thr Lys Asp Tyr Tyr Met His
1 5

<210> 3668
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3668

ttcaacacca aggactacta tatgcac 27

<210> 3669
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3669
Trp Ile Gly Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 3670
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3670
tggatcggcc ctgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 3671
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3671
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3672
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3672
gcgagggatg gatacgctag atattacttt gactac 36

<210> 3673
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3673
gacatcgtga tgacccagtc tccagactcc ctggctgtgc ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagcctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggttgag atcaaa 336

<210> 3674
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3674
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Pro Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
                85   90   95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 3675
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 3675
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1   5   10   15

Ala

<210> 3676
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 3676
aagtccagcc agagcctttt aaacagcaga accagaaaga actacttagc t   51

<210> 3677
<211> 7
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3677
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3678
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3678
tgggcatcta cccgggaatc c 21

<210> 3679
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3679
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 3680
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3680
aagcaatctt attctcggag aact 24

<210> 3681

<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3681
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggcc 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaaat ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgctagat attactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3682
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3682
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 3683
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3683
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 3684
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3684
ttcaacatca aggactacta tatgcac 27

<210> 3685
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3685
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 3686
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3686
tggatcgacc ttgaaaatgg taacacaatc tatgacccga aatttcaggg c 51

<210> 3687
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3687
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3688
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3688
gcgagagatg gatacgctag atattacttt gactac 36

<210> 3689
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region nucleic acid sequence

<400> 3689
gacatcgtaa tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca ggtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctatccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggttgag atcaaa 336

<210> 3690
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3690
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Arg Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ile Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3691
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3691
Arg Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3692
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3692
aggtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3693
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3693
Trp Ala Ser Ile Arg Glu Ser
1 5

<210> 3694
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3694
tgggcatcta tccgggaatc c 21

<210> 3695
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3695
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 3696
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3696
aagcaatctt attctcggag aact 24

<210> 3697
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3697
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgctagat attactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3698
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3698
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 3699
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3699
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 3700
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3700
ttcaacatca aggactacta tatgcac 27

<210> 3701
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3701
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 3702
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3702
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 3703
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3703
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3704
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3704
gcgagagatg gatacgctag atattacttt gactac 36

<210> 3705
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3705
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattttcgg 300

agagctttcg gcggagggac caaggttgag atcaaa 336

<210> 3706
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3706
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Phe Arg Arg Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3707
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3707
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3708
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3708
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3709
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3709
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3710
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3710
tgggcatcta cccgggaatc c 21

<210> 3711
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3711
Lys Gln Ser Tyr Phe Arg Arg Ala
1 5

<210> 3712
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3712
aagcaatctt attttcggag agct 24

<210> 3713
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3713
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggcc 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaaat ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgctagat attactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3714
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3714

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 3715
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 3715
Phe Asn Ile Lys Asp Tyr Tyr Met His
1               5


<210> 3716
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
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<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3716
ttcaacatca aggactacta tatgcac 27

<210> 3717
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3717
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 3718
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3718
tggatcgacc ttgaaaatgg taacacaatc tatgacccga aatttcaggg c 51

<210> 3719
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3719
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3720
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3720
gcgagagatg gatacgctag atattacttt gactac 36

<210> 3721
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3721
gacatcgtaa tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca ggtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggttgag atcaaa 336

<210> 3722
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3722
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Arg Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3723
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3723
Arg Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3724
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3724
aggtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3725
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3725
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3726
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3726
tgggcatcta cccgggaatc c 21

<210> 3727
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3727
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 3728
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3728

aagcaatctt attctcggag aact 24

<210> 3729
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3729
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgctagat attactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3730
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3730
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 3731
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3731
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 3732
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3732
ttcaacatca aggactacta tatgcac 27

<210> 3733
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3733
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 3734
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3734
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 3735
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3735
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3736
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3736
gcgagagatg gatacgctag atattacttt gactac 36

<210> 3737
<211> 336
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3737
ggcatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 3738
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3738
Gly Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3739
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3739
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3740
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3740
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3741
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3741
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3742

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3742
tgggcatcta cccgggaatc c 21

<210> 3743
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3743
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 3744
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3744
aagcaatctt attctcggag aact 24

<210> 3745
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3745
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggcc 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaaat ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgctagat attactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3746
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3746

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala
1				5					10					15	

Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Phe	Asn	Ile	Lys	Asp	Tyr
		20					25					30			

Tyr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Arg	Leu	Glu	Trp	Met
		35					40					45			

Gly	Trp	Ile	Asp	Leu	Glu	Asn	Gly	Asn	Thr	Ile	Tyr	Asp	Pro	Lys	Phe
	50					55					60				

Gln	Gly	Arg	Val	Thr	Ile	Thr	Arg	Asp	Thr	Ser	Ala	Ser	Thr	Ala	Tyr
65				70					75					80	

Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	

Ala	Arg	Asp	Gly	Tyr	Ala	Arg	Tyr	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly
			100					105					110		

Thr	Leu	Val	Thr	Val	Ser	Ser
		115				

<210> 3747
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3747
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 3748
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3748
ttcaacatca aggactacta tatgcac 27

<210> 3749
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3749
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 3750
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3750
tggatcgacc ttgaaaatgg taacacaatc tatgacccga aatttcaggg c 51

<210> 3751
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3751
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3752
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3752
gcgagagatg gatacgctag atattacttt gactac 36

<210> 3753
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3753
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacggcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggttgag atcaaa 336

<210> 3754
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3754
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Gly
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3755
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3755

Lys Ser Ser Gln Ser Leu Leu Asn Gly Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3756
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3756
aagtccagcc agagtctttt aaacggcaga accagaaaga actacttagc t 51

<210> 3757
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3757
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3758
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3758
tgggcatcta cccgggaatc c 21

<210> 3759
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3759
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 3760
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3760
aagcaatctt attctcggag aact 24

<210> 3761
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3761
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggcc 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg acaatggtaa cacaatctat 180

gacccgaaat ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgctagat attactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3762
<211> 119
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3762
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Asp Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 3763
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3763
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 3764
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3764
ttcaacatca aggactacta tatgcac 27

<210> 3765
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3765
Trp Ile Asp Leu Asp Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 3766
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3766
tggatcgacc ttgacaatgg taacacaatc tatgacccga aatttcaggg c 51

<210> 3767
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3767

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3768
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3768
gcgagagatg gatacgctag atattacttt gactac 36

<210> 3769
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3769
gacatcgtga tgacccagtc tccagactcc ctggctgtgc ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagcctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggttgag atcaaa 336

<210> 3770
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3770
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Pro Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
            20   25   30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
                85   90   95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 3771
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 3771
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1   5   10   15

Ala

<210> 3772
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 3772
aagtccagcc agagcctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3773
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3773
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3774
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3774
tgggcatcta cccgggaatc c 21

<210> 3775
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3775
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 3776
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3776
aagcaatctt attctcggag aact 24

<210> 3777
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3777
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggcc 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaaat ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atccgaagac acggcggtgt actactgcgc gagagatgga 300

tacgctagat attactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3778
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3778
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 3779
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3779
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 3780
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3780
ttcaacatca aggactacta tatgcac 27

<210> 3781
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3781
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 3782
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3782
tggatcgacc ttgaaaatgg taacacaatc tatgacccga aatttcaggg c 51

<210> 3783
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3783
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3784
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3784
gcgagagatg gatacgctag atattacttt gactac 36

<210> 3785
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3785
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta acggcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggactg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggttgag atcaaa 336

<210> 3786
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3786
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Gly
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Thr Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3787
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3787
Lys Ser Ser Gln Ser Leu Leu Asn Gly Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3788
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3788
aagtccagcc agagtctttt aaacggcaga accagaaaga actacttagc t 51

<210> 3789
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3789
Trp Ala Ser Thr Arg Glu Ser

1 5

<210> 3790
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3790
tgggcatcta cccgggaatc c 21

<210> 3791
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3791
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 3792
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3792
aagcaatctt attctcggag aact 24

<210> 3793
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3793
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggcc 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaaat ttcagggcag ggtcaccata accaggaaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgctagat attactttga ctactggggc caaggaaccc tggtcaccgt ttcctca 357

<210> 3794
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3794
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asn Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
        115

<210> 3795
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 3795
Phe Asn Ile Lys Asp Tyr Tyr Met His
1   5

<210> 3796
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3796
ttcaacatca aggactacta tatgcac   27

<210> 3797
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H2 amino acid sequence

<400> 3797
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1   5   10   15

Gly

<210> 3798
<211> 51
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3798
tggatcgacc ttgaaaatgg taacacaatc tatgacccga aatttcaggg c 51

<210> 3799
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3799
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3800
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3800
gcgagagatg gatacgctag atattacttt gactac 36

<210> 3801
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3801
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggttgag atcaaa 336

<210> 3802
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3802
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3803
<211> 17
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3803
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3804
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3804
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3805
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3805
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3806
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3806
tgggcatcta cccgggaatc c 21

<210> 3807
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3807
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 3808
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3808
aagcaatctt attctcggag aact 24

<210> 3809
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3809
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgctagat attactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3810
<211> 119

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3810
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
            20   25   30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35   40   45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
    50   55   60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65   70   75   80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Leu Val Thr Val Ser Ser
        115

<210> 3811
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3811
Phe Asn Ile Lys Asp Tyr Tyr Met His
1   5

<210> 3812
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3812
ttcaacatca aggactacta tatgcac 27

<210> 3813
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3813
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 3814
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3814
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 3815
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3815
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3816
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3816
gcgagagatg gatacgctag atattacttt gactac 36

<210> 3817
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3817
gacatcgtga tgacccagtc tccagactcc ctggctgtgc ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagcctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggttgag atcaaa 336

<210> 3818
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3818
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Pro Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3819
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3819
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3820
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3820
aagtccagcc agagcctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3821
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3821
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3822
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3822
tgggcatcta cccgggaatc c 21

<210> 3823
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3823
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 3824
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3824
aagcaatctt attctcggag aact 24

<210> 3825
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3825
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgctagat attactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3826
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3826
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 3827
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3827
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 3828
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3828
ttcaacatca aggactacta tatgcac 27

<210> 3829

<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3829
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 3830
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3830
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 3831
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3831
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3832
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3832
gcgagagatg gatacgctag atattacttt gactac 36

<210> 3833
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3833
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3834
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3834
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3835
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3835
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3836
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3836
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3837
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region CDR L2 amino acid sequence

<400> 3837
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3838
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3838
tgggcatcta cccgggaatc c 21

<210> 3839
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3839
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 3840
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3840
aagcaatctt attctcggag aact 24

<210> 3841
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3841
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggact caacatcaag gactactata tgcactgggt gcgacaggcc 120

cctggacaaa ggcttgagtg gatgggatgg atcggctctg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc gagagatgga 300

tacgctagat attacttcga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3842
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3842
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Leu Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Gly Ser Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 3843
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3843
Leu Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 3844
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3844
ctcaacatca aggactacta tatgcac 27

<210> 3845
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3845
Trp Ile Gly Ser Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 3846
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3846
tggatcggct ctgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 3847
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3847
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3848
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3848
gcgagagatg gatacgctag atattacttc gactac 36

<210> 3849
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3849
gacatcgtga tgacccagtc tccagactcc ctggctgtgc ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagcctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggttgag atcaaa 336

<210> 3850
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3850
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Pro Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3851
<211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3851
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3852
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3852
aagtccagcc agagcctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3853
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3853
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3854
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3854
tgggcatcta cccgggaatc c 21

<210> 3855
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3855
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 3856
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3856
aagcaatctt attctcggag aact 24

<210> 3857
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3857
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggact caacatcaag gactactata tgcactgggt gcgacaggcc 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaaat ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgctagat attactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3858
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3858
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Leu Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 3859
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3859
Leu Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 3860
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3860
ctcaacatca aggactacta tatgcac 27

<210> 3861
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3861
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 3862
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3862
tggatcgacc ttgaaaatgg taacacaatc tatgacccga aatttcaggg c 51

<210> 3863
<211> 12

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3863
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3864
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3864
gcgagagatg gatacgctag atattacttt gactac 36

<210> 3865
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3865
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 3866
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3866
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3867
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3867
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3868
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3868
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 3869
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3869
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3870
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3870
tgggcatcta cccgggaatc c 21

<210> 3871
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3871
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 3872
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3872
aagcaatctt attctcggag aact 24

<210> 3873
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3873
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ccggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacaccaag gactactata tgcactgggt gcgacaggcc 120

cccgggcaaa ggcttgagtg gatgggatgg atcggccctg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag gtctgaagac acggcggtgt actactgcgc gagggatgga 300

tacgctagat attactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3874
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3874
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Thr Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Gly Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 3875
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3875
Phe Asn Thr Lys Asp Tyr Tyr Met His
1 5

<210> 3876
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3876

ttcaacacca aggactacta tatgcac 27

<210> 3877
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3877
Trp Ile Gly Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 3878
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3878
tggatcggcc ctgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 3879
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3879
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3880
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3880
gcgagggatg gatacgctag atattacttt gactac 36

<210> 3881
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3881
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacaacagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggttgag atcaaa 336

<210> 3882
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3882
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Asn
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
                85   90   95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 3883
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 3883
Lys Ser Ser Gln Ser Leu Leu Asn Asn Arg Thr Arg Lys Asn Tyr Leu
1   5   10   15

Ala

<210> 3884
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 3884
aagtccagcc agagtctttt aaacaacaga accagaaaga actacttagc t   51

<210> 3885
<211> 7
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3885
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3886
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3886
tgggcatcta cccgggaatc c 21

<210> 3887
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3887
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 3888
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3888
aagcaatctt attctcggag aact 24

<210> 3889

<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3889
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggcc 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaaat ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgctagat attactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3890
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3890
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 3891
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3891
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 3892
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3892
ttcaacatca aggactacta tatgcac 27

<210> 3893
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3893
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 3894
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3894
tggatcgacc ttgaaaatgg taacacaatc tatgacccga aatttcaggg c 51

<210> 3895
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3895
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3896
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3896
gcgagagatg gatacgctag atattacttt gactac 36

<210> 3897
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region nucleic acid sequence

<400> 3897
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattttcgg 300

agagctttcg gcggagggac caaggttgag atcaaa 336

<210> 3898
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3898
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Phe Arg Arg Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3899
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3899
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3900
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3900
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3901
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3901
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3902
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3902
tgggcatcta cccgggaatc c 21

<210> 3903
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3903
Lys Gln Ser Tyr Phe Arg Arg Ala
1 5

<210> 3904
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3904
aagcaatctt attttcggag agct 24

<210> 3905
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3905
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

gcctgcaagg cttctggatc caatatcaag gactactatg tgcactgggt gcgacaggcc 120

cctggacaaa ggcttgagtg gatgggatgg atcggccctg aaaatggtaa cacagtctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgctagat attactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3906
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3906
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ala Cys Lys Ala Ser Gly Ser Asn Ile Lys Asp Tyr
20 25 30

Tyr Val His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Gly Pro Glu Asn Gly Asn Thr Val Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 3907
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3907
Ser Asn Ile Lys Asp Tyr Tyr Val His
1 5

<210> 3908
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3908
tccaatatca aggactacta tgtgcac 27

<210> 3909
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3909
Trp Ile Gly Pro Glu Asn Gly Asn Thr Val Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 3910
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3910
tggatcggcc ctgaaaatgg taacacagtc tatgacccga agtttcaggg c 51

<210> 3911
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3911
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3912
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3912
gcgagagatg gatacgctag atattacttt gactac 36

<210> 3913
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3913
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3914
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3914
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3915
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3915
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3916
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3916
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3917
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3917
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3918
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3918
tgggcatcta cccgggaatc c 21

<210> 3919
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3919
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 3920
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3920
aagcaatctt attctctgag aact 24

<210> 3921
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3921
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcacc agccactata tacactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atctaccctg gtgatggtag cacaaagtac 180

aacgagaagt tcaagggcag agtcaccatg accgcggaca agtccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc tagagatggc 300

tcatattact ttgactactg gggccaagga accctggtca ccgtctcctc a 351

<210> 3922
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3922

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser His
            20                  25                  30


Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Gly Arg Val Thr Met Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Gly Ser Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser
        115


<210> 3923
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 3923
Tyr Thr Phe Thr Ser His Tyr Ile His
1               5


<210> 3924
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
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<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3924
tacaccttca ccagccacta tatacac 27

<210> 3925
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3925
Trp Ile Tyr Pro Gly Asp Gly Ser Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 3926
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3926
tggatctacc ctggtgatgg tagcacaaag tacaacgaga agttcaaggg c 51

<210> 3927
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3927
Ala Arg Asp Gly Ser Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3928
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3928
gctagagatg gctcatatta ctttgactac 30

<210> 3929
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3929
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3930
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3930
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3931
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3931
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3932
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3932
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3933
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3933
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3934
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3934
tgggcatcta cccgggaatc c 21

<210> 3935
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3935
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 3936
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3936

aagcaatctt attctctgag aact 24

<210> 3937
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3937
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcacc agctcctata tacactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gataggatgg atctaccctg gtaatgttga cacaaggtac 180

aacgagaagt tcaagggcag agtcaccata accgcggaca agtccgcgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc gagggattac 300

ggatactact ttgactactg gggccaagga accctggtca ccgtctcctc a 351

<210> 3938
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3938
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Ser
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Gly Asn Val Asp Thr Arg Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Tyr Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 3939
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3939
Tyr Thr Phe Thr Ser Ser Tyr Ile His
1 5

<210> 3940
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3940
tacaccttca ccagctccta tatacac 27

<210> 3941
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3941
Trp Ile Tyr Pro Gly Asn Val Asp Thr Arg Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 3942
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3942
tggatctacc ctggtaatgt tgacacaagg tacaacgaga agttcaaggg c 51

<210> 3943
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3943
Ala Arg Asp Tyr Gly Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3944
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3944
gcgagggatt acggatacta ctttgactac 30

<210> 3945
<211> 336
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3945
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3946
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3946
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3947
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3947
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3948
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3948
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3949
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3949
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3950

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3950
tgggcatcta cccgggaatc c 21

<210> 3951
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3951
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 3952
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3952
aagcaatctt attctctgag aact 24

<210> 3953
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3953
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggcc 120

cctggacaaa ggcttgagtg gataggatgg atcgaccctg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accgcggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc tagagacggt 300

tacgccagat attactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3954
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3954
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 3955
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3955
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 3956
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3956
ttcaacatca aggactacta tatgcac 27

<210> 3957
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3957
Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 3958
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3958
tggatcgacc ctgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 3959
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3959
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3960
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3960
gctagagacg gttacgccag atattacttt gactac 36

<210> 3961
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3961
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtggag atcaaa 336

<210> 3962
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3962
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3963
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3963

Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3964
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3964
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 3965
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3965
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3966
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3966
tgggcatcta cccgggaatc c 21

<210> 3967
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3967
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 3968
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3968
aagcaatctt attctctgag aact 24

<210> 3969
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3969
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat attactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3970
<211> 119
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3970
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 3971
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3971
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 3972
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3972
ttcaacatca aggactacta tatgcac 27

<210> 3973
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3973
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 3974
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3974
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 3975
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3975

Ala Arg Asp Gly Tyr Gly Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 3976
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3976
gcgagagatg gatacgggag atattacttt gactac 36

<210> 3977
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3977
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 3978
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3978
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
            20   25   30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
                85   90   95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 3979
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 3979
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1   5   10   15

Ala

<210> 3980
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 3980
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 3981
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3981
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 3982
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3982
tgggcatcta cccgggaatc c 21

<210> 3983
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3983
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 3984
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 3984
aagcaatctt attctcggag aact 24

<210> 3985
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 3985
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgctagat attactttga catttggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 3986
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 3986
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Ile Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 3987
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 3987
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 3988
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 3988
ttcaacatca aggactacta tatgcac 27

<210> 3989
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 3989
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 3990
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 3990
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 3991
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 3991
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Ile
1 5 10

<210> 3992
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 3992
gcgagagatg gatacgctag atattacttt gacatt 36

<210> 3993
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 3993
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 3994
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 3994
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 3995
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 3995
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 3996
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 3996
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 3997
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 3997
Trp Ala Ser Thr Arg Glu Ser

1 5

<210> 3998
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 3998
tgggcatcta cccgggaatc c 21

<210> 3999
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 3999
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4000
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4000
aagcaatctt attctcggag aact 24

<210> 4001
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4001
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat attactttga cgcttggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4002
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4002
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Tyr Phe Asp Ala Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
        115

<210> 4003
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 4003
Phe Asn Ile Lys Asp Tyr Tyr Met His
1   5

<210> 4004
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4004
ttcaacatca aggactacta tatgcac   27

<210> 4005
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H2 amino acid sequence

<400> 4005
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1   5   10   15

Gly

<210> 4006
<211> 51
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4006
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4007
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4007
Ala Arg Asp Gly Tyr Gly Arg Tyr Tyr Phe Asp Ala
1 5 10

<210> 4008
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4008
gcgagagatg gatacgggag atattacttt gacgct 36

<210> 4009
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4009
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4010
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4010
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4011
<211> 17
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4011
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4012
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4012
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4013
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4013
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4014
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4014
tgggcatcta cccgggaatc c 21

<210> 4015
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4015
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4016
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4016
aagcaatctt attctcggag aact 24

<210> 4017
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4017
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgctagat attttttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4018
<211> 119

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4018
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
            20   25   30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35   40   45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
    50   55   60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65   70   75   80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Asp Gly Tyr Ala Arg Tyr Phe Phe Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Leu Val Thr Val Ser Ser
        115

<210> 4019
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4019
Phe Asn Ile Lys Asp Tyr Tyr Met His
1   5

<210> 4020
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4020
ttcaacatca aggactacta tatgcac 27

<210> 4021
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4021
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4022
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4022
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4023
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4023
Ala Arg Asp Gly Tyr Ala Arg Tyr Phe Phe Asp Tyr
1 5 10

<210> 4024
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4024
gcgagagatg gatacgctag atatttttt gactac 36

<210> 4025
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4025
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4026
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4026
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1   5   10   15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
            20   25   30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
                85   90   95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 4027
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 4027
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1   5   10   15

Ala

<210> 4028
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4028
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4029
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4029
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4030
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4030
tgggcatcta cccgggaatc c 21

<210> 4031
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4031
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4032
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4032
aagcaatctt attctcggag aact 24

<210> 4033
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4033
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat attttttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4034
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4034
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4035
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4035
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4036
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4036
ttcaacatca aggactacta tatgcac 27

<210> 4037

<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4037
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4038
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4038
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4039
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4039
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Phe Asp Tyr
1 5 10

<210> 4040
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4040
gcgagagatg gatacgggag atatttttt gactac 36

<210> 4041
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4041
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttggct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4042
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4042
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4043
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4043
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4044
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4044
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttggc t 51

<210> 4045
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region CDR L2 amino acid sequence

<400> 4045
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4046
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4046
tgggcatcta cccgggaatc c 21

<210> 4047
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4047
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4048
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4048
aagcaatctt attctcggag aact 24

<210> 4049
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4049
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat attactacga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4050
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4050
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Tyr Tyr Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4051
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4051
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4052
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4052
ttcaacatca aggactacta tatgcac 27

<210> 4053
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4053
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4054
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4054
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4055
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4055
Ala Arg Asp Gly Tyr Gly Arg Tyr Tyr Tyr Asp Tyr
1 5 10

<210> 4056
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4056
gcgagagatg gatacgggag atattactac gactac 36

<210> 4057
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4057
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4058
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4058
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4059
<211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4059
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4060
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4060
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4061
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4061
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4062
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4062
tgggcatcta cccgggaatc c 21

<210> 4063
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4063
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4064
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4064
aagcaatctt attctcggag aact 24

<210> 4065
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4065
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat attactacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4066
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4066
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Tyr Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4067
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4067
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4068
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4068
ttcaacatca aggactacta tatgcac 27

<210> 4069
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4069
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4070
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4070
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4071
<211> 12

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4071
Ala Arg Asp Gly Tyr Gly Arg Tyr Tyr Tyr Asp Val
1 5 10

<210> 4072
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4072
gcgagagatg gatacgggag atattactac gacgtg 36

<210> 4073
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4073
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4074
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4074
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4075
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4075
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4076
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4076
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4077
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4077
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4078
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4078
tgggcatcta cccgggaatc c 21

<210> 4079
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4079
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4080
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4080
aagcaatctt attctcggag aact 24

<210> 4081
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4081
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4082
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4082
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4083
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4083
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4084
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4084

ttcaacatca aggactacta tatgcac 27

<210> 4085
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4085
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4086
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4086
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4087
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4087
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Tyr
1 5 10

<210> 4088
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4088
gcgagagatg gatacgggag atatttttac gactac 36

<210> 4089
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4089
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4090
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4090
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4091
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4091
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4092
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4092
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4093
<211> 7
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4093
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4094
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4094
tgggcatcta cccgggaatc c 21

<210> 4095
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4095
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4096
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4096
aagcaatctt attctcggag aact 24

<210> 4097

<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4097
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat attttttga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4098
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4098
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Phe Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4099
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4099
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4100
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4100
ttcaacatca aggactacta tatgcac 27

<210> 4101
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4101
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4102
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4102
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4103
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4103
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Phe Asp Val
1 5 10

<210> 4104
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4104
gcgagagatg gatacgggag atatttttt gacgtg 36

<210> 4105
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region nucleic acid sequence

<400> 4105
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4106
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4106
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4107
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4107
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4108
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4108
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4109
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4109
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4110
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4110
tgggcatcta cccgggaatc c 21

<210> 4111
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4111
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4112
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4112
aagcaatctt attctcggag aact 24

<210> 4113
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4113
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgctagat attttttga catatggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4114
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4114
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ala Arg Tyr Phe Phe Asp Ile Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4115
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4115
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4116
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4116
ttcaacatca aggactacta tatgcac 27

<210> 4117
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4117
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4118
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4118
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4119
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4119
Ala Arg Asp Gly Tyr Ala Arg Tyr Phe Phe Asp Ile
1 5 10

<210> 4120
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4120
gcgagagatg gatacgctag atatttttt gacata 36

<210> 4121
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4121
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4122
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4122
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4123
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4123
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4124
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4124
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4125
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4125
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4126
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4126
tgggcatcta cccgggaatc c 21

<210> 4127
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4127
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4128
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4128
aagcaatctt attctcggag aact 24

<210> 4129
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4129
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgctagat attttttga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4130
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4130

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Gly Tyr Ala Arg Tyr Phe Phe Asp Val Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 4131
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 4131
Phe Asn Ile Lys Asp Tyr Tyr Met His
1               5


<210> 4132
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
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<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4132
ttcaacatca aggactacta tatgcac 27

<210> 4133
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4133
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4134
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4134
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4135
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4135
Ala Arg Asp Gly Tyr Ala Arg Tyr Phe Phe Asp Val
1 5 10

<210> 4136
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4136
gcgagagatg gatacgctag atatttttt gacgtg 36

<210> 4137
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4137
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4138
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4138
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
                85   90   95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 4139
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 4139
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1   5   10   15

Ala

<210> 4140
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 4140
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t   51

<210> 4141
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4141
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4142
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4142
tgggcatcta cccgggaatc c 21

<210> 4143
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4143
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4144
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4144

aagcaatctt attctcggag aact 24

<210> 4145
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4145
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgctagat atttttacga cgtctggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4146
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4146
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ala Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4147
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4147
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4148
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4148
ttcaacatca aggactacta tatgcac 27

<210> 4149
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4149
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4150
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4150
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4151
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4151
Ala Arg Asp Gly Tyr Ala Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4152
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4152
gcgagagatg gatacgctag atatttttac gacgtc 36

<210> 4153
<211> 336
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4153
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4154
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4154
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4155
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4155
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4156
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4156
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4157
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4157
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4158

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4158
tgggcatcta cccgggaatc c 21

<210> 4159
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4159
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4160
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4160
aagcaatctt attctcggag aact 24

<210> 4161
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4161
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4162
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4162
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4163
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4163
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4164
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4164
ttcaacatca aggactacta tatgcac 27

<210> 4165
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4165
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4166
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4166
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4167
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4167
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4168
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4168
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 4169
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4169
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4170
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4170
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4171
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4171

Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4172
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4172
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4173
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4173
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4174
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4174
tgggcatcta cccgggaatc c 21

<210> 4175
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4175
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4176
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4176
aagcaatctt attctcggag aact 24

<210> 4177
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4177
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgctagat atttttacga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4178
<211> 119
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4178
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ala Arg Tyr Phe Tyr Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4179
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4179
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4180
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4180
ttcaacatca aggactacta tatgcac 27

<210> 4181
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4181
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4182
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4182
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4183
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4183

Ala Arg Asp Gly Tyr Ala Arg Tyr Phe Tyr Asp Tyr
1 5 10

<210> 4184
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4184
gcgagagatg gatacgctag atatttttac gactac 36

<210> 4185
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4185
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4186
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4186
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
            20   25   30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
                85   90   95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 4187
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 4187
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1   5   10   15

Ala

<210> 4188
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 4188
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4189
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4189
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4190
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4190
tgggcatcta cccgggaatc c 21

<210> 4191
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4191
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4192
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4192
aagcaatctt attctcggag aact 24

<210> 4193
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4193
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4194
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4194
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4195
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4195
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4196
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4196
ttcaacatca aggactacta tatgcac 27

<210> 4197
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4197
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4198
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4198
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4199
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4199
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4200
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4200
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 4201
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4201
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4202
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4202
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4203
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4203
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4204
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4204
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4205
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4205
Trp Ala Ser Thr Arg Glu Ser

1 5

<210> 4206
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4206
tgggcatcta cccgggaatc c 21

<210> 4207
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4207
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4208
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4208
aagcaatctt attctcggag aact 24

<210> 4209
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4209
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccctg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4210
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4210
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
        115

<210> 4211
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 4211
Phe Asn Ile Lys Asp Tyr Tyr Met His
1   5

<210> 4212
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4212
ttcaacatca aggactacta tatgcac   27

<210> 4213
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H2 amino acid sequence

<400> 4213
Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1   5   10   15

Gly

<210> 4214
<211> 51
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4214
tggatcgacc ctgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4215
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4215
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4216
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4216
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 4217
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4217
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4218
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4218
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4219
<211> 17
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4219
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4220
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4220
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4221
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4221
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4222
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4222
tgggcatcta cccgggaatc c 21

<210> 4223
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4223
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4224
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4224
aagcaatctt attctcggag aact 24

<210> 4225
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4225
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggcc 120

cctggacaaa ggcttgagtg gataggatgg atcgaccctg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accgcggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc tagagacggt 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4226
<211> 119

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4226
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
            20   25   30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Ile
        35   40   45

Gly Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
    50   55   60

Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Ala Ser Thr Ala Tyr
65   70   75   80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
            100   105   110

Thr Leu Val Thr Val Ser Ser
        115

<210> 4227
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4227
Phe Asn Ile Lys Asp Tyr Tyr Met His
1   5

<210> 4228
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4228
ttcaacatca aggactacta tatgcac 27

<210> 4229
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4229
Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4230
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4230
tggatcgacc ctgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4231
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4231
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4232
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4232
gctagagacg gttacgggag atatttttac gacgtg 36

<210> 4233
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4233
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4234
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4234
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4235
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4235
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4236
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4236
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4237
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4237
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4238
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4238
tgggcatcta cccgggaatc c 21

<210> 4239
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4239
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4240
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4240
aagcaatctt attctcggag aact 24

<210> 4241
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4241
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4242
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4242
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4243
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4243
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4244
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4244
ttcaacatca aggactacta tatgcac 27

<210> 4245

<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4245
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4246
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4246
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4247
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4247
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4248
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4248
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 4249
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4249
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4250
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4250
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4251
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4251
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4252
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4252
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4253
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region CDR L2 amino acid sequence

<400> 4253
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4254
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4254
tgggcatcta cccgggaatc c 21

<210> 4255
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4255
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 4256
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4256
aagcaatctt attctctgag aact 24

<210> 4257
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4257
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccctg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4258
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4258
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4259
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4259
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4260
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4260
ttcaacatca aggactacta tatgcac 27

<210> 4261
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4261
Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4262
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4262
tggatcgacc ctgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4263
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4263
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4264
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4264
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 4265
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4265
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4266
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4266
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4267
<211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4267
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4268
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4268
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4269
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4269
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4270
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4270
tgggcatcta cccgggaatc c 21

<210> 4271
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4271
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 4272
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4272
aagcaatctt attctctgag aact 24

<210> 4273
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4273
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggcc 120

cctggacaaa ggcttgagtg gataggatgg atcgaccctg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accgcggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc tagagacggt 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4274
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4274
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4275
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4275
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4276
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4276
ttcaacatca aggactacta tatgcac 27

<210> 4277
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4277
Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4278
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4278
tggatcgacc ctgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4279
<211> 12

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4279
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4280
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4280
gctagagacg gttacgggag atatttttac gacgtg 36

<210> 4281
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4281
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4282
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4282
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4283
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4283
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4284
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4284
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4285
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4285
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4286
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4286
tgggcatcta cccgggaatc c 21

<210> 4287
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4287
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 4288
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4288
aagcaatctt attctctgag aact 24

<210> 4289
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4289
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aagaaggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4290
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4290
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

```
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Asp Pro Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 4291
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 4291
Phe Asn Ile Lys Asp Tyr Tyr Met His
1               5


<210> 4292
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4292
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ttcaacatca aggactacta tatgcac 27

<210> 4293
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4293
Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4294
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4294
tggatcgacc ttgaagaagg taacacaatc tatgacccga agtttcaggg c 51

<210> 4295
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4295
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4296
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4296
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 4297
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4297
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta gaaagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4298
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4298
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Glu Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4299
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4299
Lys Ser Ser Gln Ser Leu Leu Glu Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4300
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4300
aagtccagcc agagtctttt agaaagcaga accggaaaga actacttagc t 51

<210> 4301
<211> 7
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4301
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4302
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4302
tgggcatcta cccgggaatc c 21

<210> 4303
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4303
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4304
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4304
aagcaatctt attctcggag aact 24

<210> 4305

<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4305
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

caaccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4306
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4306
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Gln Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4307
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4307
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4308
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4308
ttcaacatca aggactacta tatgcac 27

<210> 4309
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4309
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Gln Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4310
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4310
tggatcgacc ttgaaaatgg taacacaatc tatcaaccga agtttcaggg c 51

<210> 4311
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4311
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4312
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4312
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 4313
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region nucleic acid sequence

<400> 4313
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta gaaagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4314
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4314
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Glu Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4315
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4315
Lys Ser Ser Gln Ser Leu Leu Glu Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4316
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4316
aagtccagcc agagtctttt agaaagcaga accggaaaga actacttagc t 51

<210> 4317
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4317
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4318
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4318
tgggcatcta cccgggaatc c 21

<210> 4319
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4319
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4320
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4320
aagcaatctt attctcggag aact 24

<210> 4321
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4321
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagaagga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4322
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4322
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4323
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4323
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4324
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4324
ttcaacatca aggactacta tatgcac 27

<210> 4325
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4325
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4326
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4326
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4327
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4327
Ala Arg Glu Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4328
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4328
gcgagagaag gatacgggag atatttttac gacgtg 36

<210> 4329
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4329
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta gaaagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4330
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4330
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Glu Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4331
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4331
Lys Ser Ser Gln Ser Leu Leu Glu Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4332
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4332
aagtccagcc agagtctttt agaaagcaga accggaaaga actacttagc t 51

<210> 4333
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4333
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4334
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4334
tgggcatcta cccgggaatc c 21

<210> 4335
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4335
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4336
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4336
aagcaatctt attctcggag aact 24

<210> 4337
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4337
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aagaaggtaa cacaatctat 180

caaccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4338
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4338

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Gln Pro Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 4339
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 4339
Phe Asn Ile Lys Asp Tyr Tyr Met His
1               5


<210> 4340
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
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<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4340
ttcaacatca aggactacta tatgcac 27

<210> 4341
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4341
Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Gln Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4342
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4342
tggatcgacc ttgaagaagg taacacaatc tatcaaccga agtttcaggg c 51

<210> 4343
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4343
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4344
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4344
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 4345
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4345
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta gaaagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4346
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4346
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Glu Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4347
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4347
Lys Ser Ser Gln Ser Leu Leu Glu Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4348
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4348
aagtccagcc agagtctttt agaaagcaga accggaaaga actacttagc t 51

<210> 4349
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4349
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4350
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4350
tgggcatcta cccgggaatc c 21

<210> 4351
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4351
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4352
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4352

aagcaatctt attctcggag aact 24

<210> 4353
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4353
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

caaccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagaagga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4354
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4354
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Gln Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4355
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4355
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4356
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4356
ttcaacatca aggactacta tatgcac 27

<210> 4357
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4357
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Gln Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4358
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4358
tggatcgacc ttgaaaatgg taacacaatc tatcaaccga agtttcaggg c 51

<210> 4359
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4359
Ala Arg Glu Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4360
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4360
gcgagagaag gatacgggag atatttttac gacgtg 36

<210> 4361
<211> 336
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4361
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta gaaagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4362
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4362
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Glu Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4363
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4363
Lys Ser Ser Gln Ser Leu Leu Glu Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4364
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4364
aagtccagcc agagtctttt agaaagcaga accggaaaga actacttagc t 51

<210> 4365
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4365
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4366

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4366
tgggcatcta cccgggaatc c 21

<210> 4367
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4367
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4368
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4368
aagcaatctt attctcggag aact 24

<210> 4369
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4369
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aagaaggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagaagga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4370
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4370
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4371
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4371
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4372
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4372
ttcaacatca aggactacta tatgcac 27

<210> 4373
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4373
Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4374
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4374
tggatcgacc ttgaagaagg taacacaatc tatgacccga agtttcaggg c 51

<210> 4375
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4375
Ala Arg Glu Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4376
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4376
gcgagagaag gatacgggag atatttttac gacgtg 36

<210> 4377
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4377
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta gaaagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4378
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4378
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Glu Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4379
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4379

Lys Ser Ser Gln Ser Leu Leu Glu Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4380
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4380
aagtccagcc agagtctttt agaaagcaga accggaaaga actacttagc t 51

<210> 4381
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4381
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4382
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4382
tgggcatcta cccgggaatc c 21

<210> 4383
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4383
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4384
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4384
aagcaatctt attctcggag aact 24

<210> 4385
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4385
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aagaaggtaa cacaatctat 180

caaccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagaagga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4386
<211> 119
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4386
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Gln Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4387
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4387
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4388
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4388
ttcaacatca aggactacta tatgcac 27

<210> 4389
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4389
Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Gln Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4390
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4390
tggatcgacc ttgaagaagg taacacaatc tatcaaccga agtttcaggg c 51

<210> 4391
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4391

Ala Arg Glu Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4392
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4392
gcgagagaag gatacgggag atatttttac gacgtg 36

<210> 4393
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4393
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta gaaagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4394
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4394
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Glu Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4395
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4395
Lys Ser Ser Gln Ser Leu Leu Glu Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4396
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4396
aagtccagcc agagtctttt agaaagcaga accggaaaga actacttagc t 51

<210> 4397
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4397
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4398
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4398
tgggcatcta cccgggaatc c 21

<210> 4399
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4399
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4400
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4400
aagcaatctt attctcggag aact 24

<210> 4401
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4401
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4402
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4402
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4403
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4403
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4404
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4404
ttcaacatca aggactacta tatgcac 27

<210> 4405
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4405
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4406
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4406
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4407
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4407
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4408
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4408
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 4409
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4409
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta gaaagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4410
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4410
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Glu Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4411
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4411
Lys Ser Ser Gln Ser Leu Leu Glu Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4412
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4412
aagtccagcc agagtctttt agaaagcaga accggaaaga actacttagc t 51

<210> 4413
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4413
Trp Ala Ser Thr Arg Glu Ser

1 5

<210> 4414
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4414
tgggcatcta cccgggaatc c 21

<210> 4415
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4415
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4416
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4416
aagcaatctt attctcggag aact 24

<210> 4417
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4417
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aagaaggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4418
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4418
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
        115

<210> 4419
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 4419
Phe Asn Ile Lys Asp Tyr Tyr Met His
1   5

<210> 4420
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4420
ttcaacatca aggactacta tatgcac   27

<210> 4421
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H2 amino acid sequence

<400> 4421
Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1   5   10   15

Gly

<210> 4422
<211> 51
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4422
tggatcgacc ttgaagaagg taacacaatc tatgacccga agtttcaggg c 51

<210> 4423
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4423
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4424
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4424
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 4425
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4425
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4426
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4426
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4427
<211> 17
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4427
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4428
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4428
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4429
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4429
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4430
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4430
tgggcatcta cccgggaatc c 21

<210> 4431
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4431
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4432
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4432
aagcaatctt attctcggag aact 24

<210> 4433
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4433
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

caaccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4434
<211> 119

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4434
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Gln Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4435
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4435
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4436
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4436
ttcaacatca aggactacta tatgcac 27

<210> 4437
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4437
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Gln Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4438
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4438
tggatcgacc ttgaaaatgg taacacaatc tatcaaccga agtttcaggg c 51

<210> 4439
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4439
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4440
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4440
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 4441
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4441
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4442
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4442
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4443
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4443
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4444
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4444
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4445
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4445
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4446
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4446
tgggcatcta cccgggaatc c 21

<210> 4447
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4447
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4448
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4448
aagcaatctt attctcggag aact 24

<210> 4449
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4449
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagaagga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4450
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4450
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4451
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4451
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4452
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4452
ttcaacatca aggactacta tatgcac 27

<210> 4453

<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4453
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4454
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4454
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4455
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4455
Ala Arg Glu Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4456
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4456
gcgagagaag gatacgggag atatttttac gacgtg 36

<210> 4457
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4457
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4458
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4458
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4459
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4459
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4460
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4460
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4461
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region CDR L2 amino acid sequence

<400> 4461
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4462
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4462
tgggcatcta cccgggaatc c 21

<210> 4463
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4463
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4464
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4464
aagcaatctt attctcggag aact 24

<210> 4465
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4465
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aagaaggtaa cacaatctat 180

caaccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4466
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4466
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Gln Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4467
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4467
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4468
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4468
ttcaacatca aggactacta tatgcac 27

<210> 4469
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4469
Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Gln Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4470
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4470
tggatcgacc ttgaagaagg taacacaatc tatcaaccga agtttcaggg c 51

<210> 4471
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4471
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4472
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4472
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 4473
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4473
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4474
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4474
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4475
<211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4475
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4476
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4476
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4477
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4477
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4478
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4478
tgggcatcta cccgggaatc c 21

<210> 4479
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4479
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4480
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4480
aagcaatctt attctcggag aact 24

<210> 4481
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4481
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

caaccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagaagga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4482
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4482
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Gln Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4483
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4483
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4484
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4484
ttcaacatca aggactacta tatgcac 27

<210> 4485
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4485
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Gln Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4486
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4486
tggatcgacc ttgaaaatgg taacacaatc tatcaaccga agtttcaggg c 51

<210> 4487
<211> 12

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4487
Ala Arg Glu Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4488
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4488
gcgagagaag gatacgggag atatttttac gacgtg 36

<210> 4489
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4489
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4490
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4490
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4491
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4491
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4492
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4492
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4493
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4493
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4494
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4494
tgggcatcta cccgggaatc c 21

<210> 4495
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4495
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4496
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4496
aagcaatctt attctcggag aact 24

<210> 4497
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4497
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aagaaggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagaagga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4498
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4498
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
            20   25   30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35   40   45

Gly Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Asp Pro Lys Phe
    50   55   60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65   70   75   80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Glu Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
            100   105   110

Thr Leu Val Thr Val Ser Ser
        115

<210> 4499
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 4499
Phe Asn Ile Lys Asp Tyr Tyr Met His
1   5

<210> 4500
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4500

ttcaacatca aggactacta tatgcac 27

<210> 4501
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4501
Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4502
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4502
tggatcgacc ttgaagaagg taacacaatc tatgacccga agtttcaggg c 51

<210> 4503
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4503
Ala Arg Glu Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4504
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4504
gcgagagaag gatacgggag atatttttac gacgtg 36

<210> 4505
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4505
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4506
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4506
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
                85   90   95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 4507
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 4507
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1   5   10   15

Ala

<210> 4508
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 4508
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t   51

<210> 4509
<211> 7
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4509
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4510
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4510
tgggcatcta cccgggaatc c 21

<210> 4511
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4511
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4512
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4512
aagcaatctt attctcggag aact 24

<210> 4513

<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4513
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aagaaggtaa cacaatctat 180

caaccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagaagga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4514
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4514
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Gln Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4515
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4515
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4516
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4516
ttcaacatca aggactacta tatgcac 27

<210> 4517
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4517
Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Gln Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4518
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4518
tggatcgacc ttgaagaagg taacacaatc tatcaaccga agtttcaggg c 51

<210> 4519
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4519
Ala Arg Glu Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4520
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4520
gcgagagaag gatacgggag atatttttac gacgtg 36

<210> 4521
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region nucleic acid sequence

<400> 4521
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4522
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4522
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4523
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4523
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4524
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4524
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4525
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4525
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4526
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4526
tgggcatcta cccgggaatc c 21

<210> 4527
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4527
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4528
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4528
aagcaatctt attctcggag aact 24

<210> 4529
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4529
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4530
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4530
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4531
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4531
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4532
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4532
ttcaacatca aggactacta tatgcac 27

<210> 4533
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4533
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4534
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4534
tggatcgacc ttgaaaatgc taacacaatc tatgacccga agtttcaggg c 51

<210> 4535
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4535
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4536
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4536
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 4537
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4537
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4538
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4538
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4539
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4539
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4540
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4540
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 4541
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4541
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4542
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4542
tgggcatcta cccgggaatc c 21

<210> 4543
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4543
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4544
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4544
aagcaatctt attctcggag aact 24

<210> 4545
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4545
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4546
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4546

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Ala Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 4547
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 4547
Phe Asn Ile Lys Asp Tyr Tyr Met His
1               5


<210> 4548
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
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<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4548
ttcaacatca aggactacta tatgcac 27

<210> 4549
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4549
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 4550
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4550
tggatcgacc ttgaaaatgg taacacaatc tatgacgcta agtttcaggg c 51

<210> 4551
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4551
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4552
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4552
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 4553
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4553
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4554
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4554
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
                85   90   95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 4555
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 4555
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1   5   10   15

Ala

<210> 4556
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 4556
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t   51

<210> 4557
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4557
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4558
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4558
tgggcatcta cccgggaatc c 21

<210> 4559
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4559
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4560
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4560

aagcaatctt attctcggag aact 24

<210> 4561
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4561
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgct 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4562
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4562
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4563
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4563
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4564
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4564
ttcaacatca aggactacta tatgcac 27

<210> 4565
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4565
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4566
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4566
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4567
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4567
Ala Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4568
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4568
gcgagagatg cttacgggag atatttttac gacgtg 36

<210> 4569
<211> 336
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4569
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta acgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4570
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4570
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4571
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4571
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4572
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4572
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 4573
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4573
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4574

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4574
tgggcatcta cccgggaatc c 21

<210> 4575
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4575
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4576
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4576
aagcaatctt attctcggag aact 24

<210> 4577
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4577
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgct 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4578
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4578
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4579
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4579
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4580
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4580
ttcaacatca aggactacta tatgcac 27

<210> 4581
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4581
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 4582
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4582
tggatcgacc ttgaaaatgg taacacaatc tatgacgcta agtttcaggg c 51

<210> 4583
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4583
Ala Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4584
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4584
gcgagagatg cttacgggag atatttttac gacgtg 36

<210> 4585
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4585
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4586
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4586
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4587
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4587

Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4588
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4588
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 4589
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4589
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4590
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4590
tgggcatcta cccgggaatc c 21

<210> 4591
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4591
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4592
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4592
aagcaatctt attctcggag aact 24

<210> 4593
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4593
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgct 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4594
<211> 119
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4594
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4595
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4595
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4596
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4596
ttcaacatca aggactacta tatgcac 27

<210> 4597
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4597
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4598
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4598
tggatcgacc ttgaaaatgc taacacaatc tatgacccga agtttcaggg c 51

<210> 4599
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4599

Ala Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4600
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4600
gcgagagatg cttacgggag atatttttac gacgtg 36

<210> 4601
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4601
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4602
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4602
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
            20   25   30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
                85   90   95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 4603
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 4603
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1   5   10   15

Ala

<210> 4604
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 4604
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 4605
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4605
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4606
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4606
tgggcatcta cccgggaatc c 21

<210> 4607
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4607
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4608
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4608
aagcaatctt attctcggag aact 24

<210> 4609
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4609
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cctctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4610
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4610
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4611
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4611
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4612
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4612
ttcaacatca aggactacta tatgcac 27

<210> 4613
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4613
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4614
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4614
tggatcgacc ttgaaaatgc taacacaatc tatgacccga agtttcaggg c 51

<210> 4615
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4615
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4616
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4616
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 4617
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4617
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4618
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4618
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4619
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4619
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4620
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4620
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4621
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4621
Trp Ala Ser Thr Arg Glu Ser

1 5

<210> 4622
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4622
tgggcatcta cccgggaatc c 21

<210> 4623
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4623
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4624
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4624
aagcaatctt attctcggag aact 24

<210> 4625
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4625
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4626
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4626
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
        115

<210> 4627
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 4627
Phe Asn Ile Lys Asp Tyr Tyr Met His
1   5

<210> 4628
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4628
ttcaacatca aggactacta tatgcac   27

<210> 4629
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H2 amino acid sequence

<400> 4629
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1   5   10   15

Gly

<210> 4630
<211> 51
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4630
tggatcgacc ttgaaaatgg taacacaatc tatgacgcta agtttcaggg c 51

<210> 4631
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4631
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4632
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4632
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 4633
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4633
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4634
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4634
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4635
<211> 17
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4635
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4636
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4636
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4637
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4637
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4638
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4638
tgggcatcta cccgggaatc c 21

<210> 4639
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4639
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4640
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4640
aagcaatctt attctcggag aact 24

<210> 4641
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4641
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgct 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4642
<211> 119

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4642
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
            20   25   30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35   40   45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
    50   55   60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65   70   75   80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
            100   105   110

Thr Leu Val Thr Val Ser Ser
        115

<210> 4643
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4643
Phe Asn Ile Lys Asp Tyr Tyr Met His
1   5

<210> 4644
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4644
ttcaacatca aggactacta tatgcac 27

<210> 4645
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4645
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4646
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4646
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4647
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4647
Ala Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4648
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4648
gcgagagatg cttacgggag atatttttac gacgtg 36

<210> 4649
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4649
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4650
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4650
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4651
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4651
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4652
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4652
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4653
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4653
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4654
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4654
tgggcatcta cccgggaatc c 21

<210> 4655
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4655
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4656
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4656
aagcaatctt attctcggag aact 24

<210> 4657
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4657
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4658
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4658
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4659
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4659
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4660
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4660
ttcaacatca aggactacta tatgcac 27

<210> 4661

<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4661
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 4662
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4662
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 4663
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4663
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4664
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4664
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 4665
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4665
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4666
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4666
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4667
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4667
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4668
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4668
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4669
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region CDR L2 amino acid sequence

<400> 4669
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4670
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4670
tgggcatcta cccgggaatc c 21

<210> 4671
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4671
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4672
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4672
aagcaatctt attctcggag aact 24

<210> 4673
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4673
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgct 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4674
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4674
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4675
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4675
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4676
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4676
ttcaacatca aggactacta tatgcac 27

<210> 4677
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4677
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 4678
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4678
tggatcgacc ttgaaaatgg taacacaatc tatgacgcta agtttcaggg c 51

<210> 4679
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4679
Ala Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4680
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4680
gcgagagatg cttacgggag atatttttac gacgtg 36

<210> 4681
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4681
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4682
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4682
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4683
<211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4683
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4684
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4684
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4685
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4685
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4686
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4686
tgggcatcta cccgggaatc c 21

<210> 4687
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4687
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4688
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4688
aagcaatctt attctcggag aact 24

<210> 4689
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4689
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgct 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4690
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4690
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4691
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4691
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4692
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4692
ttcaacatca aggactacta tatgcac 27

<210> 4693
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4693
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4694
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4694
tggatcgacc ttgaaaatgc taacacaatc tatgacccga agtttcaggg c 51

<210> 4695
<211> 12

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4695
Ala Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4696
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4696
gcgagagatg cttacgggag atatttttac gacgtg 36

<210> 4697
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4697
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4698
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4698
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4699
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4699
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4700
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4700
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4701
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4701
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4702
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4702
tgggcatcta cccgggaatc c 21

<210> 4703
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4703
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4704
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4704
aagcaatctt attctcggag aact 24

<210> 4705
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4705
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgct 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4706
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4706
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4707
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4707
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4708
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4708

ttcaacatca aggactacta tatgcac 27

<210> 4709
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4709
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 4710
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4710
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 4711
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4711
Ala Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4712
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4712
gcgagagatg cttacgggag atatttttac gacgtg 36

<210> 4713
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4713
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4714
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4714
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
                85   90   95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 4715
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 4715
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1   5   10   15

Ala

<210> 4716
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 4716
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t   51

<210> 4717
<211> 7
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4717
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4718
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4718
tgggcatcta cccgggaatc c 21

<210> 4719
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4719
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4720
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4720
aagcaatctt attctcggag aact 24

<210> 4721

<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4721
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4722
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4722
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4723
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4723
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4724
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4724
ttcaacatca aggactacta tatgcac 27

<210> 4725
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4725
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4726
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4726
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4727
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4727
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4728
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4728
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 4729
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region nucleic acid sequence

<400> 4729
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4730
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4730
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4731
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4731
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4732
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4732
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4733
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4733
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4734
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4734
tgggcatcta cccgggaatc c 21

<210> 4735
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4735
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4736
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4736
aagcaatctt attctcggag aact 24

<210> 4737
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4737
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4738
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4738
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4739
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4739
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4740
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4740
ttcaacatca aggactacta tatgcac 27

<210> 4741
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4741
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4742
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4742
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4743
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4743
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4744
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4744
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 4745
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4745
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4746
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4746
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4747
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4747
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4748
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4748
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4749
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4749
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4750
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4750
tgggcatcta cccgggaatc c 21

<210> 4751
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4751
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4752
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4752
aagcaatctt attctcggag aact 24

<210> 4753
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4753
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4754
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4754

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 4755
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 4755
Phe Asn Ile Lys Asp Tyr Tyr Met His
1               5


<210> 4756
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
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<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4756
ttcaacatca aggactacta tatgcac 27

<210> 4757
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4757
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4758
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4758
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4759
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4759
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4760
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4760
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 4761
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4761
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4762
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4762
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
                85   90   95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 4763
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 4763
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1   5   10   15

Ala

<210> 4764
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 4764
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t   51

<210> 4765
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4765
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4766
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4766
tgggcatcta cccgggaatc c 21

<210> 4767
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4767
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4768
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4768

aagcaatctt attctcggag aact 24

<210> 4769
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4769
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4770
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4770
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4771
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4771
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4772
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4772
ttcaacatca aggactacta tatgcac 27

<210> 4773
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4773
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4774
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4774
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4775
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4775
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4776
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4776
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 4777
<211> 336
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4777
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4778
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4778
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4779
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4779
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4780
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4780
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4781
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4781
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4782

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4782
tgggcatcta cccgggaatc c 21

<210> 4783
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4783
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4784
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4784
aagcaatctt attctcggag aact 24

<210> 4785
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4785
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4786
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4786
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4787
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4787
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4788
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4788
ttcaacatca aggactacta tatgcac 27

<210> 4789
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4789
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4790
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4790
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4791
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4791
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4792
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4792
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 4793
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4793
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4794
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4794
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4795
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4795

Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4796
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4796
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4797
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4797
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4798
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4798
tgggcatcta cccgggaatc c 21

<210> 4799
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4799
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4800
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4800
aagcaatctt attctcggag aact 24

<210> 4801
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4801
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4802
<211> 119
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4802
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4803
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4803
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4804
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4804
ttcaacatca aggactacta tatgcac 27

<210> 4805
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4805
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4806
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4806
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4807
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4807

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4808
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4808
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 4809
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4809
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4810
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4810
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
            20   25   30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
                85   90   95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 4811
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 4811
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1   5   10   15

Ala

<210> 4812
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 4812
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4813
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4813
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4814
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4814
tgggcatcta cccgggaatc c 21

<210> 4815
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4815
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4816
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4816
aagcaatctt attctcggag aact 24

<210> 4817
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4817
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4818
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4818
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4819
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4819
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4820
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4820
ttcaacatca aggactacta tatgcac 27

<210> 4821
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4821
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4822
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4822
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4823
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4823
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4824
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4824
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 4825
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4825
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4826
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4826
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4827
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4827
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4828
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4828
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4829
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4829
Trp Ala Ser Thr Arg Glu Ser

1 5

<210> 4830
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4830
tgggcatcta cccgggaatc c 21

<210> 4831
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4831
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4832
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4832
aagcaatctt attctcggag aact 24

<210> 4833
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4833
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4834
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4834
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
        115

<210> 4835
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 4835
Phe Asn Ile Lys Asp Tyr Tyr Met His
1   5

<210> 4836
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4836
ttcaacatca aggactacta tatgcac   27

<210> 4837
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H2 amino acid sequence

<400> 4837
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1   5   10   15

Gly

<210> 4838
<211> 51
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4838
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4839
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4839
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4840
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4840
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 4841
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4841
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4842
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4842
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4843
<211> 17
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4843
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4844
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4844
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4845
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4845
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4846
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4846
tgggcatcta cccgggaatc c 21

<210> 4847
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4847
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4848
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4848
aagcaatctt attctcggag aact 24

<210> 4849
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4849
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4850
<211> 119

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4850
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4851
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4851
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4852
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4852
ttcaacatca aggactacta tatgcac 27

<210> 4853
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4853
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4854
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4854
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4855
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4855
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4856
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4856
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 4857
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4857
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4858
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4858
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4859
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4859
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4860
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4860
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4861
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4861
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4862
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4862
tgggcatcta cccgggaatc c 21

<210> 4863
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4863
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4864
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4864
aagcaatctt attctcggag aact 24

<210> 4865
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4865
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4866
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4866
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4867
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4867
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4868
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4868
ttcaacatca aggactacta tatgcac 27

<210> 4869

<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4869
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4870
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4870
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4871
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4871
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4872
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4872
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 4873
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4873
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4874
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4874
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4875
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4875
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4876
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4876
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4877
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region CDR L2 amino acid sequence

<400> 4877
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4878
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4878
tgggcatcta cccgggaatc c 21

<210> 4879
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4879
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4880
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4880
aagcaatctt attctcggag aact 24

<210> 4881
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4881
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4882
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4882
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4883
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4883
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4884
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4884
ttcaacatca aggactacta tatgcac 27

<210> 4885
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4885
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4886
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4886
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4887
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4887
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4888
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4888
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 4889
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4889
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4890
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4890
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4891
<211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4891
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4892
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4892
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4893
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4893
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4894
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4894
tgggcatcta cccgggaatc c 21

<210> 4895
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4895
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4896
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4896
aagcaatctt attctcggag aact 24

<210> 4897
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4897
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4898
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4898
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4899
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4899
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4900
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4900
ttcaacatca aggactacta tatgcac 27

<210> 4901
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4901
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4902
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4902
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4903
<211> 12

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4903
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4904
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4904
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 4905
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4905
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4906
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4906
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4907
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4907
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4908
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4908
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4909
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4909
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4910
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4910
tgggcatcta cccgggaatc c 21

<210> 4911
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4911
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4912
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4912
aagcaatctt attctcggag aact 24

<210> 4913
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4913
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4914
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4914
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4915
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4915
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4916
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4916

ttcaacatca aggactacta tatgcac 27

<210> 4917
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4917
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4918
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4918
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4919
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4919
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4920
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4920
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 4921
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4921
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4922
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4922
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
                85   90   95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 4923
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 4923
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1   5   10   15

Ala

<210> 4924
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 4924
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t   51

<210> 4925
<211> 7
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4925
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4926
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4926
tgggcatcta cccgggaatc c 21

<210> 4927
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4927
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4928
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4928
aagcaatctt attctcggag aact 24

<210> 4929

<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4929
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4930
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4930
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4931
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4931
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4932
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4932
ttcaacatca aggactacta tatgcac 27

<210> 4933
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4933
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4934
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4934
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4935
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4935
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4936
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4936
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 4937
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region nucleic acid sequence

<400> 4937
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4938
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4938
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4939
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4939
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4940
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4940
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4941
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4941
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4942
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4942
tgggcatcta cccgggaatc c 21

<210> 4943
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4943
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4944
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4944
aagcaatctt attctcggag aact 24

<210> 4945
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4945
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcagtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4946
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4946
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4947
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4947
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4948
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4948
ttcaacatca aggactacta tatgcac 27

<210> 4949
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4949
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4950
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4950
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4951
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4951
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4952
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4952
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 4953
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4953
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 4954
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4954
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4955
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4955
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4956
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4956
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4957
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4957
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4958
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4958
tgggcatcta cccgggaatc c 21

<210> 4959
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4959
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4960
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4960
aagcaatctt attctcggag aact 24

<210> 4961
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4961
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaat gtcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4962
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4962

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 4963
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 4963
Phe Asn Ile Lys Asp Tyr Tyr Met His
1               5


<210> 4964
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
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<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4964
ttcaacatca aggactacta tatgcac 27

<210> 4965
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4965
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4966
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4966
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4967
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4967
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4968
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4968
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 4969
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4969
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gctgtgggac caaggtcgag atcaaa 336

<210> 4970
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4970
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
                85   90   95

Ser Tyr Ser Arg Arg Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 4971
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 4971
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1   5   10   15

Ala

<210> 4972
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 4972
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t   51

<210> 4973
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4973
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4974
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4974
tgggcatcta cccgggaatc c 21

<210> 4975
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4975
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4976
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4976

aagcaatctt attctcggag aact 24

<210> 4977
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4977
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaat gtcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4978
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4978
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4979
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4979
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4980
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4980
ttcaacatca aggactacta tatgcac 27

<210> 4981
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4981
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4982
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4982
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4983
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4983
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 4984
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 4984
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 4985
<211> 336
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 4985
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gctgtgggac caaggtcgag atcaaa 336

<210> 4986
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 4986
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 4987
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 4987
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 4988
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 4988
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 4989
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 4989
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 4990

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 4990
tgggcatcta cccgggaatc c 21

<210> 4991
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 4991
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 4992
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 4992
aagcaatctt attctcggag aact 24

<210> 4993
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 4993
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaat gtcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 4994
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 4994
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 4995
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 4995
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 4996
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 4996
ttcaacatca aggactacta tatgcac 27

<210> 4997
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 4997
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 4998
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region CDR H2 nucleic acid sequence

<400> 4998
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 4999
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 4999
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 5000
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5000
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 5001
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5001
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gctgtgggac caaggtcgag atcaaa 336

<210> 5002
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5002
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5003
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5003

Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5004
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5004
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 5005
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5005
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5006
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5006
tgggcatcta cccgggaatc c 21

<210> 5007
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5007
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 5008
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5008
aagcaatctt attctcggag aact 24

<210> 5009
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5009
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaat gtcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5010
<211> 119
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5010
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5011
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5011
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 5012
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5012
ttcaacatca aggactacta tatgcac 27

<210> 5013
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5013
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 5014
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5014
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 5015
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5015

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 5016
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5016
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 5017
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5017
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gctgtgggac caaggtcgag atcaaa 336

<210> 5018
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5018
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
            20   25   30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
                85   90   95

Ser Tyr Ser Arg Arg Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 5019
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 5019
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1   5   10   15

Ala

<210> 5020
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 5020
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 5021
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5021
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5022
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5022
tgggcatcta cccgggaatc c 21

<210> 5023
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5023
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 5024
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5024
aagcaatctt attctcggag aact 24

<210> 5025
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5025
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaat gtcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5026
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5026
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5027
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5027
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 5028
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5028
ttcaacatca aggactacta tatgcac 27

<210> 5029
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5029
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 5030
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5030
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 5031
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5031
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 5032
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5032
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 5033
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5033
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gctgtgggac caaggtcgag atcaaa 336

<210> 5034
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5034
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5035
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5035
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5036
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5036
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 5037
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5037
Trp Ala Ser Thr Arg Glu Ser

1 5

<210> 5038
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5038
tgggcatcta cccgggaatc c 21

<210> 5039
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5039
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 5040
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5040
aagcaatctt attctcggag aact 24

<210> 5041
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5041
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaat gtcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgatgt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5042
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5042
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Met Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
        115

<210> 5043
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 5043
Phe Asn Ile Lys Asp Tyr Tyr Met His
1   5

<210> 5044
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5044
ttcaacatca aggactacta tatgcac   27

<210> 5045
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H2 amino acid sequence

<400> 5045
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Met Phe Gln
1   5   10   15

Gly

<210> 5046
<211> 51
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5046
tggatcgacc ttgaaaatgg taacacaatc tatgacccga tgtttcaggg c 51

<210> 5047
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5047
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 5048
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5048
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 5049
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5049
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gctgtgggac caaggtcgag atcaaa 336

<210> 5050
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5050
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5051
<211> 17
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5051
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5052
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5052
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 5053
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5053
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5054
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5054
tgggcatcta cccgggaatc c 21

<210> 5055
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5055
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 5056
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5056
aagcaatctt attctcggag aact 24

<210> 5057
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5057
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaat gtcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5058
<211> 119

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5058
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
            20   25   30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
        35   40   45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
    50   55   60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65   70   75   80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
            100   105   110

Thr Leu Val Thr Val Ser Ser
        115

<210> 5059
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5059
Phe Asn Ile Lys Asp Tyr Tyr Met His
1   5

<210> 5060
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5060
ttcaacatca aggactacta tatgcac 27

<210> 5061
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5061
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 5062
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5062
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 5063
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5063
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 5064
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5064
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 5065
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5065
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gctgtgggac caaggtcgag atcaaa 336

<210> 5066
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5066
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5067
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5067
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5068
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5068
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 5069
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5069
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5070
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5070
tgggcatcta cccgggaatc c 21

<210> 5071
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5071
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 5072
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5072
aagcaatctt attctcggag aact 24

<210> 5073
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5073
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaat gtcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5074
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5074
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5075
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5075
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 5076
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5076
ttcaacatca aggactacta tatgcac 27

<210> 5077

<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5077
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 5078
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5078
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 5079
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5079
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 5080
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5080
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 5081
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5081
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gctgtgggac caaggtcgag atcaaa 336

<210> 5082
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5082
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5083
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5083
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5084
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5084
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 5085
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region CDR L2 amino acid sequence

<400> 5085
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5086
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5086
tgggcatcta cccgggaatc c 21

<210> 5087
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5087
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 5088
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5088
aagcaatctt attctcggag aact 24

<210> 5089
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5089
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaat gtcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5090
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5090
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5091
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5091
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 5092
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5092
ttcaacatca aggactacta tatgcac 27

<210> 5093
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5093
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 5094
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5094
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 5095
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5095
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 5096
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5096
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 5097
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5097
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gctgtgggac caaggtcgag atcaaa 336

<210> 5098
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5098
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5099
<211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5099
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5100
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5100
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 5101
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5101
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5102
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5102
tgggcatcta cccgggaatc c 21

<210> 5103
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5103
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 5104
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5104
aagcaatctt attctcggag aact 24

<210> 5105
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5105
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaat gtcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5106
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5106
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5107
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5107
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 5108
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5108
ttcaacatca aggactacta tatgcac 27

<210> 5109
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5109
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 5110
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5110
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 5111
<211> 12

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5111
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 5112
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5112
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 5113
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5113
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gctgtgggac caaggtcgag atcaaa 336

<210> 5114
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5114
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5115
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5115
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5116
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5116
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 5117
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5117
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5118
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5118
tgggcatcta cccgggaatc c 21

<210> 5119
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5119
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 5120
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5120
aagcaatctt attctcggag aact 24

<210> 5121
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5121
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaat gtcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5122
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5122
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

```
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 5123
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 5123
Phe Asn Ile Lys Asp Tyr Tyr Met His
1               5


<210> 5124
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5124
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ttcaacatca aggactacta tatgcac 27

<210> 5125
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5125
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 5126
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5126
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 5127
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5127
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 5128
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5128
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 5129
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5129
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gctgtgggac caaggtcgag atcaaa 336

<210> 5130
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5130
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5131
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5131
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5132
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5132
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 5133
<211> 7
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5133
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5134
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5134
tgggcatcta cccgggaatc c 21

<210> 5135
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5135
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 5136
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5136
aagcaatctt attctcggag aact 24

<210> 5137

<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5137
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaat gtcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5138
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5138
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5139
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5139
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 5140
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5140
ttcaacatca aggactacta tatgcac 27

<210> 5141
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5141
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 5142
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5142
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 5143
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5143
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 5144
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5144
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 5145
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region nucleic acid sequence

<400> 5145
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gctgtgggac caaggtcgag atcaaa 336

<210> 5146
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5146
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5147
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5147
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5148
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5148
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 5149
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5149
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5150
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5150
tgggcatcta cccgggaatc c 21

<210> 5151
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5151
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 5152
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5152
aagcaatctt attctcggag aact 24

<210> 5153
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5153
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaat gtcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5154
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5154
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5155
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5155
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 5156
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5156
ttcaacatca aggactacta tatgcac 27

<210> 5157
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5157
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 5158
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5158
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 5159
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5159
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 5160
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5160
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 5161
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5161
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gctgtgggac caaggtcgag atcaaa 336

<210> 5162
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5162
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5163
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5163
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5164
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5164
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 5165
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5165
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5166
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5166
tgggcatcta cccgggaatc c 21

<210> 5167
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5167
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 5168
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5168
aagcaatctt attctcggag aact 24

<210> 5169
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5169
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggaggat gtcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5170
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5170

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gly Cys Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5171
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5171
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 5172
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5172
ttcaacatca aggactacta tatgcac 27

<210> 5173
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5173
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 5174
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5174
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 5175
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5175
Ala Arg Asp Gly Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 5176
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5176
gcgagagatg gatacgggag atatttttac gacgtg 36

<210> 5177
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5177
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gctgtgggac caaggtcgag atcaaa 336

<210> 5178
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5178
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5179
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5179
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5180
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5180
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 5181
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5181
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5182
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5182
tgggcatcta cccgggaatc c 21

<210> 5183
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5183
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 5184
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5184

aagcaatctt attctcggag aact 24

<210> 5185
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5185
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgct 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5186
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5186
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5187
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5187
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 5188
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5188
ttcaacatca aggactacta tatgcac 27

<210> 5189
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5189
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 5190
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5190
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 5191
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5191
Ala Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 5192
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5192
gcgagagatg cttacgggag atatttttac gacgtg 36

<210> 5193
<211> 336
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5193
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta acgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5194
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5194
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5195
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5195
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5196
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5196
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 5197
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5197
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5198

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5198
tgggcatcta cccgggaatc c 21

<210> 5199
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5199
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 5200
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5200
aagcaatctt attctcggag aact 24

<210> 5201
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5201
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgg tagagatgcg 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5202
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5202
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Gly Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5203
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5203
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 5204
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5204
ttcaacatca aggactacta tatgcac 27

<210> 5205
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5205
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 5206
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5206
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 5207
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5207
Gly Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 5208
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5208
ggtagagatg cgtacgggag atatttttac gacgtg 36

<210> 5209
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5209
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5210
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5210
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5211
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5211

Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5212
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5212
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 5213
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5213
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5214
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5214
tgggcatcta cccgggaatc c 21

<210> 5215
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5215
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 5216
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5216
aagcaatctt attctcggag aact 24

<210> 5217
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5217
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aagagggcaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgct 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5218
<211> 119
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5218
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5219
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5219
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 5220
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5220
ttcaacatca aggactacta tatgcac 27

<210> 5221
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5221
Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 5222
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5222
tggatcgacc ttgaagaggg caacacaatc tatgacgcta agtttcaggg c 51

<210> 5223
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5223

Ala Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 5224
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5224
gcgagagatg cttacgggag atatttttac gacgtg 36

<210> 5225
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5225
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5226
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5226
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
            20   25   30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
                85   90   95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 5227
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 5227
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1   5   10   15

Ala

<210> 5228
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 5228
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 5229
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5229
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5230
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5230
tgggcatcta cccgggaatc c 21

<210> 5231
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5231
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 5232
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5232
aagcaatctt attctcggag aact 24

<210> 5233
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5233
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aagagggcaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgg tagagatgcg 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5234
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5234
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Gly Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5235
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5235
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 5236
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5236
ttcaacatca aggactacta tatgcac 27

<210> 5237
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5237
Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 5238
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5238
tggatcgacc ttgaagaggg caacacaatc tatgacgcta agtttcaggg c 51

<210> 5239
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5239
Gly Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 5240
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5240
ggtagagatg cgtacgggag atatttttac gacgtg 36

<210> 5241
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5241
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta acgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5242
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5242
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5243
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5243
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5244
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5244
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 5245
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5245
Trp Ala Ser Thr Arg Glu Ser

1 5

<210> 5246
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5246
tgggcatcta cccgggaatc c 21

<210> 5247
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5247
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 5248
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5248
aagcaatctt attctcggag aact 24

<210> 5249
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5249
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatcgt 300

tacggggctt atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5250
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5250
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Tyr Gly Ala Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
        115

<210> 5251
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 5251
Phe Asn Ile Lys Asp Tyr Tyr Met His
1   5

<210> 5252
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5252
ttcaacatca aggactacta tatgcac   27

<210> 5253
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H2 amino acid sequence

<400> 5253
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1   5   10   15

Gly

<210> 5254
<211> 51
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5254
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 5255
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5255
Ala Arg Asp Arg Tyr Gly Ala Tyr Phe Tyr Asp Val
1 5 10

<210> 5256
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5256
gcgagagatc gttacggggc ttatttttac gacgtg 36

<210> 5257
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5257
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5258
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5258
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5259
<211> 17
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5259
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5260
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5260
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 5261
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5261
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5262
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5262
tgggcatcta cccgggaatc c 21

<210> 5263
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5263
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 5264
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5264
aagcaatctt attctcggag aact 24

<210> 5265
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5265
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgtg 300

ttggggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5266
<211> 119

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5266
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
            20   25   30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35   40   45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
    50   55   60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65   70   75   80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Asp Val Leu Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
            100   105   110

Thr Leu Val Thr Val Ser Ser
        115

<210> 5267
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5267
Phe Asn Ile Lys Asp Tyr Tyr Met His
1   5

<210> 5268
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5268
ttcaacatca aggactacta tatgcac 27

<210> 5269
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5269
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 5270
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5270
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 5271
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5271
Ala Arg Asp Val Leu Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 5272
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5272
gcgagagatg tgttggggag atatttttac gacgtg 36

<210> 5273
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5273
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5274
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5274
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5275
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5275
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5276
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5276
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 5277
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5277
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5278
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5278
tgggcatcta cccgggaatc c 21

<210> 5279
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5279
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 5280
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5280
aagcaatctt attctcggag aact 24

<210> 5281
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5281
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatcag 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5282
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5282
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gln Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5283
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5283
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 5284
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5284
ttcaacatca aggactacta tatgcac 27

<210> 5285

<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5285
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 5286
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5286
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 5287
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5287
Ala Arg Asp Gln Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 5288
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5288
gcgagagatc agtacgggag atatttttac gacgtg 36

<210> 5289
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5289
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5290
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5290
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5291
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5291
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5292
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5292
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 5293
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region CDR L2 amino acid sequence

<400> 5293
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5294
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5294
tgggcatcta cccgggaatc c 21

<210> 5295
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5295
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 5296
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5296
aagcaatctt attctcggag aact 24

<210> 5297
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5297
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aagagggcaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgtg 300

ttggggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5298
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5298
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Val Leu Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5299
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5299
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 5300
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5300
ttcaacatca aggactacta tatgcac 27

<210> 5301
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5301
Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 5302
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5302
tggatcgacc ttgaagaggg caacacaatc tatgacgcta agtttcaggg c 51

<210> 5303
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5303
Ala Arg Asp Val Leu Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 5304
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5304
gcgagagatg tgttggggag atatttttac gacgtg 36

<210> 5305
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5305
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5306
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5306
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5307
<211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5307
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5308
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5308
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 5309
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5309
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5310
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5310
tgggcatcta cccgggaatc c 21

<210> 5311
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5311
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 5312
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5312
aagcaatctt attctcggag aact 24

<210> 5313
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5313
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgtg 300

tacgggagat atttttacga cctttggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5314
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5314
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Val Tyr Gly Arg Tyr Phe Tyr Asp Leu Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5315
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5315
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 5316
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5316
ttcaacatca aggactacta tatgcac 27

<210> 5317
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5317
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 5318
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5318
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 5319
<211> 12

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5319
Ala Arg Asp Val Tyr Gly Arg Tyr Phe Tyr Asp Leu
1 5 10

<210> 5320
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5320
gcgagagatg tgtacgggag atatttttac gacctt 36

<210> 5321
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5321
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5322
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5322
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5323
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5323
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5324
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5324
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 5325
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5325
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5326
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5326
tgggcatcta cccgggaatc c 21

<210> 5327
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5327
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 5328
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5328
aagcaatctt attctcggag aact 24

<210> 5329
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5329
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgcg 300

tacgggggggt atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5330
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5330
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
            20   25   30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35   40   45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
    50   55   60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65   70   75   80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Asp Ala Tyr Gly Gly Tyr Phe Tyr Asp Val Trp Gly Gln Gly
            100   105   110

Thr Leu Val Thr Val Ser Ser
        115

<210> 5331
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 5331
Phe Asn Ile Lys Asp Tyr Tyr Met His
1   5

<210> 5332
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5332

ttcaacatca aggactacta tatgcac 27

<210> 5333
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5333
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 5334
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5334
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 5335
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5335
Ala Arg Asp Ala Tyr Gly Gly Tyr Phe Tyr Asp Val
1 5 10

<210> 5336
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5336
gcgagagatg cgtacggggg gtatttttac gacgtg 36

<210> 5337
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5337
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5338
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5338
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5339
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5339
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5340
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5340
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 5341
<211> 7
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5341
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5342
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5342
tgggcatcta cccgggaatc c 21

<210> 5343
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5343
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 5344
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5344
aagcaatctt attctcggag aact 24

<210> 5345

<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5345
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagataat 300

tacgggggt atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5346
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5346
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Asn Tyr Gly Gly Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5347
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5347
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 5348
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5348
ttcaacatca aggactacta tatgcac 27

<210> 5349
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5349
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 5350
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5350
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 5351
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5351
Ala Arg Asp Asn Tyr Gly Gly Tyr Phe Tyr Asp Val
1 5 10

<210> 5352
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5352
gcgagagata attacggggg gtatttttac gacgtg 36

<210> 5353
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region nucleic acid sequence

<400> 5353
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5354
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5354
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5355
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5355
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5356
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5356
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 5357
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5357
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5358
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5358
tgggcatcta cccgggaatc c 21

<210> 5359
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5359
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 5360
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5360
aagcaatctt attctcggag aact 24

<210> 5361
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5361
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgct 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5362
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5362
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5363
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5363
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 5364
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5364
ttcaacatca aggactacta tatgcac 27

<210> 5365
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5365
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 5366
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5366
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 5367
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5367
Ala Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 5368
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5368
gcgagagatg cttacgggag atatttttac gacgtg 36

<210> 5369
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5369
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5370
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5370
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5371
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5371
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5372
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5372
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 5373
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5373
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5374
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5374
tgggcatcta cccgggaatc c 21

<210> 5375
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5375
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 5376
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5376
aagcaatctt attctctgag aact 24

<210> 5377
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5377
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgg tagagatgcg 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5378
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5378

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Gly Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5379
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5379
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 5380
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5380
ttcaacatca aggactacta tatgcac 27

<210> 5381
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5381
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 5382
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5382
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 5383
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5383
Gly Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 5384
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5384
ggtagagatg cgtacgggag atatttttac gacgtg 36

<210> 5385
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5385
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5386
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5386
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

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Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45


Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60


Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80


Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
                85                  90                  95


Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


<210> 5387
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 5387
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1               5                   10                  15


Ala



<210> 5388
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 5388
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t                51
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<210> 5389
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5389
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5390
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5390
tgggcatcta cccgggaatc c 21

<210> 5391
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5391
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 5392
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5392

aagcaatctt attctctgag aact 24

<210> 5393
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5393
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aagagggcaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgct 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5394
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5394
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5395
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5395
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 5396
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5396
ttcaacatca aggactacta tatgcac 27

<210> 5397
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5397
Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 5398
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5398
tggatcgacc ttgaagaggg caacacaatc tatgacgcta agtttcaggg c 51

<210> 5399
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5399
Ala Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 5400
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5400
gcgagagatg cttacgggag atatttttac gacgtg 36

<210> 5401
<211> 336
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5401
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta acgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5402
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5402
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5403
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5403
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5404
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5404
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 5405
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5405
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5406

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5406
tgggcatcta cccgggaatc c 21

<210> 5407
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5407
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 5408
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5408
aagcaatctt attctctgag aact 24

<210> 5409
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5409
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgg tagagatgcg 300

tacgggctgt atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5410
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5410
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Gly Arg Asp Ala Tyr Gly Leu Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5411
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5411
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 5412
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5412
ttcaacatca aggactacta tatgcac 27

<210> 5413
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5413
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 5414
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5414
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 5415
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5415
Gly Arg Asp Ala Tyr Gly Leu Tyr Phe Tyr Asp Val
1 5 10

<210> 5416
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5416
ggtagagatg cgtacgggct gtatttttac gacgtg 36

<210> 5417
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5417
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5418
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5418
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5419
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5419

Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5420
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5420
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 5421
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5421
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5422
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5422
tgggcatcta cccgggaatc c 21

<210> 5423
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5423
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 5424
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5424
aagcaatctt attctctgag aact 24

<210> 5425
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5425
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgtg 300

ttggggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5426
<211> 119
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5426
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Val Leu Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5427
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5427
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 5428
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5428
ttcaacatca aggactacta tatgcac 27

<210> 5429
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5429
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 5430
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5430
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 5431
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5431

Ala Arg Asp Val Leu Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 5432
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5432
gcgagagatg tgttggggag atatttttac gacgtg 36

<210> 5433
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5433
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5434
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5434
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
            20   25   30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
                85   90   95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 5435
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 5435
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1   5   10   15

Ala

<210> 5436
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 5436
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 5437
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5437
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5438
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5438
tgggcatcta cccgggaatc c 21

<210> 5439
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5439
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 5440
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5440
aagcaatctt attctctgag aact 24

<210> 5441
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5441
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aagagggcaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatcgt 300

tacggggctt atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5442
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5442
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Tyr Gly Ala Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5443
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5443
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 5444
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5444
ttcaacatca aggactacta tatgcac 27

<210> 5445
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5445
Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 5446
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5446
tggatcgacc ttgaagaggg caacacaatc tatgacgcta agtttcaggg c 51

<210> 5447
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5447
Ala Arg Asp Arg Tyr Gly Ala Tyr Phe Tyr Asp Val
1 5 10

<210> 5448
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5448
gcgagagatc gttacggggc ttatttttac gacgtg 36

<210> 5449
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5449
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta acgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5450
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5450
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5451
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5451
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5452
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5452
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 5453
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5453
Trp Ala Ser Thr Arg Glu Ser

1 5

<210> 5454
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5454
tgggcatcta cccgggaatc c 21

<210> 5455
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5455
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 5456
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5456
aagcaatctt attctctgag aact 24

<210> 5457
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5457
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aagagggcaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgg tagagatgcg 300

tacgggctgt atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5458
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5458
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Gly Arg Asp Ala Tyr Gly Leu Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
        115

<210> 5459
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 5459
Phe Asn Ile Lys Asp Tyr Tyr Met His
1   5

<210> 5460
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5460
ttcaacatca aggactacta tatgcac   27

<210> 5461
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H2 amino acid sequence

<400> 5461
Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1   5   10   15

Gly

<210> 5462
<211> 51
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5462
tggatcgacc ttgaagaggg caacacaatc tatgacgcta agtttcaggg c 51

<210> 5463
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5463
Gly Arg Asp Ala Tyr Gly Leu Tyr Phe Tyr Asp Val
1 5 10

<210> 5464
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5464
ggtagagatg cgtacgggct gtatttttac gacgtg 36

<210> 5465
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5465
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5466
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5466
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5467
<211> 17
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5467
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5468
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5468
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 5469
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5469
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5470
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5470
tgggcatcta cccgggaatc c 21

<210> 5471
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5471
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 5472
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5472
aagcaatctt attctctgag aact 24

<210> 5473
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5473
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aagagggcaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgtg 300

ttggggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5474
<211> 119

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5474
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
            20   25   30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35   40   45

Gly Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Asp Ala Lys Phe
    50   55   60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65   70   75   80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Asp Val Leu Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
            100   105   110

Thr Leu Val Thr Val Ser Ser
        115

<210> 5475
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5475
Phe Asn Ile Lys Asp Tyr Tyr Met His
1   5

<210> 5476
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5476
ttcaacatca aggactacta tatgcac 27

<210> 5477
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5477
Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 5478
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5478
tggatcgacc ttgaagaggg caacacaatc tatgacgcta agtttcaggg c 51

<210> 5479
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5479
Ala Arg Asp Val Leu Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 5480
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5480
gcgagagatg tgttggggag atatttttac gacgtg 36

<210> 5481
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5481
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5482
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5482
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5483
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5483
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5484
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5484
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 5485
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5485
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5486
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5486
tgggcatcta cccgggaatc c 21

<210> 5487
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5487
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 5488
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5488
aagcaatctt attctctgag aact 24

<210> 5489
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5489
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgtg 300

tacgggagat atttttacga cctttggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5490
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5490
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Val Tyr Gly Arg Tyr Phe Tyr Asp Leu Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5491
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5491
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 5492
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5492
ttcaacatca aggactacta tatgcac 27

<210> 5493

<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5493
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 5494
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5494
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 5495
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5495
Ala Arg Asp Val Tyr Gly Arg Tyr Phe Tyr Asp Leu
1 5 10

<210> 5496
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5496
gcgagagatg tgtacgggag atatttttac gacctt 36

<210> 5497
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5497
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5498
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5498
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5499
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5499
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5500
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5500
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 5501
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region CDR L2 amino acid sequence

<400> 5501
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5502
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5502
tgggcatcta cccgggaatc c 21

<210> 5503
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5503
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 5504
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5504
aagcaatctt attctctgag aact 24

<210> 5505
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5505
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagataat 300

tacgggggggt atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5506
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5506
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Asn Tyr Gly Gly Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5507
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5507
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 5508
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5508
ttcaacatca aggactacta tatgcac 27

<210> 5509
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5509
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 5510
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5510
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 5511
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5511
Ala Arg Asp Asn Tyr Gly Gly Tyr Phe Tyr Asp Val
1 5 10

<210> 5512
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5512
gcgagagata attacggggg gtatttttac gacgtg 36

<210> 5513
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5513
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5514
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5514
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5515
<211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5515
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5516
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5516
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 5517
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5517
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5518
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5518
tgggcatcta cccgggaatc c 21

<210> 5519
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5519
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 5520
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5520
aagcaatctt attctctgag aact 24

<210> 5521
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5521
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgct 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5522
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5522
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5523
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5523
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 5524
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5524
ttcaacatca aggactacta tatgcac 27

<210> 5525
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5525
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 5526
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5526
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 5527
<211> 12

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5527
Ala Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 5528
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5528
gcgagagatg cttacgggag atatttttac gacgtg 36

<210> 5529
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5529
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctatc 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5530
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5530
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Ile Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5531
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5531
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5532
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5532
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 5533
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5533
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5534
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5534
tgggcatcta cccgggaatc c 21

<210> 5535
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5535
Lys Gln Ser Tyr Ser Ile Arg Thr
1 5

<210> 5536
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5536
aagcaatctt attctatcag aact 24

<210> 5537
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5537
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgtg 300

ttggggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5538
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5538
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
            20   25   30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35   40   45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
    50   55   60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65   70   75   80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Asp Val Leu Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
            100   105   110

Thr Leu Val Thr Val Ser Ser
        115

<210> 5539
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 5539
Phe Asn Ile Lys Asp Tyr Tyr Met His
1   5

<210> 5540
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5540

ttcaacatca aggactacta tatgcac 27

<210> 5541
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5541
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 5542
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5542
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 5543
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5543
Ala Arg Asp Val Leu Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 5544
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5544
gcgagagatg tgttggggag atatttttac gacgtg 36

<210> 5545
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5545
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctatc 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5546
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5546
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Ile Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5547
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5547
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5548
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5548
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 5549
<211> 7
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5549
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5550
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5550
tgggcatcta cccgggaatc c 21

<210> 5551
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5551
Lys Gln Ser Tyr Ser Ile Arg Thr
1 5

<210> 5552
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5552
aagcaatctt attctatcag aact 24

<210> 5553

<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5553
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatcag 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5554
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5554
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gln Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5555
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5555
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 5556
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5556
ttcaacatca aggactacta tatgcac 27

<210> 5557
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5557
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 5558
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5558
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 5559
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5559
Ala Arg Asp Gln Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 5560
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5560
gcgagagatc agtacgggag atatttttac gacgtg 36

<210> 5561
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region nucleic acid sequence

<400> 5561
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctatc 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5562
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5562
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Ile Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5563
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5563
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5564
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5564
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 5565
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5565
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5566
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5566
tgggcatcta cccgggaatc c 21

<210> 5567
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5567
Lys Gln Ser Tyr Ser Ile Arg Thr
1 5

<210> 5568
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5568
aagcaatctt attctatcag aact 24

<210> 5569
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5569
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aagagggcaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatcgt 300

tacggggctt atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5570
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5570
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Tyr Gly Ala Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5571
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5571
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 5572
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5572
ttcaacatca aggactacta tatgcac 27

<210> 5573
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5573
Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 5574
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5574
tggatcgacc ttgaagaggg caacacaatc tatgacgcta agtttcaggg c 51

<210> 5575
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5575
Ala Arg Asp Arg Tyr Gly Ala Tyr Phe Tyr Asp Val
1 5 10

<210> 5576
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5576
gcgagagatc gttacggggc ttatttttac gacgtg 36

<210> 5577
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5577
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctatc 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5578
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5578
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Ile Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5579
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5579
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5580
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5580
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 5581
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5581
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5582
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5582
tgggcatcta cccgggaatc c 21

<210> 5583
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5583
Lys Gln Ser Tyr Ser Ile Arg Thr
1 5

<210> 5584
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5584
aagcaatctt attctatcag aact 24

<210> 5585
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5585
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aagagggcaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatcag 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5586
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5586

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Asp Ala Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Gln Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 5587
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 5587
Phe Asn Ile Lys Asp Tyr Tyr Met His
1               5


<210> 5588
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
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<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5588
ttcaacatca aggactacta tatgcac 27

<210> 5589
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5589
Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 5590
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5590
tggatcgacc ttgaagaggg caacacaatc tatgacgcta agtttcaggg c 51

<210> 5591
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5591
Ala Arg Asp Gln Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 5592
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5592
gcgagagatc agtacgggag atatttttac gacgtg 36

<210> 5593
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5593
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctatc 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5594
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5594
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Ile Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5595
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5595
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5596
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5596
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 5597
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5597
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5598
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5598
tgggcatcta cccgggaatc c 21

<210> 5599
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5599
Lys Gln Ser Tyr Ser Ile Arg Thr
1 5

<210> 5600
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5600

aagcaatctt attctatcag aact 24

<210> 5601
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5601
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgtg 300

tacgggagat atttttacga cctttggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5602
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5602
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Val Tyr Gly Arg Tyr Phe Tyr Asp Leu Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5603
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5603
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 5604
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5604
ttcaacatca aggactacta tatgcac 27

<210> 5605
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5605
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 5606
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5606
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 5607
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5607
Ala Arg Asp Val Tyr Gly Arg Tyr Phe Tyr Asp Leu
1 5 10

<210> 5608
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5608
gcgagagatg tgtacgggag atatttttac gacctt 36

<210> 5609
<211> 336
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5609
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctatc 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5610
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5610
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Ile Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5611
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5611
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5612
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5612
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 5613
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5613
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5614

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5614
tgggcatcta cccgggaatc c 21

<210> 5615
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5615
Lys Gln Ser Tyr Ser Ile Arg Thr
1 5

<210> 5616
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5616
aagcaatctt attctatcag aact 24

<210> 5617
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5617
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgcg 300

tacgggggggt atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5618
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5618
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Ala Tyr Gly Gly Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5619
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5619
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 5620
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5620
ttcaacatca aggactacta tatgcac 27

<210> 5621
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5621
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 5622
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5622
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 5623
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5623
Ala Arg Asp Ala Tyr Gly Gly Tyr Phe Tyr Asp Val
1 5 10

<210> 5624
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5624
gcgagagatg cgtacggggg gtatttttac gacgtg 36

<210> 5625
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5625
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctatc 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5626
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5626
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Ile Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5627
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5627

Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5628
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5628
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 5629
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5629
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5630
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5630
tgggcatcta cccgggaatc c 21

<210> 5631
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5631
Lys Gln Ser Tyr Ser Ile Arg Thr
1 5

<210> 5632
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5632
aagcaatctt attctatcag aact 24

<210> 5633
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5633
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagataat 300

tacgggggt atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5634
<211> 119
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5634
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Asn Tyr Gly Gly Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5635
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5635
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 5636
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5636
ttcaacatca aggactacta tatgcac 27

<210> 5637
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5637
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 5638
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5638
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 5639
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5639

Ala Arg Asp Asn Tyr Gly Gly Tyr Phe Tyr Asp Val
1 5 10

<210> 5640
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5640
gcgagagata attacggggg gtatttttac gacgtg 36

<210> 5641
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5641
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctatc 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5642
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5642
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
            20   25   30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
                85   90   95

Ser Tyr Ser Ile Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 5643
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 5643
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1   5   10   15

Ala

<210> 5644
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 5644
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 5645
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5645
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5646
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5646
tgggcatcta cccgggaatc c 21

<210> 5647
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5647
Lys Gln Ser Tyr Ser Ile Arg Thr
1 5

<210> 5648
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5648
aagcaatctt attctatcag aact 24

<210> 5649
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5649
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aagagggcaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgg tagagatgcg 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5650
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5650
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Gly Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5651
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5651
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 5652
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5652
ttcaacatca aggactacta tatgcac 27

<210> 5653
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5653
Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 5654
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5654
tggatcgacc ttgaagaggg caacacaatc tatgacgcta agtttcaggg c 51

<210> 5655
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5655
Gly Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 5656
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5656
ggtagagatg cgtacgggag atatttttac gacgtg 36

<210> 5657
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5657
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta gaaagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5658
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5658
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Glu Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5659
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5659
Lys Ser Ser Gln Ser Leu Leu Glu Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5660
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5660
aagtccagcc agagtctttt agaaagcaga accggaaaga actacttagc t 51

<210> 5661
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5661
Trp Ala Ser Thr Arg Glu Ser

1 5

<210> 5662
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5662
tgggcatcta cccgggaatc c 21

<210> 5663
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5663
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 5664
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5664
aagcaatctt attctctgag aact 24

<210> 5665
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5665
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aagagggcaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgtg 300

ttggggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5666
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5666
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Val Leu Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
        115

<210> 5667
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 5667
Phe Asn Ile Lys Asp Tyr Tyr Met His
1   5

<210> 5668
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5668
ttcaacatca aggactacta tatgcac   27

<210> 5669
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H2 amino acid sequence

<400> 5669
Trp Ile Asp Leu Glu Glu Gly Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1   5   10   15

Gly

<210> 5670
<211> 51
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5670
tggatcgacc ttgaagaggg caacacaatc tatgacgcta agtttcaggg c 51

<210> 5671
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5671
Ala Arg Asp Val Leu Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 5672
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5672
gcgagagatg tgttggggag atatttttac gacgtg 36

<210> 5673
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5673
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta gaaagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5674
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5674
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Glu Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5675
<211> 17
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5675
Lys Ser Ser Gln Ser Leu Leu Glu Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5676
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5676
aagtccagcc agagtctttt agaaagcaga accggaaaga actacttagc t 51

<210> 5677
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5677
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5678
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5678
tgggcatcta cccgggaatc c 21

<210> 5679
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5679
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 5680
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5680
aagcaatctt attctctgag aact 24

<210> 5681
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5681
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagataat 300

tacgggggt atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5682
<211> 119

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5682
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
            20   25   30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35   40   45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
    50   55   60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65   70   75   80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Asp Asn Tyr Gly Gly Tyr Phe Tyr Asp Val Trp Gly Gln Gly
            100   105   110

Thr Leu Val Thr Val Ser Ser
        115

<210> 5683
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5683
Phe Asn Ile Lys Asp Tyr Tyr Met His
1   5

<210> 5684
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5684
ttcaacatca aggactacta tatgcac 27

<210> 5685
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5685
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 5686
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5686
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 5687
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5687
Ala Arg Asp Asn Tyr Gly Gly Tyr Phe Tyr Asp Val
1 5 10

<210> 5688
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5688
gcgagagata attacggggg gtatttttac gacgtg 36

<210> 5689
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5689
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta gaaagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctctg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5690
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5690
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Glu Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Leu Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5691
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5691
Lys Ser Ser Gln Ser Leu Leu Glu Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5692
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5692
aagtccagcc agagtctttt agaaagcaga accggaaaga actacttagc t 51

<210> 5693
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5693
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5694
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5694
tgggcatcta cccgggaatc c 21

<210> 5695
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5695
Lys Gln Ser Tyr Ser Leu Arg Thr
1 5

<210> 5696
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5696
aagcaatctt attctctgag aact 24

<210> 5697
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5697
gaagtgaagc tgcagcagtc tggggctgag cttgtgaggc caggggcctt agtcaagttg 60

tcctgcaaag cttctgactt caacattaaa gactactata tgcactgggt gaagcagagg 120

cctgaacagg gcctggagtg gattggatgg attgatcctg agaatggtaa tactatatat 180

gacccgaagt tccagggcaa ggccagtata acagcagaca catcctccaa cacagcctac 240

ctgcagctca gcagcctgac atctgaggac actgccgtct attactgtgg tagggatggt 300

aactactttt ttgactactg gggccaaggc accacggtca ccgtctcctc a 351

<210> 5698
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5698
Glu Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
1 5 10 15

Leu Val Lys Leu Ser Cys Lys Ala Ser Asp Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Lys Ala Ser Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Gly Arg Asp Gly Asn Tyr Phe Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

<210> 5699
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5699
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 5700
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5700
ttcaacatta aagactacta tatgcac 27

<210> 5701

<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5701
Trp Ile Asp Pro Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 5702
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5702
tggattgatc ctgagaatgg taatactata tgacccga agttccaggg c 51

<210> 5703
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5703
Gly Arg Asp Gly Asn Tyr Phe Phe Asp Tyr
1 5 10

<210> 5704
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5704
ggtagggatg gtaactactt ttttgactac 30

<210> 5705
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5705
gacatccagc tgactcagtc tccatcctcc ctggctgtgt cagcaggaga gaaggtcact 60

atgagctgca aatccagtca gagtctgctc aacagtagaa cccgaaagaa ctacttggct 120

tggtaccagc agaaaccagg gcagtctcct aaactgctga tctactgggc atccactagg 180

gaatctggag tccctgatcg cttcacaggc agtggatctg ggacagattt cactctcacc 240

atcagcagtg tgcaggctga agacctggca gtttattact gcaagcaatc ttataatctt 300

cggacgttcg gtggagggac caagctggag ctgaaa 336

<210> 5706
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5706
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys
100 105 110

<210> 5707
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5707
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5708
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5708
aaatccagtc agagtctgct caacagtaga acccgaaaga actacttggc t 51

<210> 5709
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region CDR L2 amino acid sequence

<400> 5709
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5710
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5710
tgggcatcca ctagggaatc t 21

<210> 5711
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5711
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 5712
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5712
aagcaatctt ataatcttcg gacg 24

<210> 5713
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5713
gaagtgcagc tgcagcagtc aggacctgag ctggtgaagc ctggggcttc agtgaggatc 60

tcctgcaagg cttctgacta caccttcaca agctactata ttcactgggt gaagcagagg 120

cctggacagg gacttgagtg gattggatgg atttatcctg gaaatgttaa tactaagtac 180

aatgagaatt tcaaggacaa ggccacactg actgcagaca aatcctccag cacagcctac 240

atgcacctca gcagcctgac ctctgaggac tctgcggtct atttctgtgc aagagatgat 300

ggttactact ttgactactg gggccaaggc accacggtca ccgtctcctc a 351

<210> 5714
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5714
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Arg Ile Ser Cys Lys Ala Ser Asp Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Asn Phe
50 55 60

Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met His Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Asp Asp Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

<210> 5715
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5715
Tyr Thr Phe Thr Ser Tyr Tyr Ile His
1 5

<210> 5716
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5716
tacaccttca caagctacta tattcac 27

<210> 5717
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5717
Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Asn Phe Lys
1 5 10 15

Asp

<210> 5718
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5718
tggatttatc ctggaaatgt taatactaag tacaatgaga atttcaagga c 51

<210> 5719
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5719
Ala Arg Asp Asp Gly Tyr Tyr Phe Asp Tyr
1 5 10

<210> 5720
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5720
gcaagagatg atggttacta ctttgactac 30

<210> 5721
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5721
gacatccagc tgacccagtc tccatcctcc ctggctgtgt cagcaggaga gaaggtcact 60

atgagctgca aatccagtca gagtctgctc aacagtagaa cccgaaagaa ctacttggct 120

tggtaccagc agaaaccagg gcagtctcct aaactgctga tctactgggc atccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg ggacagattt cactctcacc 240

atcagcagtg tgcaggctga agacctggca gtttattact gcaagcaatc ttataatctt 300

cggacgttcg gtggaggcac aaagctggaa atcaaa 336

<210> 5722
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5722
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 5723
<211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5723
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5724
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5724
aaatccagtc agagtctgct caacagtaga acccgaaaga actacttggc t 51

<210> 5725
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5725
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5726
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5726
tgggcatcca ctagggaatc t 21

<210> 5727
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5727
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 5728
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5728
aagcaatctt ataatcttcg gacg 24

<210> 5729
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5729
caagtcaagc tggagcagtc tggacctgag ctggtgaagc ctggggcttc agtgaagatg 60

tcctgcaagg cttctggcta caccttcaca aactactata tacactgggt gaagcagagg 120

cctggacagg gacttgagtg gattggatgg atttatcctg aagatggtaa tactaaatac 180

aatgagaaat tcaagggcaa gaccacactg actgcagaca aatcctccag cacagcctac 240

atgttgctca gcagcctgac ctctgaggac tctgcgatct atttctgtgc aaggaataac 300

ggtagtagct atgctatgga ctactggggc caaggcacca cggtcaccgt ctcctca 357

<210> 5730
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5730
Gln Val Lys Leu Glu Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Glu Asp Gly Asn Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Leu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Ile Tyr Phe Cys
85 90 95

Ala Arg Asn Asn Gly Ser Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 5731
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5731
Tyr Thr Phe Thr Asn Tyr Tyr Ile His
1 5

<210> 5732
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5732
tacaccttca caaactacta tatacac 27

<210> 5733
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5733
Trp Ile Tyr Pro Glu Asp Gly Asn Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 5734
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5734
tggatttatc ctgaagatgg taatactaaa tacaatgaga aattcaaggg c 51

<210> 5735
<211> 12

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5735
Ala Arg Asn Asn Gly Ser Ser Tyr Ala Met Asp Tyr
1 5 10

<210> 5736
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5736
gcaaggaata acggtagtag ctatgctatg gactac 36

<210> 5737
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5737
ggcatccagc tgactcagtc tccatcctcc ctggctgtgt cagcaggaga gaaggtcact 60

atgagctgca aatccagtca gagtctgctc aacagtagaa cccgaaagaa ctacttggct 120

tggtaccagc agaaaccagg gcagtctcct aaactgctga tctactgggc atccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg ggacagattt cactctcacc 240

atcagcagtg tgcaggctga agacctggca gtttattact gcaagcagtc ttataatctt 300

cggacgttcg gtggagggac caagctggag ctgaaa 336

<210> 5738
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5738
Gly Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys
100 105 110

<210> 5739
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5739
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5740
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5740
aaatccagtc agagtctgct caacagtaga acccgaaaga actacttggc t 51

<210> 5741
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5741
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5742
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5742
tgggcatcca ctagggaatc t 21

<210> 5743
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5743
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 5744
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5744
aagcagtctt ataatcttcg gacg 24

<210> 5745
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5745
caagtacagc tggagcagtc aggacctgag ctggtgaagc ctggggcttc agtgaggata 60

tcctgcaagg cttctggcta caccttcaca agctactata tacactgggt gaggcagagg 120

cctggtcagg gacttgagtg gattggatgg atttttcctg gaaatgttaa tactaagtac 180

aatgagaagt tcaagggcaa ggccacactg actgcagaca aatcctccag cacagcctac 240

atgcagctca gcagcctgac ctctgaggac tctgcggtct atttctgtgc aagagatggt 300

aactactcct ttgcttactg gggccaaggc accacggtca ccgtctcctc a 351

<210> 5746
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5746
Gln Val Gln Leu Glu Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Arg Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Phe Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Asp Gly Asn Tyr Ser Phe Ala Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

<210> 5747
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5747
Tyr Thr Phe Thr Ser Tyr Tyr Ile His
1 5

<210> 5748
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5748

tacaccttca caagctacta tatacac 27

<210> 5749
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5749
Trp Ile Phe Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 5750
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5750
tggatttttc ctggaaatgt taatactaag tacaatgaga agttcaaggg c 51

<210> 5751
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5751
Ala Arg Asp Gly Asn Tyr Ser Phe Ala Tyr
1 5 10

<210> 5752
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5752
gcaagagatg gtaactactc ctttgcttac 30

<210> 5753
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5753
gacattcagc tcactcagtc tccatcctcc ctggctgtgt cagcaggaga gaaggtcact 60

atgagctgca aatccagtca gagtctgctc aacagtagaa cccgaaagaa ctacttggct 120

tggtaccagc aaaaaccagg gcagtctcct aaactgctga tctactgggc atccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg ggacagattt cactctcacc 240

atcagcagtg tgcaggctga agacctggca gtttattact gcaagcaatc ttataatctt 300

cggacgttcg gtggagggac aaagctggaa ataaaa 336

<210> 5754
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5754
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Lys Gln
                85   90   95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105   110

<210> 5755
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 5755
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1   5   10   15

Ala

<210> 5756
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 5756
aaatccagtc agagtctgct caacagtaga acccgaaaga actacttggc t   51

<210> 5757
<211> 7
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5757
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5758
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5758
tgggcatcca ctagggaatc t 21

<210> 5759
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5759
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 5760
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5760
aagcaatctt ataatcttcg gacg 24

<210> 5761

<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5761
caggtgaagc tggagcagtc tggacctgag ctggtgaagc ctggggcttc agtgaggata 60

tcctgcaagg cttctggcta caccttcaca acctactata tacactgggt gaagcagagg 120

cctggacagg gacttgagtg gattggatgg atttatcctg gaaatgttaa tgctaagtac 180

aatgagaagt tcaagggcaa ggccacactg actgcagaca aatcctccag cacagcctac 240

atgcagctca gcagcctgac ctctgaggac tctgcggtct atttctgtgc aagagatgat 300

gggtactact ttgactactg gggccaaggc accacggtca ccgtctcctc a 351

<210> 5762
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5762
Gln Val Lys Leu Glu Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Arg Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr
20 25 30

Tyr Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Gly Asn Val Asn Ala Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Asp Asp Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

<210> 5763
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5763
Tyr Thr Phe Thr Thr Tyr Tyr Ile His
1 5

<210> 5764
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5764
tacaccttca caacctacta tatacac 27

<210> 5765
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5765
Trp Ile Tyr Pro Gly Asn Val Asn Ala Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 5766
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5766
tggatttatc ctggaaatgt taatgctaag tacaatgaga agttcaaggg c 51

<210> 5767
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5767
Ala Arg Asp Asp Gly Tyr Tyr Phe Asp Tyr
1 5 10

<210> 5768
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5768
gcaagagatg atgggtacta ctttgactac 30

<210> 5769
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region nucleic acid sequence

<400> 5769
gacatccagc tgactcagtc tccatcctcc ctggctgtgt cagcaggaga gaaggtcact 60

atgagctgca aatccagtca gagtctgctc aacagtagaa cccgaaagaa ctacttggct 120

tggtaccagc agaaaccagg gcagtctcct aaactgctga tctactgggc atccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg ggacagattt cactctcacc 240

atcagcagtg tgcaggctga agacctggca gtttattact gcaagcaatc ttataatctt 300

cggacgttcg gtggaggcac aaagctggaa ataaa 336

<210> 5770
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5770
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Asn Lys
100 105 110

<210> 5771
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5771
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5772
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5772
aaatccagtc agagtctgct caacagtaga acccgaaaga actacttggc t 51

<210> 5773
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5773
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5774
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5774
tgggcatcca ctagggaatc t 21

<210> 5775
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5775
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 5776
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5776
aagcaatctt ataatcttcg gacg 24

<210> 5777
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5777
gaggtccagc tgcaacaatc aggacctgag ctggtgaagc ctggggcctc agtgagggta 60

tcctgcaagg cttctggcta caccttcaca agctactata tacactgggt gaagcagagg 120

cctggacagg gacttgagtg gattggatgg atttatcctg gaaatgttaa tactcagtac 180

aatgagaagt tcaagggcaa ggccacactg actgcagaca aatcctccag cacaacctac 240

atgcagctca gcagcctgac ctctgaggac tctgcggtct atttctgtgc aagagatggt 300

gattactact ttgactactg gggccaaggc accacggtca ccgtctcctc a 351

<210> 5778
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5778
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Arg Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Gln Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Thr Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Asp Gly Asp Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

<210> 5779
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5779
Tyr Thr Phe Thr Ser Tyr Tyr Ile His
1 5

<210> 5780
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5780
tacaccttca caagctacta tatacac 27

<210> 5781
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5781
Trp Ile Tyr Pro Gly Asn Val Asn Thr Gln Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 5782
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5782
tggatttatc ctggaaatgt taatactcag tacaatgaga agttcaaggg c 51

<210> 5783
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5783
Ala Arg Asp Gly Asp Tyr Tyr Phe Asp Tyr
1 5 10

<210> 5784
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5784
gcaagagatg gtgattacta ctttgactac 30

<210> 5785
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5785
ggcattcagc tgacccagtc tccatcctcc ctggctgtgt cagcaggaga gaaggtcact 60

atgacctgca aatccagtca gagtctgctc aacagtagaa cccgaaagaa ctacttggct 120

tggtaccagc agaaaccagg gcagtctcct aaactgctga tctactgggc atccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg ggacagattt cactctcacc 240

atcagcagtg tgcaggctga agacctggca gtttattact gcaagcaatc ttataatctt 300

cggacgttcg gtggaggcac aaagttggaa ataaaa 336

<210> 5786
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5786
Gly Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
1 5 10 15

Glu Lys Val Thr Met Thr Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 5787
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5787
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5788
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5788
aaatccagtc agagtctgct caacagtaga acccgaaaga actacttggc t 51

<210> 5789
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5789
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5790
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5790
tgggcatcca ctagggaatc t 21

<210> 5791
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5791
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 5792
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5792
aagcaatctt ataatcttcg gacg 24

<210> 5793
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5793
gaggtcaagc tgcaggagtc tggacctgag ctggtgaagc ctggggcttc agtgaggata 60

tcctgcaagg cttctggcta caccttcaca agctactata tacactgggt gaagcagagg 120

cctggacagg gacttgagtg gattggatgg atttatcctg gaaatgttaa tactaagtac 180

aatgagaagt tcaagggcaa ggccacactg actgcagaca aatcctccag cacagcctac 240

atgcagctca gcagcctgac ctctgaggac tctgcggtct atttctgtgc aagagatggt 300

gattacttct ttgactactg gggccaaggc accacggtca ccgtctcctc a 351

<210> 5794
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5794

Glu Val Lys Leu Gln Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Arg Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Asp Gly Asp Tyr Phe Phe Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

<210> 5795
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5795
Tyr Thr Phe Thr Ser Tyr Tyr Ile His
1 5

<210> 5796
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5796
tacaccttca caagctacta tatacac 27

<210> 5797
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5797
Trp Ile Tyr Pro Gly Asn Val Asn Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 5798
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5798
tggatttatc ctggaaatgt taatactaag tacaatgaga agttcaaggg c 51

<210> 5799
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5799
Ala Arg Asp Gly Asp Tyr Phe Phe Asp Tyr
1 5 10

<210> 5800
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5800
gcaagagatg gtgattactt ctttgactac 30

<210> 5801
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5801
gacatccagc tcacccagtc tccatcctcc ctggctgtgt cagcaggaga gaaggtcact 60

atgagctgca aatccagtca gagtctgctc aacagtagaa cccaaaagaa ctacttggct 120

tggtaccagc agaaaccagg gcagtctcct aaactgctga tctactgggc atccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg ggacagattt cactctcacc 240

atcagcagtg tgcaggctga agacctggca gtttattact gcaagcaatc ttataatctt 300

cggacgttcg gtggaggcac caagctgaaa atcaaa 336

<210> 5802
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5802
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Leu Lys Ile Lys
100 105 110

<210> 5803
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5803
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gln Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5804
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5804
aaatccagtc agagtctgct caacagtaga acccaaaaga actacttggc t 51

<210> 5805
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5805
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5806
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5806
tgggcatcca ctagggaatc t 21

<210> 5807
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5807
Lys Gln Ser Tyr Asn Leu Arg Thr
1 5

<210> 5808
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5808

aagcaatctt ataatcttcg gacg 24

<210> 5809
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5809
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctggagggtc cctgaaactc 60

tcctgtgcag cctctggatt caccttcaat aaatacgcca tgaactgggt ccgccaggct 120

ccagggaagg ggctggagtg ggttgcccgt attagaagca aatataacaa ttacgccaca 180

tactacgccg actctgtgaa agacagattc accatctcaa gagatgattc aaagaacaca 240

gcgtatctgc aaatgaacaa cctgaaaacc gaggacacgg cggtgtacta ctgcgtgagg 300

cacggcaact tcgggaattc ctatatttca tactgggcct actggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 5810
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5810
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 5811
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5811
Phe Thr Phe Asn Lys Tyr Ala Met Asn
1 5

<210> 5812
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5812
ttcaccttca ataaatacgc catgaac 27

<210> 5813
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region CDR H2 amino acid sequence

<400> 5813
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 5814
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5814
cgtattagaa gcaaatataa caattacgcc acatactacg ccgactctgt gaaagac 57

<210> 5815
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5815
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr
1 5 10 15

<210> 5816
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5816
gtgaggcacg gcaacttcgg gaattcctat atttcatact gggcctac 48

<210> 5817

<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5817
cagactgtgg tgactcagga gccctcactg actgtgtccc caggagggac agtcactctc 60

acctgtggct ccagcactgg agctgtcacc agtggtaatt atcccaactg ggtccagcag 120

aagcctggcc aagcccccag gggactgatt ggtggtacaa aattcctggc ccccgggaca 180

cctgcccggt tctcaggctc cctccttggg ggcaaagctg ccctgaccct ttcgggtgtg 240

cagcctgagg atgaggctga gtattactgc gtgctctggt atagtaatcg gtgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 5818
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5818
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly
20 25 30

Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val
65 70 75 80

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
85 90 95

Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 5819
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5819
Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
1 5 10

<210> 5820
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5820
ggctccagca ctggagctgt caccagtggt aattatccca ac 42

<210> 5821
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5821
Gly Thr Lys Phe Leu Ala Pro
1 5

<210> 5822
<211> 21
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5822
ggtacaaaat tcctggcccc c 21

<210> 5823
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5823
Val Leu Trp Tyr Ser Asn Arg Trp Val
1 5

<210> 5824
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5824
gtgctctggt atagtaatcg gtgggtg 27

<210> 5825
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5825
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctggagggtc cctgaaactc 60

tcctgtgcag cctctggatt caccttcaat aaatacgcca tgaactgggt ccgccaggct 120

ccagggaagg ggctggagtg ggttgcccgt attagaagca aatataacaa ttacgccaca 180

tactacgccg actctgtgaa agacagattc accatctcaa gagatgattc aaagaacaca 240

gcgtatctgc aaatgaacaa cctgaaaacc gaggacacgg cggtgtacta ctgcgtgagg 300

cacggcaact tcgggaattc ctatatttca tactgggcct actggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 5826
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5826

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5				10					15		

Ser	Leu	Lys	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Asn	Lys	Tyr
		20					25					30			

Ala	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
	35					40					45				

Ala	Arg	Ile	Arg	Ser	Lys	Tyr	Asn	Asn	Tyr	Ala	Thr	Tyr	Tyr	Ala	Asp
50					55					60					

Ser	Val	Lys	Asp	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	Asn	Thr
65				70				75					80		

Ala	Tyr	Leu	Gln	Met	Asn	Asn	Leu	Lys	Thr	Glu	Asp	Thr	Ala	Val	Tyr
			85					90					95		

Tyr	Cys	Val	Arg	His	Gly	Asn	Phe	Gly	Asn	Ser	Tyr	Ile	Ser	Tyr	Trp
		100					105					110			

Ala	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser			
	115					120					125				

<210> 5827
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5827
Phe Thr Phe Asn Lys Tyr Ala Met Asn
1 5

<210> 5828
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5828
ttcaccttca ataaatacgc catgaac 27

<210> 5829
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5829
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 5830
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5830
cgtattagaa gcaaatataa caattacgcc acatactacg ccgactctgt gaaagac 57

<210> 5831
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5831
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr
1 5 10 15

<210> 5832
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5832
gtgaggcacg gcaacttcgg gaattcctat atttcatact gggcctac 48

<210> 5833
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5833
cagactgtgg tgactcagga gccctcactg actgtgtccc caggagggac agtcactctc 60

acctgtggct ccagcactgg agctgtcacc agtggtaatt atcccaactg ggtccagcag 120

aagcctggcc aagcccccag gggactgatt ggtggtacaa aattcctggc ccccgggaca 180

cctgcccggt tctcaggctc cctccttggg ggcaaagctg ccctgaccct ttcgggtgtg 240

cagcctgagg atgaggctga gtattactgc gtgctctggt atagtaatcg gtgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 5834
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5834
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly
20 25 30

Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val
65 70 75 80

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn
85 90 95

Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 5835
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5835

Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
1 5 10

<210> 5836
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5836
ggctccagca ctggagctgt caccagtggt aattatccca ac 42

<210> 5837
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5837
Gly Thr Lys Phe Leu Ala Pro
1 5

<210> 5838
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5838
ggtacaaaat tcctggcccc c 21

<210> 5839
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5839
Val Leu Trp Tyr Ser Asn Arg Trp Val
1 5

<210> 5840
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5840
gtgctctggt atagtaatcg gtgggtg 27

<210> 5841
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5841
gaggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggatt caccttcacc agctactata tacactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gataggatgg atctaccctg aaaatgataa cacaaagtac 180

aacgagaagt tcaaggacag agtcaccata accgcggaca cgtccacgag cacagcctac 240

ctggagctga gcagcctgag atctgaggac acggcggtgt actactgcgc cagggacgga 300

tattctagat attactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5842
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5842

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe Thr Ser Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Pro Glu Asn Asp Asn Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Leu Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ser Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5843
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5843
Phe Thr Phe Thr Ser Tyr Tyr Ile His
1 5

<210> 5844
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5844
ttcaccttca ccagctacta tatacac 27

<210> 5845
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5845
Trp Ile Tyr Pro Glu Asn Asp Asn Thr Lys Tyr Asn Glu Lys Phe Lys
1 5 10 15

Asp

<210> 5846
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5846
tggatctacc ctgaaaatga taacacaaag tacaacgaga agttcaagga c 51

<210> 5847
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5847
Ala Arg Asp Gly Tyr Ser Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 5848
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5848
gccagggacg gatattctag atattacttt gactac 36

<210> 5849
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5849
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccagaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagtctcct aagctgctca tttactggac atctacccgg 180

aagtccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtaagcaaag cttcatcctt 300

aggacgttcg gccaagggac caaggtggaa atcaaa 336

<210> 5850
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5850
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg Lys Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Phe Ile Leu Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5851
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5851
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5852
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5852
aagtccagcc agagtctttt aaacagcaga accagaaaga actacttagc t 51

<210> 5853
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5853
Trp Thr Ser Thr Arg Lys Ser
1 5

<210> 5854
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5854
tggacatcta cccggaagtc c 21

<210> 5855
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5855
Lys Gln Ser Phe Ile Leu Arg Thr
1 5

<210> 5856
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5856

aagcaaagct tcatccttag gacg 24

<210> 5857
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5857
gaagtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgat gattatacca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attagttgga atagtggtag cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa gtccctgtat 240

ctgcaaatga acagtctgag agctgaggac acggcgttgt actactgcgc caaggacaat 300

tccggatacg gccactacta ctacggtatg gacgtctggg ggcaagggac cacggtcacc 360

gtcgcctca 369

<210> 5858
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5858
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Asp Asn Ser Gly Tyr Gly His Tyr Tyr Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ala Ser
115 120

<210> 5859
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5859
Phe Thr Phe Asp Asp Tyr Thr Met His
1 5

<210> 5860
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5860
ttcacctttg atgattatac catgcac 27

<210> 5861
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region CDR H2 amino acid sequence

<400> 5861
Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 5862
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5862
ggtattagtt ggaatagtgg tagcataggc tatgcggact ctgtgaaggg c 51

<210> 5863
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5863
Ala Lys Asp Asn Ser Gly Tyr Gly His Tyr Tyr Tyr Gly Met Asp Val
1 5 10 15

<210> 5864
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5864
gccaaggaca attccggata cggccactac tactacggta tggacgtc 48

<210> 5865

<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5865
gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcaacttag cctggtacca gcagaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240

gaagattttg cagtttatta ctgtcaacat tacatcaatt ggcctctcac tttcggcgga 300

gggaccaagg tggagatcaa a 321

<210> 5866
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5866
Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln His Tyr Ile Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 5867
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5867
Arg Ala Ser Gln Ser Val Ser Ser Asn Leu Ala
1 5 10

<210> 5868
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5868
agggccagtc agagtgttag cagcaactta gcc 33

<210> 5869
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5869
Gly Ala Ser Thr Arg Ala Thr
1 5

<210> 5870
<211> 21
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5870
ggtgcatcca ccagggccac t 21

<210> 5871
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5871
Gln His Tyr Ile Asn Trp Pro Leu Thr
1 5

<210> 5872
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5872
caacattaca tcaattggcc tctcact 27

<210> 5873
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5873
gaagtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcggatc cctgagactc 60

tcctgtgcag ccactggatt cacctttgat gatttcacca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attagttgga atagtggtag cataggctat 180

gtggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag agctgaggac acggcgttgt actactgcgc caaggacaac 300

agcggatacg gctactacta ctacggtatg gacgtctggg ggcaagggac cacggtcacc 360

gtctcctca 369

<210> 5874
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5874

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5				10					15		

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Thr	Gly	Phe	Thr	Phe	Asp	Asp	Phe
		20					25					30			

Thr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
	35					40					45				

Ser	Gly	Ile	Ser	Trp	Asn	Ser	Gly	Ser	Ile	Gly	Tyr	Val	Asp	Ser	Val
	50					55					60				

Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr
65				70					75					80	

Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Leu	Tyr	Tyr	Cys
				85					90					95	

Ala	Lys	Asp	Asn	Ser	Gly	Tyr	Gly	Tyr	Tyr	Tyr	Tyr	Gly	Met	Asp	Val
			100					105					110		

Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser					
			115					120							

<210> 5875
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5875
Phe Thr Phe Asp Asp Phe Thr Met His
1 5

<210> 5876
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5876
ttcacctttg atgatttcac catgcac 27

<210> 5877
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5877
Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Val Asp Ser Val Lys
1 5 10 15

Gly

<210> 5878
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5878
ggtattagtt ggaatagtgg tagcataggc tatgtggact ctgtgaaggg c 51

<210> 5879
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5879
Ala Lys Asp Asn Ser Gly Tyr Gly Tyr Tyr Tyr Tyr Gly Met Asp Val
1 5 10 15

<210> 5880
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5880
gccaaggaca acagcggata cggctactac tactacggta tggacgtc 48

<210> 5881
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5881
gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca cagtgttagc agaaactcag cctggtacca gcagaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240

gaagattttg caatttatta ctgtcaacag tataataatt ggccgctcac tttcggcgga 300

gggaccaagg tggagatcaa a 321

<210> 5882
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5882
Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser His Ser Val Ser Arg Asn
20 25 30

Ser Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Ile Tyr Tyr Cys Gln Gln Tyr Asn Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 5883
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5883

Arg Ala Ser His Ser Val Ser Arg Asn Ser Ala
1 5 10

<210> 5884
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5884
agggccagtc acagtgttag cagaaactca gcc 33

<210> 5885
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5885
Gly Ala Ser Thr Arg Ala Thr
1 5

<210> 5886
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5886
ggtgcatcca ccagggccac t 21

<210> 5887
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5887
Gln Gln Tyr Asn Asn Trp Pro Leu Thr
1 5

<210> 5888
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5888
caacagtata ataattggcc gctcact 27

<210> 5889
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5889
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctggatt caccttcaga agctatgcca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcaatg gtatactatg atggaaataa tcaatactat 180

gcagactccg tgaggggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgacgac acggcggtgt acttctgcgc tagaggtcct 300

ggctataact ggttggaccc ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> 5890
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5890

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Met Val Tyr Tyr Asp Gly Asn Asn Gln Tyr Tyr Ala Asp Ser Val
50 55 60

Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 5891
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5891
Phe Thr Phe Arg Ser Tyr Ala Met His
1 5

<210> 5892
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5892
ttcaccttca gaagctatgc catgcac 27

<210> 5893
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5893
Met Val Tyr Tyr Asp Gly Asn Asn Gln Tyr Tyr Ala Asp Ser Val Arg
1 5 10 15

Gly

<210> 5894
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5894
atggtatact atgatggaaa taatcaatac tatgcagact ccgtgagggg c 51

<210> 5895
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5895
Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro
1 5 10

<210> 5896
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5896
gctagaggtc ctggctataa ctggttggac ccc 33

<210> 5897
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5897
gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agaaacttag cctggtacca gcagaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc 180

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctgcagtct 240

gaagattttg cagtttatta ctgtcaacag tacaacaatt ggcctctcac tttcggcgga 300

gggaccaagg tggtgatcaa a 321

<210> 5898
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5898
Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Arg Asn
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Val Ile Lys
100 105

<210> 5899
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5899
Arg Ala Ser Gln Ser Val Ser Arg Asn Leu Ala
1 5 10

<210> 5900
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5900
agggccagtc agagtgttag cagaaactta gcc 33

<210> 5901
<211> 7
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5901
Gly Ala Ser Thr Arg Ala Thr
1 5

<210> 5902
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5902
ggtgcatcca ccagggccac t 21

<210> 5903
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5903
Gln Gln Tyr Asn Asn Trp Pro Leu Thr
1 5

<210> 5904
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5904
caacagtaca acaattggcc tctcact 27

<210> 5905

<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5905
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

gcctgtgtag cgtctggatt caccttcaga agctatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctgcagtg ggtggcaatg atatactatg atggaaagaa taaatactat 180

gcagactccg tgaggggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acaacctgag agtcgaggac acggcgatgt acttctgcgc cagaggtcca 300

ggctataact ggttggaccc ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> 5906
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5906
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Gln Trp Val
35 40 45

Ala Met Ile Tyr Tyr Asp Gly Lys Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Asn Leu Arg Val Glu Asp Thr Ala Met Tyr Phe Cys
85 90 95

Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 5907
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5907
Phe Thr Phe Arg Ser Tyr Gly Met His
1 5

<210> 5908
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5908
ttcaccttca gaagctatgg catgcac 27

<210> 5909
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5909
Met Ile Tyr Tyr Asp Gly Lys Asn Lys Tyr Tyr Ala Asp Ser Val Arg
1 5 10 15

Gly

<210> 5910
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5910
atgatatact atgatggaaa gaataaatac tatgcagact ccgtgagggg c 51

<210> 5911
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5911
Ala Arg Gly Pro Gly Tyr Asn Trp Leu Asp Pro
1 5 10

<210> 5912
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5912
gccagaggtc caggctataa ctggttggac ccc 33

<210> 5913
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region nucleic acid sequence

<400> 5913
gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagaattagc agcaacttag cctggtacca gcagaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tagcccagcc 180

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctgcagtct 240

gaagatgttg cagtttatta ctgtcagcag catcataact ggcctctcac tttcggcgga 300

gggaccaagg tggagatcaa a 321

<210> 5914
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5914
Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Ile Ser Ser Asn
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ser Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln His His Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 5915
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5915
Arg Ala Ser Gln Arg Ile Ser Ser Asn Leu Ala
1 5 10

<210> 5916
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5916
agggccagtc agagaattag cagcaactta gcc 33

<210> 5917
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5917
Gly Ala Ser Thr Arg Ala Thr
1 5

<210> 5918
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5918
ggtgcatcca ccagggccac t 21

<210> 5919
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5919
Gln Gln His His Asn Trp Pro Leu Thr
1 5

<210> 5920
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5920
cagcagcatc ataactggcc tctcact 27

<210> 5921
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5921
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttaac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttatgtatcc tggtttgctt attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 5922
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5922
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 5923
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5923
Phe Thr Phe Asn Thr Tyr Ala Met Asn
1 5

<210> 5924
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5924
ttcaccttta acacatatgc catgaat 27

<210> 5925
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5925
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 5926
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5926
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 5927
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5927
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr
1 5 10 15

<210> 5928
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5928
gtcaggcacg gtaacttcgg gaacagttat gtatcctggt ttgcttat 48

<210> 5929
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5929
cagactgtgg tgacccagga gccatcgttc tcagtgtccc ctggagggac agtcacactc 60

acttgtagat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccacg cggactcatc ggcggcacaa acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaatctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 5930
<211> 109

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5930
Gln Thr Val Val Thr Gln Glu Pro Ser Phe Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ser Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 5931
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5931
Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 5932
<211> 42

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5932
agatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 5933
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5933
Gly Thr Asn Lys Arg Ala Pro
1 5

<210> 5934
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5934
ggcacaaaca agcgcgctcc t 21

<210> 5935
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5935
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 5936
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5936
gcgctgtggt acagtaacct ttgggtg 27

<210> 5937
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5937
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgctagat attactttga tgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5938
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5938
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5939
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5939
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 5940
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5940
ttcaacatca aggactacta tatgcac 27

<210> 5941
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5941
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 5942
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5942
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 5943
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5943
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Val
1 5 10

<210> 5944
<211> 36
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5944
gcgagagatg gatacgctag atattacttt gatgtg 36

<210> 5945
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5945
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5946
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5946
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5947
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5947
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5948
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5948
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 5949
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5949
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5950
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5950
tgggcatcta cccgggaatc c 21

<210> 5951
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5951
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 5952
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5952
aagcaatctt attctcggag aact 24

<210> 5953
<211> 357
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5953
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgctagat attactatga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5954
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5954
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Tyr Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5955
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5955
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 5956
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5956
ttcaacatca aggactacta tatgcac 27

<210> 5957
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5957
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 5958
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5958
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 5959
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5959
Ala Arg Asp Gly Tyr Ala Arg Tyr Tyr Tyr Asp Tyr
1 5 10

<210> 5960
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5960
gcgagagatg gatacgctag atattactat gactac 36

<210> 5961
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5961
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5962
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5962
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5963
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5963
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5964
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5964
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 5965
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5965
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5966
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region CDR L2 nucleic acid sequence

<400> 5966
tgggcatcta cccgggaatc c 21

<210> 5967
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5967
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 5968
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5968
aagcaatctt attctcggag aact 24

<210> 5969
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5969
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcag tagagatgga 300

tacgctagat attactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5970
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5970
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ser Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 5971
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 5971
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 5972
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5972
ttcaacatca aggactacta tatgcac 27

<210> 5973
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5973
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 5974
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5974
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 5975
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5975
Ser Arg Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 5976
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5976
agtagagatg gatacgctag atattacttt gactac 36

<210> 5977
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5977
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5978
<211> 112

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5978
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5979
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5979
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5980
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5980
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 5981
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5981
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5982
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5982
tgggcatcta cccgggaatc c 21

<210> 5983
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5983

Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 5984
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 5984
aagcaatctt attctcggag aact 24

<210> 5985
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 5985
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcaa tagagatgga 300

tacgctagat attactatga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 5986
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 5986
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
            20   25   30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35   40   45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
    50   55   60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65   70   75   80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Asn Arg Asp Gly Tyr Ala Arg Tyr Tyr Tyr Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Leu Val Thr Val Ser Ser
        115

<210> 5987
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 5987
Phe Asn Ile Lys Asp Tyr Tyr Met His
1   5

<210> 5988
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 5988
ttcaacatca aggactacta tatgcac 27

<210> 5989
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 5989
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 5990
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 5990
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 5991
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 5991
Asn Arg Asp Gly Tyr Ala Arg Tyr Tyr Tyr Asp Tyr
1 5 10

<210> 5992
<211> 36

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 5992
aatagagatg gatacgctag atattactat gactac 36

<210> 5993
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 5993
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 5994
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 5994
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5995
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 5995
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 5996
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 5996
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 5997

<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 5997
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 5998
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 5998
tgggcatcta cccgggaatc c 21

<210> 5999
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 5999
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 6000
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 6000
aagcaatctt attctcggag aact 24

<210> 6001
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 6001
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgga 300

tacgctagat attttttga caattggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 6002
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 6002
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Ala Arg Tyr Phe Phe Asp Asn Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 6003
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 6003
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 6004
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 6004
ttcaacatca aggactacta tatgcac 27

<210> 6005
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 6005
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln

1 5 10 15

Gly

<210> 6006
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 6006
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 6007
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 6007
Ala Arg Asp Gly Tyr Ala Arg Tyr Phe Phe Asp Asn
1 5 10

<210> 6008
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 6008
gcgagagatg gatacgctag atatttttt gacaat 36

<210> 6009
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 6009
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 6010
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 6010
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 6011
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 6011
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 6012
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 6012
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 6013
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 6013
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 6014
<211> 21
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 6014
tgggcatcta cccgggaatc c 21

<210> 6015
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 6015
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 6016
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 6016
aagcaatctt attctcggag aact 24

<210> 6017
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 6017
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatggg 300

tacgggagat attactttga ccgttggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 6018
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 6018
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Gly Arg Tyr Tyr Phe Asp Arg Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 6019
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 6019
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 6020
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 6020
ttcaacatca aggactacta tatgcac 27

<210> 6021
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 6021
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 6022
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 6022
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 6023
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 6023
Ala Arg Asp Gly Tyr Gly Arg Tyr Tyr Phe Asp Arg
1 5 10

<210> 6024
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 6024
gcgagagatg ggtacgggag atattacttt gaccgt 36

<210> 6025
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 6025
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcccccc aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 6026
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 6026
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 6027
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 6027
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 6028
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 6028
aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 6029
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 6029
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 6030
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 6030
tgggcatcta cccgggaatc c 21

<210> 6031
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 6031
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 6032
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 6032
aagcaatctt attctcggag aact 24

<210> 6033
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 6033
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatggtaa cacaatctat 180

gacccgaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgg gtcggatgga 300

tacgctagat attactttga ctactggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 6034
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 6034
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
            20   25   30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35   40   45

Gly Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe
    50   55   60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65   70   75   80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Gly Ser Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Leu Val Thr Val Ser Ser
        115

<210> 6035
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 6035
Phe Asn Ile Lys Asp Tyr Tyr Met His
1   5

<210> 6036
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 6036
ttcaacatca aggactacta tatgcac 27

<210> 6037
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 6037
Trp Ile Asp Leu Glu Asn Gly Asn Thr Ile Tyr Asp Pro Lys Phe Gln
1 5 10 15

Gly

<210> 6038
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 6038
tggatcgacc ttgaaaatgg taacacaatc tatgacccga agtttcaggg c 51

<210> 6039
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 6039
Gly Ser Asp Gly Tyr Ala Arg Tyr Tyr Phe Asp Tyr
1 5 10

<210> 6040
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 6040
gggtcggatg gatacgctag atattacttt gactac 36

<210> 6041
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 6041
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacagcagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 6042
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 6042
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

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Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
            20                  25                  30


Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45


Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60


Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80


Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
                85                  90                  95


Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


<210> 6043
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 6043
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Gly Lys Asn Tyr Leu
1               5                   10                  15


Ala



<210> 6044
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 6044
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aagtccagcc agagtctttt aaacagcaga accggaaaga actacttagc t 51

<210> 6045
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 6045
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 6046
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 6046
tgggcatcta cccgggaatc c 21

<210> 6047
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 6047
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 6048
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 6048
aagcaatctt attctcggag aact 24

<210> 6049
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 6049
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgg tagagatgcg 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 6050
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 6050
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Gly Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 6051
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 6051
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 6052
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 6052
ttcaacatca aggactacta tatgcac 27

<210> 6053
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region CDR H2 amino acid sequence

<400> 6053
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 6054
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 6054
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 6055
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 6055
Gly Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 6056
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 6056
ggtagagatg cgtacgggag atatttttac gacgtg 36

<210> 6057

<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 6057
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 6058
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 6058
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 6059
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 6059
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 6060
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 6060
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 6061
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 6061
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 6062
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 6062
tgggcatcta cccgggaatc c 21

<210> 6063
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 6063
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 6064
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 6064
aagcaatctt attctcggag aact 24

<210> 6065
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 6065
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgtg 300

ttggggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 6066
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 6066
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Val Leu Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 6067
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 6067
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 6068
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 6068
ttcaacatca aggactacta tatgcac 27

<210> 6069
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 6069
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 6070
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 6070
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 6071
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 6071
Ala Arg Asp Val Leu Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 6072
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 6072
gcgagagatg tgttggggag atatttttac gacgtg 36

<210> 6073
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 6073
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 6074
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 6074
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 6075
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 6075
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 6076
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 6076
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 6077
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 6077
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 6078
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 6078
tgggcatcta cccgggaatc c 21

<210> 6079
<211> 8

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 6079
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 6080
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 6080
aagcaatctt attctcggag aact 24

<210> 6081
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 6081
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatcag 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 6082
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 6082
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gln Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 6083
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 6083
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 6084
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 6084
ttcaacatca aggactacta tatgcac 27

<210> 6085
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 6085
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 6086
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 6086
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 6087
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 6087
Ala Arg Asp Gln Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 6088
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 6088
gcgagagatc agtacgggag atatttttac gacgtg 36

<210> 6089
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 6089
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 6090
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 6090

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Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                  10                  15


Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
            20                  25                  30


Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45


Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60


Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80


Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
                85                  90                  95


Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


<210> 6091
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 6091
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1               5                  10                  15


Ala



<210> 6092
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
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<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 6092
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 6093
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 6093
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 6094
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 6094
tgggcatcta cccgggaatc c 21

<210> 6095
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 6095
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 6096
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 6096
aagcaatctt attctcggag aact 24

<210> 6097
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 6097
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgtg 300

tacgggagat atttttacga cctttggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 6098
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 6098
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
    50   55   60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65   70   75   80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Asp Val Tyr Gly Arg Tyr Phe Tyr Asp Leu Trp Gly Gln Gly
            100   105   110

Thr Leu Val Thr Val Ser Ser
        115

<210> 6099
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 6099
Phe Asn Ile Lys Asp Tyr Tyr Met His
1   5

<210> 6100
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 6100
ttcaacatca aggactacta tatgcac   27

<210> 6101
<211> 17
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 6101
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 6102
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 6102
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 6103
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 6103
Ala Arg Asp Val Tyr Gly Arg Tyr Phe Tyr Asp Leu
1 5 10

<210> 6104
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 6104

gcgagagatg tgtacgggag atatttttac gacctt 36

<210> 6105
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 6105
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 6106
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 6106
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 6107
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 6107
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 6108
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 6108
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 6109
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 6109
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 6110
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 6110
tgggcatcta cccgggaatc c 21

<210> 6111
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 6111
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 6112
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 6112
aagcaatctt attctcggag aact 24

<210> 6113
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region nucleic acid sequence

<400> 6113
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgcg 300

tacgggggggt atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 6114
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 6114
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Ala Tyr Gly Gly Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
        115

<210> 6115
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 6115
Phe Asn Ile Lys Asp Tyr Tyr Met His
1   5

<210> 6116
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 6116
ttcaacatca aggactacta tatgcac   27

<210> 6117
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H2 amino acid sequence

<400> 6117
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1   5   10   15

Gly

<210> 6118

<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 6118
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 6119
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 6119
Ala Arg Asp Ala Tyr Gly Gly Tyr Phe Tyr Asp Val
1 5 10

<210> 6120
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 6120
gcgagagatg cgtacggggg gtatttttac gacgtg 36

<210> 6121
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 6121
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 6122
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 6122
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 6123
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 6123
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 6124
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 6124
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 6125
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 6125
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 6126
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 6126
tgggcatcta cccgggaatc c 21

<210> 6127
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 6127
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 6128
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 6128
aagcaatctt attctcggag aact 24

<210> 6129
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 6129
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagataat 300

tacgggggt atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 6130
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 6130

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Asn Tyr Gly Gly Tyr Phe Tyr Asp Val Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115
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<210> 6131
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 6131

Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 6132
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 6132
ttcaacatca aggactacta tatgcac 27

<210> 6133
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 6133
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 6134
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 6134
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 6135
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 6135
Ala Arg Asp Asn Tyr Gly Gly Tyr Phe Tyr Asp Val
1 5 10

<210> 6136
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 6136
gcgagagata attacggggg gtatttttac gacgtg 36

<210> 6137
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 6137
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 6138
<211> 112
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 6138
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 6139
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 6139
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 6140
<211> 51

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 6140
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 6141
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 6141
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 6142
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 6142
tgggcatcta cccgggaatc c 21

<210> 6143
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 6143
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 6144
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 6144
aagcaatctt attctcggag aact 24

<210> 6145
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 6145
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttaac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttatgtatcc tggtttgctt attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 6146
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 6146
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr
            20                  25                  30


Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
    50                  55                  60


Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65                  70                  75                  80


Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85                  90                  95


Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
            100                 105                 110


Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125


<210> 6147
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 6147
Phe Thr Phe Asn Thr Tyr Ala Met Asn
1               5


<210> 6148
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 6148
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ttcaccttta acacatatgc catgaat 27

<210> 6149
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 6149
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 6150
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 6150
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 6151
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 6151
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr
1 5 10 15

<210> 6152
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 6152
gtcaggcacg gtaacttcgg gaacagttat gtatcctggt ttgcttat 48

<210> 6153
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 6153
cagactgtgg tgacccagga gccatcgctc tcggtgtccc ctggagggac agtcacactc 60

acttgtagat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcccggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaatctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 6154
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 6154
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ser Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 6155
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 6155
Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 6156
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 6156
agatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 6157
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region CDR L2 amino acid sequence

<400> 6157
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 6158
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 6158
ggcacagaca agcgcgctcc c 21

<210> 6159
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 6159
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 6160
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 6160
gcgctgtggt acagtaacct ttgggtg 27

<210> 6161
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 6161
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttaac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttatgtatcc tggtttgctt attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 6162
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 6162
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 6163
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 6163
Phe Thr Phe Asn Thr Tyr Ala Met Asn
1 5

<210> 6164
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 6164
ttcaccttta acacatatgc catgaat 27

<210> 6165
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 6165
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 6166
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 6166
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 6167
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 6167
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr
1 5 10 15

<210> 6168
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 6168
gtcaggcacg gtaacttcgg gaacagttat gtatcctggt ttgcttat 48

<210> 6169
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 6169
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtagat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacaa acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaagctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 6170
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 6170
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 6171
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 6171
Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 6172
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 6172
agatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 6173
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 6173
Gly Thr Asn Lys Arg Ala Pro
1 5

<210> 6174
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 6174
ggcacaaaca agcgcgctcc t 21

<210> 6175
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 6175
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 6176
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 6176
gcgctgtggt acagtaacct ttgggtg 27

<210> 6177
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 6177
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaacag ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 6178
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 6178
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 6179
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 6179
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 6180
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 6180
ttcacctttg acacatatgc catgaat 27

<210> 6181
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 6181
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 6182
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 6182
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 6183
<211> 16

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 6183
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 6184
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 6184
gtcaggcacg gtaacttcgg gaacagttac gtatcctggt ttgctcat 48

<210> 6185
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 6185
cagactgtgg tgacccagga gccatcgttc tcagtgtccc ctggagggac agtcacactc 60

acttgtagat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacaa acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagatg atgaatctga ttattactgt gcgctgtggt acagtaacct ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 6186
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 6186
Gln Thr Val Val Thr Gln Glu Pro Ser Phe Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Asp Asp Glu Ser Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 6187
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 6187
Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 6188
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 6188
agatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 6189
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 6189
Gly Thr Asn Lys Arg Ala Pro
1 5

<210> 6190
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 6190
ggcacaaaca agcgcgctcc t 21

<210> 6191
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 6191
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 6192
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 6192
gcgctgtggt acagtaacct ttgggtg 27

<210> 6193
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 6193
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgcg 300

tacgggagat atttttacag ggtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 6194
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 6194
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Arg Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 6195
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 6195
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 6196
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 6196
ttcaacatca aggactacta tatgcac 27

<210> 6197

<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 6197
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 6198
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 6198
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 6199
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 6199
Ala Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Arg Val
1 5 10

<210> 6200
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 6200
gcgagagatg cgtacgggag atatttttac agggtg 36

<210> 6201
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 6201
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 6202
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 6202
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 6203
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 6203
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 6204
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 6204
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 6205
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region CDR L2 amino acid sequence

<400> 6205
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 6206
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 6206
tgggcatcta cccgggaatc c 21

<210> 6207
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 6207
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 6208
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 6208
aagcaatctt attctcggag aact 24

<210> 6209
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 6209
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgccc gagagatgct 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 6210
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 6210
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Pro Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 6211
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 6211
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 6212
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 6212
ttcaacatca aggactacta tatgcac 27

<210> 6213
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 6213
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 6214
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 6214
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 6215
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 6215
Pro Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 6216
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 6216
ccgagagatg cttacgggag atatttttac gacgtg 36

<210> 6217
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 6217
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 6218
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 6218
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 6219
<211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 6219
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 6220
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 6220
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 6221
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 6221
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 6222
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 6222
tgggcatcta cccgggaatc c 21

<210> 6223
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 6223
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 6224
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 6224
aagcaatctt attctcggag aact 24

<210> 6225
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 6225
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgcg 300

tacgggagat atttttacga cgggtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 6226
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 6226
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Gly Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 6227
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 6227
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 6228
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 6228
ttcaacatca aggactacta tatgcac 27

<210> 6229
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 6229
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 6230
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 6230
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 6231
<211> 12

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 6231
Ala Arg Asp Ala Tyr Gly Arg Tyr Phe Tyr Asp Gly
1 5 10

<210> 6232
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 6232
gcgagagatg cgtacgggag atatttttac gacggg 36

<210> 6233
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 6233
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 6234
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 6234
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 6235
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 6235
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 6236
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 6236
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 6237
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 6237
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 6238
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 6238
tgggcatcta cccgggaatc c 21

<210> 6239
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 6239
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 6240
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 6240
aagcaatctt attctcggag aact 24

<210> 6241
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 6241
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatcgt 300

tacggggctt atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 6242
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 6242
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
            20   25   30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35   40   45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
    50   55   60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65   70   75   80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Asp Arg Tyr Gly Ala Tyr Phe Tyr Asp Val Trp Gly Gln Gly
            100   105   110

Thr Leu Val Thr Val Ser Ser
        115

<210> 6243
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 6243
Phe Asn Ile Lys Asp Tyr Tyr Met His
1   5

<210> 6244
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 nucleic acid sequence

<400> 6244

ttcaacatca aggactacta tatgcac 27

<210> 6245
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 6245
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 6246
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 6246
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 6247
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 6247
Ala Arg Asp Arg Tyr Gly Ala Tyr Phe Tyr Asp Val
1 5 10

<210> 6248
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 6248
gcgagagatc gttacggggc ttatttttac gacgtg 36

<210> 6249
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 6249
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 6250
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 6250
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
                85   90   95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 6251
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 6251
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1   5   10   15

Ala

<210> 6252
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 6252
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t   51

<210> 6253
<211> 7
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 6253
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 6254
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 6254
tgggcatcta cccgggaatc c 21

<210> 6255
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 6255
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 6256
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 6256
aagcaatctt attctcggag aact 24

<210> 6257

<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 6257
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatcgg 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 6258
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 6258
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 6259
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 6259
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 6260
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 6260
ttcaacatca aggactacta tatgcac 27

<210> 6261
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 6261
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 6262
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 6262
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 6263
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 6263
Ala Arg Asp Arg Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 6264
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 6264
gcgagagatc ggtacgggag atatttttac gacgtg 36

<210> 6265
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Light chain variable region nucleic acid sequence

<400> 6265
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 6266
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 6266
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 6267
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 6267
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 6268
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 6268
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 6269
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 6269
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 6270
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 6270
tgggcatcta cccgggaatc c 21

<210> 6271
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 6271
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 6272
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 6272
aagcaatctt attctcggag aact 24

<210> 6273
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 6273
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagattcg 300

tacgggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 6274
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 6274
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Ser Tyr Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 6275
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 6275
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 6276
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 6276
ttcaacatca aggactacta tatgcac 27

<210> 6277
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 6277
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 6278
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 6278
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 6279
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 6279
Ala Arg Asp Ser Tyr Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 6280
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 6280
gcgagagatt cgtacgggag atatttttac gacgtg 36

<210> 6281
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 6281
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 6282
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 6282
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 6283
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 6283
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 6284
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 6284
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 6285
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 6285
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 6286
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 6286
tgggcatcta cccgggaatc c 21

<210> 6287
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 6287
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 6288
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 6288
aagcaatctt attctcggag aact 24

<210> 6289
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 6289
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgtg 300

tacgggagat atctttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 6290
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 6290

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Val Tyr Gly Arg Tyr Leu Tyr Asp Val Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210> 6291
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 6291
Phe Asn Ile Lys Asp Tyr Tyr Met His
1               5


<210> 6292
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
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<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 6292
ttcaacatca aggactacta tatgcac 27

<210> 6293
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 6293
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 6294
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 6294
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 6295
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 6295
Ala Arg Asp Val Tyr Gly Arg Tyr Leu Tyr Asp Val
1 5 10

<210> 6296
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 6296
gcgagagatg tgtacgggag atatctttac gacgtg 36

<210> 6297
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 6297
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 6298
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 6298
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
                85   90   95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 6299
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 6299
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1   5   10   15

Ala

<210> 6300
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 6300
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t   51

<210> 6301
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 6301
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 6302
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 6302
tgggcatcta cccgggaatc c 21

<210> 6303
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 6303
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 6304
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 6304

aagcaatctt attctcggag aact 24

<210> 6305
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 6305
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgc gagagatgtg 300

tacaggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 6306
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 6306
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Val Tyr Arg Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 6307
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 6307
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 6308
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 6308
ttcaacatca aggactacta tatgcac 27

<210> 6309
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 6309
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 6310
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 6310
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 6311
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 6311
Ala Arg Asp Val Tyr Arg Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 6312
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 6312
gcgagagatg tgtacaggag atatttttac gacgtg 36

<210> 6313
<211> 336
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 6313
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta acgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 6314
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 6314
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 6315
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 6315
Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 6316
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 6316
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 6317
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 6317
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 6318

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 6318
tgggcatcta cccgggaatc c 21

<210> 6319
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 6319
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 6320
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 6320
aagcaatctt attctcggag aact 24

<210> 6321
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 6321
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggatt caacatcaag gactactata tgcactgggt gcgacaggct 120

cctggacaaa ggcttgagtg gatgggatgg atcgaccttg aaaatgctaa cacaatctat 180

gacgctaagt ttcagggcag ggtcaccata accagggaca cgtccgccag cacagcctac 240

atggagctga gcagcctgag atctgaagac acggcggtgt actactgcgt gagagatctt 300

cgggggagat atttttacga cgtgtggggc caaggaaccc tggtcaccgt ctcctca 357

<210> 6322
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 6322
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Val Arg Asp Leu Arg Gly Arg Tyr Phe Tyr Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 6323
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 6323
Phe Asn Ile Lys Asp Tyr Tyr Met His
1 5

<210> 6324
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 6324
ttcaacatca aggactacta tatgcac 27

<210> 6325
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 6325
Trp Ile Asp Leu Glu Asn Ala Asn Thr Ile Tyr Asp Ala Lys Phe Gln
1 5 10 15

Gly

<210> 6326
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region CDR H2 nucleic acid sequence

<400> 6326
tggatcgacc ttgaaaatgc taacacaatc tatgacgcta agtttcaggg c 51

<210> 6327
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 6327
Val Arg Asp Leu Arg Gly Arg Tyr Phe Tyr Asp Val
1 5 10

<210> 6328
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 6328
gtgagagatc ttcgggggag atatttttac gacgtg 36

<210> 6329
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 6329
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtctttta aacgctagaa ccggaaagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagactt cactctcact 240

atcagtagcc tgcaggctga agatgtggca gtttattact gtaagcaatc ttattctcgg 300

agaactttcg gcggagggac caaggtcgag atcaaa 336

<210> 6330
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 6330
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Asn Ala
20 25 30

Arg Thr Gly Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Ser Arg Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 6331
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 6331

Lys Ser Ser Gln Ser Leu Leu Asn Ala Arg Thr Gly Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 6332
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 6332
aagtccagcc agagtctttt aaacgctaga accggaaaga actacttagc t 51

<210> 6333
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 6333
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 6334
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 6334
tgggcatcta cccgggaatc c 21

<210> 6335
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 6335
Lys Gln Ser Tyr Ser Arg Arg Thr
1 5

<210> 6336
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 6336
aagcaatctt attctcggag aact 24

<210> 6337
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 6337
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcaag 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggggtgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 6338
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 6338
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Lys
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Gly Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 6339
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 6339
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 6340
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 6340
ttcacctttg acacatatgc catgaat 27

<210> 6341
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 6341
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 6342
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 6342
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 6343
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 6343
Val Arg His Gly Asn Phe Gly Gly Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 6344
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 6344
gtcaggcacg gtaacttcgg gggtggttac gtatcctggt ttgctcat 48

<210> 6345
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 6345
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 6346
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 6346

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Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1               5                   10                  15


Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
            20                  25                  30


Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
        35                  40                  45


Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65                  70                  75                  80


Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
                85                  90                  95


His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105


<210> 6347
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 6347
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1               5                   10


<210> 6348
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 6348
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ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 6349
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 6349
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 6350
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 6350
ggcacagaca agcgcgctcc t 21

<210> 6351
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 6351
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 6352
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 6352
gcgctgtggt acagtaacca ttgggtg 27

<210> 6353
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 6353
gaggtgcagc tgttggggtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcgggaactc gtacgtttcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 6354
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 6354
Glu Val Gln Leu Leu Gly Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 6355
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 6355
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 6356
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 6356
ttcacctttg acacatatgc catgaat 27

<210> 6357
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 6357
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 6358
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 6358
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 6359
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 6359
Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 6360
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 6360
gtcaggcacg gtaacttcgg gaactcgtac gtttcctggt ttgctcat 48

<210> 6361
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 6361
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 6362
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 6362
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 6363
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 6363
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 6364
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 6364
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 6365
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 6365
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 6366

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 6366
ggcacagaca agcgcgctcc t 21

<210> 6367
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 6367
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 6368
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 6368
gcgctgtggt acagtaacca ttgggtg 27

<210> 6369
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 6369
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcggtggggg ttacgtagcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 6370
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 6370
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Gly Gly Tyr Val Ala Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 6371
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 6371
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 6372
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 6372
ttcacctttg acacatatgc catgaat 27

<210> 6373
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 6373
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 6374
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 6374
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 6375
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 6375
Val Arg His Gly Asn Phe Gly Gly Gly Tyr Val Ala Trp Phe Ala His
1 5 10 15

<210> 6376
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 6376
gtcaggcacg gtaacttcgg tgggggttac gtagcctggt ttgctcat 48

<210> 6377
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 6377
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 6378
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 6378
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 6379
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 6379
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 6380
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 6380
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 6381
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 6381
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 6382
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 6382
ggcacagaca agcgcgctcc t 21

<210> 6383
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 6383
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 6384
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 6384
gcgctgtggt acagtaacca ttgggtg 27

<210> 6385
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 6385
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtttaacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tccagggtgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 6386
<211> 125
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 6386
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Phe Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gln Gly Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 6387
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 6387
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 6388
<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 6388
ttcacctttg acacatatgc catgaat 27

<210> 6389
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 6389
Arg Ile Arg Ser Lys Phe Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 6390
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 6390
aggattagat ccaagtttaa caattacgct acatactacg cagactccgt gaaggat 57

<210> 6391
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 6391

Val Arg His Gly Asn Phe Gln Gly Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 6392
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 6392
gtcaggcacg gtaacttcca gggtggttac gtatcctggt ttgctcat 48

<210> 6393
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 6393
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 6394
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 6394
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
            20   25   30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
        35   40   45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
    50   55   60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65   70   75   80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
                85   90   95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100   105

<210> 6395
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 6395
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1   5   10

<210> 6396
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 6396
ggatcaagca ctggcgcagt cactactagt aactacgcca ac   42

<210> 6397
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 6397
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 6398
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 6398
ggcacagaca agcgcgctcc t 21

<210> 6399
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 6399
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 6400
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 6400

gcgctgtggt acagtaacca ttgggtg 27

<210> 6401
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 6401
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaacg tgggggGTGG ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 6402
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 6402
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Val Gly Gly Gly Tyr Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 6403
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 6403
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 6404
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 6404
ttcacctttg acacatatgc catgaat 27

<210> 6405
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region CDR H2 amino acid sequence

<400> 6405
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 6406
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 6406
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 6407
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 6407
Val Arg His Gly Asn Val Gly Gly Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 6408
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 6408
gtcaggcacg gtaacgtggg gggtggttac gtatcctggt ttgctcat 48

<210> 6409

<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 6409
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 6410
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 6410
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 6411
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 6411
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 6412
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 6412
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 6413
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 6413
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 6414
<211> 21
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 6414
ggcacagaca agcgcgctcc t 21

<210> 6415
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 6415
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 6416
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 6416
gcgctgtggt acagtaacca ttgggtg 27

<210> 6417
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 6417
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacgataact tcggggctgg ttacgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 6418
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 6418

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5				10					15		

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Asp	Thr	Tyr
		20					25					30			

Ala	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
	35					40					45				

Ala	Arg	Ile	Arg	Ser	Lys	Tyr	Asn	Asn	Tyr	Ala	Thr	Tyr	Tyr	Ala	Asp
	50					55					60				

Ser	Val	Lys	Asp	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	Ser	Thr
65					70				75					80	

Leu	Tyr	Leu	Gln	Met	Glu	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr
				85					90					95	

Tyr	Cys	Val	Arg	His	Asp	Asn	Phe	Gly	Ala	Gly	Tyr	Val	Ser	Trp	Phe
		100					105					110			

Ala	His	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser			
	115					120					125				

<210> 6419
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 6419
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 6420
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 6420
ttcacctttg acacatatgc catgaat 27

<210> 6421
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 6421
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 6422
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Heavy chain variable region CDR H2 nucleic acid sequence

<400> 6422
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 6423
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 6423
Val Arg His Asp Asn Phe Gly Ala Gly Tyr Val Ser Trp Phe Ala His
1 5 10 15

<210> 6424
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 6424
gtcaggcacg ataacttcgg ggctggttac gtatcctggt ttgctcat 48

<210> 6425
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 6425
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 6426
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 6426
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 6427
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 6427

Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 6428
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 6428
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 6429
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 6429
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 6430
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 6430
ggcacagaca agcgcgctcc t 21

<210> 6431
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 6431
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 6432
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 6432
gcgctgtggt acagtaacca ttgggtg 27

<210> 6433
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 6433
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtaact tcggggttgg ttacgtatcc tggtttgctt cttggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 6434
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 6434
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
            20   25   30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
    50   55   60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65   70   75   80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
                85   90   95

Tyr Cys Val Arg His Gly Asn Phe Gly Val Gly Tyr Val Ser Trp Phe
            100   105   110

Ala Ser Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120   125

<210> 6435
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Heavy chain variable region CDR H1 amino acid sequence

<400> 6435
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1   5

<210> 6436
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 6436
ttcacctttg acacatatgc catgaat 27

<210> 6437
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 6437
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 6438
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 6438
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 6439
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 6439
Val Arg His Gly Asn Phe Gly Val Gly Tyr Val Ser Trp Phe Ala Ser
1 5 10 15

<210> 6440
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 6440
gtcaggcacg gtaacttcgg ggttggttac gtatcctggt ttgcttct 48

<210> 6441
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 6441
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 6442
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 6442
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

```
Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
            20                  25                  30


Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
        35                  40                  45


Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
    50                  55                  60


Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65                  70                  75                  80


Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
                85                  90                  95


His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105


<210> 6443
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 amino acid sequence

<400> 6443
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1               5                   10


<210> 6444
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      Light chain variable region CDR L1 nucleic acid sequence

<400> 6444
ggatcaagca ctggcgcagt cactactagt aactacgcca ac                          42


<210> 6445
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<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 6445
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 6446
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 6446
ggcacagaca agcgcgctcc t 21

<210> 6447
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 6447
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 6448
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 6448
gcgctgtggt acagtaacca ttgggtg 27

<210> 6449
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 6449
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggGTC cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggttggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

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gtcaccgtct cctca 375

<210> 6450
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 6450
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Tyr Ala Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 6451
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 6451
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 6452
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 6452
ttcacctttg acacatatgc catgaat 27

<210> 6453
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 6453
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 6454
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 6454
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 6455
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 6455
Val Arg His Gly Asn Phe Gly Asn Tyr Ala Val Ser Trp Phe Ala His
1 5 10 15

<210> 6456
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 6456
gtcaggcacg gtaacttcgg gaactatgct gtatcctggt ttgctcat 48

<210> 6457
<211> 327
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 6457
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 6458
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 6458
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 6459
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 6459
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 6460
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 6460
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 6461
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 6461
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 6462
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 6462
ggcacagaca agcgcgctcc t 21

<210> 6463
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 6463
Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 6464
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 6464
gcgctgtggt acagtaacca ttgggtg 27

<210> 6465
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region nucleic acid sequence

<400> 6465
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttgac acatatgcca tgaattgggt tcgccaggct 120

ccagggaagg ggctggagtg ggtcgcaagg attagatcca agtataacaa ttacgctaca 180

tactacgcag actccgtgaa ggatcggttc accatctcca gagacgattc caagagcacg 240

ctgtatctgc aaatggaaag cctgagagcc gaggacacgg cggtgtacta ctgcgtcagg 300

cacggtagct tcgggaacca tattgtatcc tggtttgctc attggggcca aggaaccctg 360

gtcaccgtct cctca 375

<210> 6466
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region amino acid sequence

<400> 6466
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Thr
65 70 75 80

Leu Tyr Leu Gln Met Glu Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Ser Phe Gly Asn His Ile Val Ser Trp Phe
100 105 110

Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 6467
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 amino acid sequence

<400> 6467
Phe Thr Phe Asp Thr Tyr Ala Met Asn
1 5

<210> 6468
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H1 nucleic acid sequence

<400> 6468
ttcacctttg acacatatgc catgaat 27

<210> 6469
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 amino acid sequence

<400> 6469
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

<210> 6470
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H2 nucleic acid sequence

<400> 6470
aggattagat ccaagtataa caattacgct acatactacg cagactccgt gaaggat 57

<210> 6471
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 amino acid sequence

<400> 6471
Val Arg His Gly Ser Phe Gly Asn His Ile Val Ser Trp Phe Ala His
1 5 10 15

<210> 6472
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Heavy chain variable region CDR H3 nucleic acid sequence

<400> 6472
gtcaggcacg gtagcttcgg gaaccatatt gtatcctggt ttgctcat 48

<210> 6473
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region nucleic acid sequence

<400> 6473
cagactgtgg tgacccagga gccatcgctc tcagtgtccc ctggagggac agtcacactc 60

acttgtggat caagcactgg cgcagtcact actagtaact acgccaactg ggtccagcag 120

accccaggcc aggctccgcg cggactcatc ggcggcacag acaagcgcgc tcctggggtc 180

cctgatcgct tctctggctc cctgcttggg gacaaagctg ccctcaccat cacgggggcc 240

caggcagagg atgaagctga ttattactgt gcgctgtggt acagtaacca ttgggtgttc 300

ggcggaggga ccaagctgac cgtccta 327

<210> 6474
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region amino acid sequence

<400> 6474
Gln Thr Val Val Thr Gln Glu Pro Ser Leu Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Thr Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asp Lys Arg Ala Pro Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 6475
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 amino acid sequence

<400> 6475
Gly Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 6476
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L1 nucleic acid sequence

<400> 6476
ggatcaagca ctggcgcagt cactactagt aactacgcca ac 42

<210> 6477
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 amino acid sequence

<400> 6477
Gly Thr Asp Lys Arg Ala Pro
1 5

<210> 6478
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L2 nucleic acid sequence

<400> 6478
ggcacagaca agcgcgctcc t 21

<210> 6479
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 amino acid sequence

<400> 6479

Ala Leu Trp Tyr Ser Asn His Trp Val
1 5

<210> 6480
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Light chain variable region CDR L3 nucleic acid sequence

<400> 6480
gcgctgtggt acagtaacca ttgggtg 27