

ANTIBODIES AGAINST INTEGRIN ALPHA 11 BETA 1

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] The present application claims priority to U.S. Provisional Application No. 62/951,723, filed December 20, 2019; U.S. Provisional Application No. 62/983,155, filed February 28, 2020; and U.S. Provisional Application No. 63/054,717, filed July 21, 2020, each of which is incorporated herein in its entirety.

BACKGROUND

[0002] Fibrosis is a process of scarring that manifests itself in many tissues in the body, typically as a result of inflammation or tissue damage. Increased production of extracellular matrix results in organ failure and, often, death. Diseases associated with fibrosis account for approximately 45% of all deaths in industrialized nations (Wynn, T. A., 2008, *J Pathol.* 214:199-210). One such disease is Systemic Sclerosis (SSc). SSc is a complex autoimmune disease with a chronic progressive course and high interpatient variability. It is characterized by inflammation, vascular dysfunction and fibrosis. Fibrosis of the skin and visceral organs results in irreversible scarring and ultimately organ failure, accounting for high mortality. There is currently no approved targeted therapy with disease-modifying potential.

SUMMARY

[0003] The present disclosure provides novel, function-blocking antibodies against type I collagen receptor integrin alpha 11 beta 1 ($\alpha 11\beta 1$). The present disclosure also provides use of such antibodies to treat fibrotic disorders and/or cancers.

[0004] In one aspect, the present disclosure provides an anti- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, comprising an amino acid sequence selected from a group consisting of SEQ ID NO: 103-435. In another aspect, the present disclosure provides an anti- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, comprising a CDR sequence encompassed within any one of SEQ ID NO: 103-207, 209, 211, 213, 216, 218, 220, 223, 225, 228, 233, 234, 236, 240, 241, 245, 247, 253, 255, 257, 259, 261, 265, 267, 269, 271, 275, 277, 279, 281, 283, 287,

289, 291, 293, 296, 300, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 325, 327, 329, 334, 336, 338, 340, 342, 344, 348, 351, 353, 355, 358, 360, 361, 364, 366, 368, 369, 374, 376, 377, 379, 380, 381, 383, 384, 385, 387, 389, 392, 393, 396, 398, 400, 402, 405, 408, 411, or 413-435. In another aspect, the present disclosure provides an anti- $\alpha 1 \beta 1$ antibody, or antigen-binding fragment thereof, comprising CDR1, CDR2, and CDR3 encompassed within any one of SEQ ID NO: 103-206, or 413-435. In some embodiments, an anti- $\alpha 1 \beta 1$ antibody, or antigen-binding fragment thereof, comprises an amino acid sequence selected from a group consisting of SEQ ID NO: 103-114, 207-311, and 312-435. In some embodiments, an anti- $\alpha 1 \beta 1$ antibody, or antigen-binding fragment thereof, comprises a CDR sequence encompassed within any one of SEQ ID NO: 103-114, 207, 209, 211, 213, 216, 218, 220, 223, 225, 228, 233, 234, 236, 240, 241, 245, 247, 253, 255, 257, 259, 261, 265, 267, 269, 271, 275, 277, 279, 281, 283, 287, 289, 291, 293, 296, 300, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 325, 327, 329, 334, 336, 338, 340, 342, 344, 348, 351, 353, 355, 358, 360, 361, 364, 366, 368, 369, 374, 376, 377, 379, 380, 381, 383, 384, 385, 387, 389, 392, 393, 396, 398, 400, 402, 405, 408, 411, or 413-435. In some embodiments, an anti- $\alpha 1 \beta 1$ antibody, or antigen-binding fragment thereof, comprises one or more CDR sequences encompassed within any one of SEQ ID NO: 103-114, or 413-434. In some embodiments, an anti- $\alpha 1 \beta 1$ antibody, or antigen-binding fragment thereof, comprises CDR1, CDR2, and CDR3 encompassed within any one of SEQ ID NO: 103-114 or 413-434.

[0005] In some embodiments, an anti- $\alpha 1 \beta 1$ antibody, or antigen-binding fragment thereof, is a monoclonal antibody, or antigen-binding fragment thereof. In some embodiments, an anti- $\alpha 1 \beta 1$ antibody, or antigen-binding fragment thereof, is a humanized antibody, or antigen-binding fragment thereof. In some embodiments, an anti- $\alpha 1 \beta 1$ antibody, or antigen-binding fragment thereof, reduces interaction of $\alpha 1 \beta 1$ with collagen in human $\alpha 1 \beta 1$ -expressing cells. In some embodiments, an anti- $\alpha 1 \beta 1$ antibody, or antigen-binding fragment thereof, competes with an antibody, or antigen-binding fragment thereof, described herein.

[0006] In another aspect, the present disclosure provides a nucleic acid, comprising a nucleic acid sequence encoding an antibody, or antigen-binding fragment thereof, described herein. In some embodiments, a nucleic acid sequence comprises a sequence selected from a group consisting of SEQ ID NO: 1-102.

[0007] In another aspect, the present disclosure provides a vector comprising a nucleic acid described herein.

[0008] In another aspect, the present disclosure provides a host cell comprising a nucleic acid described herein or a vector described herein.

[0009] In another aspect, the present disclosure provides a method of producing an antibody, or antigen-binding fragment thereof, comprising culturing a host cell described herein under conditions suitable for expression of the antibody or antigen-binding fragment thereof.

[0010] In another aspect, the present disclosure provides a method of treating a subject having or at risk of a fibrotic disorder, the method comprising administering to a subject in need thereof a therapeutically effective amount of an antibody, or antigen-binding fragment thereof, described herein. In some embodiments, a fibrotic disorder is idiopathic pulmonary fibrosis (IPF), chronic kidney disease, diabetic cardiomyopathy, primary sclerosing cholangitis (PSC), primary biliary cirrhosis (PBC), non-alcoholic fatty liver disease (NAFLD/NASH), Crohn's disease, ulcerative colitis, or systemic sclerosis.

[0011] In another aspect, the present disclosure provides a method of treating a subject having or at risk of cancer, the method comprising administering to a subject in need thereof a therapeutically effective amount of an antibody, or antigen-binding fragment thereof, described herein. In some embodiments, the cancer is one or more of head and neck squamous cell carcinomas, pancreatic ductal adenocarcinoma, non-small cell lung cancer, adrenocortical carcinoma, acute myeloid leukemia, bladder urothelial carcinoma, invasive breast carcinoma, cervical squamous cell carcinoma, cholangiocarcinoma, colorectal adenocarcinoma, diffuse large B-cell lymphoma, esophageal adenocarcinoma, glioblastoma multiforme, liver hepatocellular carcinoma, lung adenocarcinoma, lung squamous cell carcinoma, skin cutaneous melanoma, mesothelioma, ovarian serous cystadenocarcinoma, pheochromocytoma and paraganglioma, prostate adenocarcinoma, sarcoma, stomach adenocarcinoma, testicular germ cell tumors, thymoma, thyroid carcinoma, uterine corpus endometrial carcinoma, uterine carcinosarcoma, uveal melanoma, kidney renal clear cell carcinoma, kidney chromophobe, and kidney renal papillary cell carcinoma.

BRIEF DESCRIPTION OF THE DRAWING

[0012] The present teachings described herein will be more fully understood from the following description of various illustrative embodiments, when read together with the accompanying drawings. It should be understood that the drawings described below are for illustration purposes only and are not intended to limit the scope of the present teachings in any way.

[0013] **Figure 1** shows representations of an integrin structure. The panels illustrate the structure of collagen-binding integrins and three different conformations integrins can exist in on the surface of a cell.

[0014] **Figure 2A** shows a chart illustrating an ELISA analysis of binding of exemplary mouse monoclonal antibodies to human $\alpha 1 \beta 1$.

[0015] **Figure 2B** shows a chart illustrating an exemplary ELISA analysis of binding of mouse monoclonal antibodies to mouse $\alpha 1 \beta 1$.

[0016] **Figure 3A** shows a graph illustrating an ELISA analysis of binding of exemplary rat monoclonal antibodies to a human $\alpha 1 \beta 1$ I domain.

[0017] **Figure 3B** shows a graph illustrating an ELISA analysis of binding of exemplary mouse monoclonal antibodies to a human $\alpha 1 \beta 1$ I domain.

[0018] **Figure 4A** shows a graph illustrating an FACS analysis of binding of exemplary rat monoclonal antibodies to CHO-K1 cells expressing human $\alpha 1 \beta 1$.

[0019] **Figure 4B** shows a graph illustrating an FACS analysis of binding of exemplary mouse monoclonal antibodies to CHO-K1 cells expressing human $\alpha 1 \beta$.

[0020] **Figure 5** shows graphs illustrating a FACS analysis of binding of exemplary mouse monoclonal antibodies to human pulmonary fibroblasts (HPFs) and myofibroblasts (MF).

[0021] **Figure 6A** shows graphs illustrating the ability of exemplary rat monoclonal antibodies to inhibit adhesion of CHO-K1 cells expressing human $\alpha 1$ to rat tail type I collagen.

[0022] **Figure 6B** shows graphs illustrating the ability of exemplary rabbit monoclonal antibodies to inhibit adhesion of CHO-K1 cells expressing human $\alpha 1$ to rat tail type I collagen.

[0023] **Figure 6C** shows graphs illustrating the ability of exemplary mouse monoclonal antibodies to inhibit adhesion of CHO-K1 cells expressing human $\alpha 1$ to rat tail type I collagen.

[0024] **Figure 7A** shows a graph illustrating the ability of exemplary rat monoclonal antibodies to inhibit Fibroblast-to-Myofibroblasts Transition (FMT) as measured by percent inhibition of α SMA upregulation.

[0025] **Figure 7B** shows a graph illustrating the ability of exemplary rabbit monoclonal antibodies to inhibit Fibroblast-to-Myofibroblasts Transition (FMT) as measured by percent inhibition of α SMA upregulation.

[0026] **Figure 7C** shows a graph illustrating the ability of exemplary mouse monoclonal antibodies to inhibit Fibroblast-to-Myofibroblasts Transition (FMT) as measured by percent inhibition of α SMA upregulation.

[0027] **Figure 8** shows graphs illustrating the ability of exemplary monoclonal antibodies to inhibit CHO-K1 human α 11-mediated rat tail type I collagen gel contraction.

[0028] **Figure 9** shows graphs illustrating the affinity of exemplary monoclonal antibodies for human α 11 β 1 via surface plasmon resonance (SPR).

[0029] **Figure 10A** and **Figure 10B** show graphs illustrating the affinity of exemplary monoclonal antibodies for human α 11 β 1 via surface plasmon resonance (SPR).

[0030] **Figure 11A** and **Figure 11B** show graphs illustrating the binding ability of selected rabbit, rat, mouse and human monoclonal antibodies to α 11 β 1 expressed on the surface of CHO cells.

[0031] **Figure 12** shows graphs illustrating a FACS analysis of binding of exemplary monoclonal antibodies to human pulmonary fibroblasts (HPFs) and myofibroblasts (MF).

[0032] **Figure 13** shows a graph and table illustrating a FACS analysis of binding of exemplary monoclonal antibodies to human myofibroblasts (MF).

[0033] **Figure 14** shows a graph illustrating the binding ability of selected monoclonal antibodies to α 11 β 1 expressed on the surface of CHO cells.

[0034] **Figure 15A** and **Figure 15B** show graphs illustrating the ability of exemplary monoclonal antibodies to inhibit adhesion of CHO cells expressing human α 11 to rat tail type I collagen.

[0035] **Figure 16** shows a graph illustrating the effect of exemplary monoclonal antibodies on xenograft growth in SCID mice.

[0036] **Figure 17A**, **Figure 17B** and **Figure 17 C** illustrate the effect of exemplary monoclonal antibodies on soluble pro-fibrogenic markers from Precision-Cut Liver Slices (PCLS).

DETAILED DESCRIPTION

[0037] The present disclosure is based, in part, on the discovery of novel antibodies that selectively bind to $\alpha 11\beta 1$. The disclosure also relates to nucleic acids encoding said antibodies and methods of use in the treatment of fibrosis and diseases comprising a fibrotic component.

Fibrosis and Diseases

[0038] Fibrosis is a process of scarring that manifests itself in many tissues in the body, typically as a result of inflammation or tissue damage. Increased production of extracellular matrix results in organ failure and, often, death. Diseases associated with fibrosis account for approximately 45% of all deaths in industrialized nations (Wynn, T. A., 2008, *J Pathol.* 214:199-210). One such disease is Systemic Sclerosis (SSc). SSc is a complex autoimmune disease with a chronic progressive course and high interpatient variability. It is characterized by inflammation, vascular dysfunction and fibrosis. Fibrosis of the skin and visceral organs results in irreversible scarring and ultimately organ failure, accounting for high mortality. There is currently no approved targeted therapy with disease-modifying potential.

[0039] The cells responsible for producing extracellular matrix (ECM) for tissue repair (and in fibrosis) are a specialized type of fibroblasts called myofibroblasts (MF). Although mechanisms of fibrosis have been extensively studied, this complex process is far from well understood. In order to focus on the most important drivers of fibrosis, published patient-derived datasets (SSc patient data and normal controls) were interrogated using an *in-house* derived novel data analysis methodology. This analysis lead to the identification of the type I collagen-binding integrin alpha 11 beta 1 ($\alpha 11\beta 1$) as one of the top targets for modulating fibrosis.

[0040] To this date, there are no truly disease-modifying therapeutics for fibrosis. Two of the approved therapies for idiopathic pulmonary fibrosis (IPF), nintedanib and pirfenidone, work poorly and do not modify the disease, and there is no approved therapy for systemic sclerosis (SSc) to date. In some embodiments, a fibrotic disorder is or comprises idiopathic pulmonary fibrosis (IPF), chronic kidney disease, diabetic cardiomyopathy, primary sclerosing cholangitis (PSC), primary biliary cirrhosis (PBC), non-alcoholic fatty liver disease (NAFLD/NASH), Crohn's disease, ulcerative colitis, or systemic sclerosis (SSc). In some embodiments, a fibrotic disorder is or comprises atrial fibrosis, endomyocardial fibrosis, arthrofibrosis, mediastinal fibrosis, myelofibrosis, progressive massive fibrosis, retroperitoneal fibrosis or skeletal muscle fibrosis.

[0041] One clinical feature of the tumor microenvironment is the interaction between tumor and stroma, which mainly relies on various integrins that interact with ECM components as well as growth factors. Such interaction can influence tumor survival, progression and eventually metastasis. $\alpha 1 \beta 1$ has been reported to be overexpressed in cancer-associated fibroblasts (CAFs) of metastatic tumors, and its expression has been correlated with aggressive tumors in patients. For example, integrin $\alpha 11$ was overexpressed in the stroma of most head and neck squamous cell carcinomas (HNSCC) and correlated positively with alpha smooth muscle actin expression (Parajuli et al., J. Oral Pathol. Med. 46:267-275 (2017)). Integrin $\alpha 11$ was also overexpressed by CAFs in Pancreatic Ductal Adenocarcinoma (PDAC) stroma (Schnittert et al., FASEB J. 33:6609-6621 (2019)). In addition, integrin $\alpha 1 \beta 1$ overexpression in the tumor stroma has been associated with tumor growth and metastatic potential of non-small cell lung cancer (NSCLC), and high expression of ITGA11 (gene encoding integrin alpha-11 in humans) was associated with lower recurrence-free survival in all NSCLC patients; the same study showed that $\alpha 11$ overexpression in lung cancer cell lines resulted in increased migration and invasion (Ando et al., Cancer Sci. 111:200-208 (2020)).

Integrins

[0042] Integrins are a large family of type I transmembrane heterodimeric glycoprotein receptors and act as major receptors for cell adhesion. The integrin family of receptors plays key roles in modulating signal transduction pathways that control cell adhesion, migration, proliferation, differentiation and apoptosis. There are 18 α and 8 β subunits, which combine to

form 24 integrin heterodimers. Each integrin receptor comprises two non-covalently bound subunits, α and β . Integrins $\alpha 1\beta 1$, $\alpha 2\beta 1$, $\alpha 10\beta 1$, and $\alpha 11\beta 1$ are the primary collagen receptors. α and β subunits are transmembrane proteins with large, modular, extracellular domains, single transmembrane helices, and short cytoplasmic regions, which mediate cytoskeletal interactions. Extracellular domain of integrins are generally large, approximately 80-150 kDa structures. The extracellular domains can be seen as comprising a headpiece connected to two legs (see Figure 1 for structure of collagen-binding integrins). Collagen binding integrins contain an I domain, which serves as the ligand-binding site. The αI -domain contains a conserved “metal-ion-dependent adhesion site” (MIDAS) that binds divalent metal cations (Mg^{2+}) and plays important role in ligand binding.

[0043] Integrins can exist in three different conformations: 1) a resting, low affinity state (bent conformation, **Figure 1**, panel A) where the head piece containing ligand binding site is turned towards the membrane; 2) an extended, intermediate affinity state, where the integrin is extended but the head piece remains ‘closed’ (**Figure 1**, panel B) and 3) an extended, high affinity state where the integrin is fully activated and readily binds the ligand. The complexity of the different integrin states allows for both allosteric and ligand-blocking ways of inhibiting integrin function. As marked with a star in **Figure 1**, one of the allosteric ways to block the function of an integrin is to generate a monoclonal antibody that prevents the integrin from reaching the fully extended conformation from the extended intermediate conformation. Another allosteric option is to bind an integrin in its bent/inactive conformation and to keep it from extending to either of the two other states. A non-allosteric way of inhibiting integrin function is to bind to the I domain to prevent the integrin from attaching to collagen. Binding to the ligand binding site directly runs the risk of generating a recombinant activator of integrin function.

[0044] As cell surface receptors, integrins sense the stiffness of the surrounding matrix, triggering the cells to further produce and remodel connective tissue, which can perpetuate a fibrotic phenotype. Many integrins are overexpressed in fibrosis, but it is not clear which alpha subunit is sufficient for fibrosis to occur. $\alpha 11\beta 1$ integrin is specifically expressed on a subset of fibroblasts and myofibroblasts (i.e., terminal scar producing cells). Recent literature has provided strong evidence that $\alpha 11\beta 1$ is one of the main drivers of a fibrotic phenotype in cardiac tissue, liver, lungs and kidney (Romaine, A. et. al. Overexpression of integrin alpha 11 induces cardiac fibrosis in mice. *Acta Physiol* Feb 2018, 222(2); Bansal, R. et.al. Integrin alpha 11 in the

regulation of the myofibroblast phenotype: implications for fibrotic diseases. *Exp Mol Med*. 2017 Nov 17:49(11)). Blocking $\alpha 11\beta 1$ function may inhibit myofibroblast differentiation and extracellular matrix deposition (i.e., the major event in scar formation) and blocking $\alpha 11\beta 1$ function may provide a mechanism for local, injury-specific attenuation of fibrosis which could fundamentally change fibrotic microenvironment and modify disease progression in all diseases that have a fibrotic component.

[0045] In some embodiments, an anti- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, of the present disclosure reduces interaction of $\alpha 11\beta 1$ with collagen in human $\alpha 11\beta 1$ -expressing cells. In some embodiments, reducing interaction of $\alpha 11\beta 1$ with collagen in human $\alpha 11\beta 1$ -expressing cells comprises an anti- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, interacting with $\alpha 11\beta 1$ that is in a resting, low affinity state (bent conformation). In some embodiments, reducing interaction of $\alpha 11\beta 1$ with collagen in human $\alpha 11\beta 1$ -expressing cells comprises an anti- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, interacting with $\alpha 11\beta 1$ that is in an extended, intermediate affinity state. In some embodiments, reducing interaction of $\alpha 11\beta 1$ with collagen in human $\alpha 11\beta 1$ -expressing cells comprises an anti- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, interacting with $\alpha 11\beta 1$ that is in an extended, high affinity state.

Antibodies

[0046] The term “antibody” is used herein 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/or antibody fragments (preferably those fragments that exhibit the desired antigen-binding activity). An antibody described herein can be an immunoglobulin, heavy chain antibody, light chain antibody, LRR-based antibody, or other protein scaffold with antibody-like properties, as well as other immunological binding moiety known in the art, including, e.g., a Fab, Fab', Fab'2, Fab2, Fab3, F(ab')₂, Fd, Fv, Feb, scFv, SMIP, antibody, diabody, triabody, tetrabody, minibody, maxibody, tandab, DVD, BiTe, TandAb, or the like, or any combination thereof. The subunit structures and three-dimensional configurations of different classes of antibodies are known in the art.

[0047] A “monoclonal antibody” or “mAb” 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.

[0048] An “antigen-binding fragment” refers to a portion of an intact antibody that binds the antigen to which the intact antibody binds. An antigen-binding fragment of an antibody includes any naturally occurring, enzymatically obtainable, synthetic, or genetically engineered polypeptide or glycoprotein that specifically binds an antigen to form a complex. Exemplary antibody fragments include, but are not limited to, Fv, Fab, Fab', Fab'-SH, F(ab')₂; diabodies; linear antibodies; single-chain antibody molecules (e.g. scFv or VHH or VH or VL domains only); and multispecific antibodies formed from antibody fragments. In some embodiments, the antigen-binding fragments of the antibodies described herein are scFvs. As with full antibody molecules, antigen-binding fragments may be mono-specific or multispecific (e.g., bispecific). A multispecific antigen-binding fragment of an antibody may 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 of the same antigen.

[0049] A “multispecific antibody” refers to an antibody comprising at least two different antigen binding domains that recognize and specifically bind to at least two different antigens. A “bispecific antibody” is a type of multispecific antibody and refers to an antibody comprising two different antigen binding domains that recognize and specifically bind to at least two different antigens.

[0050] A “different antigen” 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.

[0051] 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 of an antigen and may have different biological effects. The term “epitope” also refers to a site of 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.

[0052] As used herein, “selective binding”, “selectively binds” “specific binding”, or “specifically binds” refers, with respect to an antigen binding moiety and an antigen target, preferential association of an antigen binding moiety to an antigen target and not to an entity that is not the antigen target. A certain degree of non-specific binding may occur between an antigen binding moiety and a non-target. In some embodiments, an antigen binding moiety selectively binds an antigen target if binding between the antigen binding moiety and the antigen target is greater than 2-fold, greater than 5-fold, greater than 10-fold, or greater than 100-fold as compared with binding of the antigen binding moiety and a non-target. In some embodiments, an antigen binding moiety selectively binds an antigen target if the binding affinity is less than about 10^{-5} M, less than about 10^{-6} M, less than about 10^{-7} M, less than about 10^{-8} M, or less than about 10^{-9} M.

[0053] In some embodiments, antibodies or fragments thereof that selectively bind to an identical epitope or overlapping epitope that will often cross-compete for binding to an antigen. Thus, in some embodiments, the disclosure provides an antibody or fragment thereof that cross-competes with an exemplary antibody or fragment thereof as disclosed herein. In some embodiments, to “cross-compete”, “compete”, “cross-competition”, or “competition” means antibodies or fragments thereof compete for the same epitope or binding site on a target. Such competition can be determined by an assay in which the reference antibody or fragment thereof prevents or inhibits specific binding of a test antibody or fragment thereof, and vice versa. Numerous types of competitive binding assays can be used to determine if a test molecule competes with a reference molecule for binding. Examples of assays that can be employed

include solid phase direct or indirect radioimmunoassay (RIA), solid phase direct or indirect enzyme immunoassay (EIA), sandwich competition assay (see, e.g., Stahli et al. (1983) *Methods in Enzymology* 9:242-253), solid phase direct biotin-avidin EIA (see, e.g., Kirkland et al., (1986) *J. Immunol.* 137:3614-9), solid phase direct labeled assay, solid phase direct labeled sandwich assay, Luminex (Jia et al. "A novel method of Multiplexed Competitive Antibody Binning for the characterization of monoclonal antibodies" *J. Immunological Methods* (2004) 288, 91-98) and surface plasmon resonance (Song et al. "Epitope Mapping of Ibalizumab, a Humanized Anti-CD4 Monoclonal Antibody with Anti-HIV-1 Activity in Infected Patients" *J. Virol.* (2010) 84, 6935-42). Usually, when a competing antibody or fragment thereof is present in excess, it will inhibit binding of a reference antibody or fragment thereof to a common antigen by at least 50%, 55%, 60%, 65%, 70%, or 75%. In some instances, binding is inhibited by at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or more.

[0054] An antibody can be an immunoglobulin molecule of four polypeptide chains, e.g., two heavy (H) chains and two light (L) chains. In some embodiments, a light chain is a lambda light chain. In some embodiments, a light chain is a kappa light chain. A heavy chain can include a heavy chain variable domain and a heavy chain constant domain. A heavy chain constant domain can include CH1, hinge, CH2, CH3, and in some instances CH4 regions. A light chain can include a light chain variable domain and a light chain constant domain. A light chain constant domain can include a CL.

[0055] A heavy chain variable domain of a heavy chain and a light chain variable domain of a light chain can typically be further subdivided into regions of variability, termed complementarity determining regions (CDRs), interspersed with regions that are more conserved, termed framework regions (FR). Such heavy chain and light chain variable domains can each include three CDRs and four framework regions, arranged from amino-terminus to carboxyl-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4, one or more of which can be engineered as described herein. The CDRs in a heavy chain are designated "CDRH1", "CDRH2", and "CDRH3", respectively, and the CDRs in a light chain are designated "CDRL1", "CDRL2", and "CDRL3".

[0056] 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, IgG2, IgG3, IgG4,

IgA1, and IgA2. The heavy chain constant domains that correspond to the different classes of immunoglobulins are called α , δ , ϵ , γ , and μ , respectively.

Exemplary Antibodies

[0057] The present disclosure provides antibodies that can include various heavy chains and light chains described herein. In some embodiments, an antibody comprises two heavy chains and light chains. In some embodiments, the present disclosure encompasses an antibody including at least one heavy chain and/or light chain as disclosed herein, at least one heavy chain and/or light chain framework domain as disclosed herein, at least one heavy chain and/or light chain CDR domain as disclosed herein, and/or any heavy chain and/or light chain constant domain as disclosed herein.

[0058] In some embodiments, an antibody disclosed herein is a homodimeric monoclonal antibody. In some embodiments, an antibody disclosed herein is a heterodimeric antibody. In some embodiments, an antibody is, e.g., a typical antibody or a diabody, triabody, tetrabody, minibody, maxibody, tandab, DVD, BiTe, scFv, TandAb scFv, Fab, Fab2, Fab3, F(ab')₂, or the like, or any combination thereof.

[0059] The present disclosure provides, among other things, an anti-integrin $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof. In some embodiments, an $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, comprises an amino acid sequence selected from a group consisting of SEQ ID NO: 103-435. In some embodiments, an anti- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, comprises a CDR sequence encompassed within any one of SEQ ID NO: 103-207, 209, 211, 213, 216, 218, 220, 223, 225, 228, 233, 234, 236, 240, 241, 245, 247, 253, 255, 257, 259, 261, 265, 267, 269, 271, 275, 277, 279, 281, 283, 287, 289, 291, 293, 296, 300, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 325, 327, 329, 334, 336, 338, 340, 342, 344, 348, 351, 353, 355, 358, 360, 361, 364, 366, 368, 369, 374, 376, 377, 379, 380, 381, 383, 384, 385, 387, 389, 392, 393, 396, 398, 400, 402, 405, 408, 411, or 413-435. In some embodiments, an anti- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, comprises CDR1, CDR2, and CDR3 encompassed within any one of SEQ ID NO: 103-206, or 413-435. In some embodiments, an anti- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, comprises an amino acid sequence selected from a group consisting of SEQ ID NO: 103-114, 207-311, and 312-435. In some embodiments, an anti- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, comprises a

CDR sequence encompassed within any one of SEQ ID NO: 103-114, 207, 209, 211, 213, 216, 218, 220, 223, 225, 228, 233, 234, 236, 240, 241, 245, 247, 253, 255, 257, 259, 261, 265, 267, 269, 271, 275, 277, 279, 281, 283, 287, 289, 291, 293, 296, 300, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 325, 327, 329, 334, 336, 338, 340, 342, 344, 348, 351, 353, 355, 358, 360, 361, 364, 366, 368, 369, 374, 376, 377, 379, 380, 381, 383, 384, 385, 387, 389, 392, 393, 396, 398, 400, 402, 405, 408, 411, or 413-435. In some embodiments, an anti- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, comprises one or more CDR sequences encompassed within any one of SEQ ID NO: 103-114, or 413-434. In some embodiments, an anti- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, comprises CDR1, CDR2, and CDR3 encompassed within any one of SEQ ID NO: 103-114, or 413-434. In some embodiments, an anti- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, is a monoclonal antibody, or antigen-binding fragment thereof. In some embodiments, an anti- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, is a humanized antibody, or antigen-binding fragment thereof. In some embodiments, an anti- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, reduces interaction of $\alpha 11\beta 1$ with collagen in human $\alpha 11\beta 1$ -expressing cells. In some embodiments, the present disclosure provides an anti- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, that competes with an antibody, or antigen-binding fragment thereof, comprising an amino acid sequence selected from a group consisting of SEQ ID NO: 103-435. In some embodiments, the present disclosure provides an anti- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, that competes with an antibody, or antigen-binding fragment thereof, comprising an amino acid sequence selected from a group consisting of SEQ ID NO: 103-435.

[0060] In some embodiments, the present disclosure provides an anti- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, comprising a heavy chain provided herein and a light chain provided herein. In some embodiments, the present disclosure provides an anti- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, comprising a heavy chain variable domain provided herein and a light chain variable region provided herein. In some embodiments, the present disclosure provides an anti- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, comprising a specific combination of heavy chain variable domain and light chain variable domain. For example, in some embodiments, an anti- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, comprises a combination of heavy chain variable domain and light chain variable domain selected from

Table 1.

Table 1. Combinations of 16E10 variant heavy chain variable regions and light chain variable regions

Light Chain Variable Region	Heavy Chain Variable Region	Description
16E10_VL (SEQ ID NO: 428)	16E10_VH (SEQ ID NO: 421)	Parental light chain variable region; Parental heavy chain variable region
16E10_VL_1 (SEQ ID NO: 429)	16E10_VH_1 (SEQ ID NO: 422)	Conservatively humanized light chain variable region; Conservatively humanized heavy chain variable region
16E10_VL_2 (SEQ ID NO: 430)	16E10_VH_2 (SEQ ID NO: 423)	Humanized light chain variable region; humanized heavy chain variable region
16E10_VL_3 (SEQ ID NO: 431)	16E10_VH_1 (SEQ ID NO: 422)	Deimmunized conservatively humanized light chain variable region; Conservatively humanized heavy chain variable region
16E10_VL_4 (SEQ ID NO: 432)	16E10_VH_2 (SEQ ID NO: 423)	Deimmunized humanized light chain variable region; Humanized heavy chain variable region
16E10_VL_1 (SEQ ID NO: 429)	16E10_VH_3 (SEQ ID NO: 424)	Conservatively humanized light chain variable region; Deimmunized conservatively humanized heavy chain variable region
16E10_VL_2 (SEQ ID NO: 430)	16E10_VH_4 (SEQ ID NO: 425)	Humanized light chain variable region; Deimmunized humanized heavy chain variable region
16E10_VL_3 (SEQ ID NO: 431)	16E10_VH_3 (SEQ ID NO: 424)	Deimmunized conservatively humanized light chain variable region; Deimmunized conservatively humanized heavy chain variable region
16E10_VL_4 (SEQ ID NO: 432)	16E10_VH_4 (SEQ ID NO: 425)	Deimmunized humanized light chain variable region; Deimmunized humanized heavy chain variable region
16E10_VL_5 (SEQ ID NO: 433)	16E10_VH_3 (SEQ ID NO: 424)	De-risked deimmunized conservatively humanized light chain variable region; Deimmunized conservatively humanized heavy chain variable region
16E10_VL_6 (SEQ ID NO: 434)	16E10_VH_4 (SEQ ID NO: 425)	De-risked deimmunized humanized light chain variable region; Deimmunised humanised heavy chain variable region
16E10_VL_3 (SEQ ID NO: 431)	16E10_VH_5 (SEQ ID NO: 426)	Deimmunised conservatively humanised light chain variable region; De-risked deimmunised conservatively humanised heavy chain variable region
16E10_VL_4 (SEQ ID NO: 432)	16E10_VH_6 (SEQ ID NO: 427)	Deimmunised humanised light chain variable region; De-risked deimmunised humanised heavy chain variable region
16E10_VL_5 (SEQ ID NO: 433)	16E10_VH_5 (SEQ ID NO: 426)	De-risked deimmunised conservatively humanised light chain variable region; De-risked deimmunised

		conservatively humanised heavy chain variable region
16E10_VL_6 (SEQ ID NO: 434)	16E10_VH_6 (SEQ ID NO: 427)	De-risked deimmunised humanised light chain variable region; De-risked deimmunised humanised heavy chain variable region

[0061] In some embodiments, the present disclosure provides an anti- α 11 β 1 antibody, or antigen-binding fragment thereof, comprising between 1 and 30 (e.g., 1, 2, 3, 4, 5, 10, or more) additions, deletions, or substitutions relative to an anti- α 11 β 1 antibody, or antigen-binding fragment thereof, wherein the anti- α 11 β 1 antibody comprises an amino acid sequence selected from a group consisting of SEQ ID NO: 103-158, 413, 414 and 421-434 and, e.g., the antibody or fragment selectively binds α 11 β 1. In some embodiments, the present disclosure provides an anti- α 11 β 1 antibody, or antigen-binding fragment thereof, comprising between 1 and 30 additions, deletions, or substitutions relative to an anti- α 11 β 1 antibody, or antigen-binding fragment thereof, wherein the anti- α 11 β 1 antibody comprises an amino acid sequence selected from a group consisting of SEQ ID NO: 103-114, 413, 414 and 421-434 and, e.g., the antibody or fragment selectively binds α 11 β 1. In some embodiments, the present disclosure provides an anti- α 11 β 1 antibody, or antigen-binding fragment thereof, comprising an amino acid sequence having at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence selected from a group consisting of SEQ ID NO: 103-158, 413, 414 and 421-434 and, e.g., the antibody or fragment selectively binds α 11 β 1. In some embodiments, the present disclosure provides an anti- α 11 β 1 antibody, or antigen-binding fragment thereof, comprising an amino acid sequence having at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence selected from a group consisting of SEQ ID NO: 103-114, 413, 414 and 421-434 and, e.g., the antibody or fragment selectively binds α 11 β 1.

[0062] In some embodiments, the present disclosure provides an anti- α 11 β 1 antibody, or antigen-binding fragment thereof, comprising between 1 and 90 (e.g., between 1 and 50, e.g., at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) additions, deletions, or substitutions relative to an anti- α 11 β 1 antibody, or antigen-binding fragment thereof, wherein the anti- α 11 β 1 antibody, or antigen-binding fragment thereof comprises an amino acid sequence selected from a group consisting of SEQ ID NO: 159-206 and 415-420 and, e.g., the antibody or fragment selectively

binds $\alpha 11\beta 1$. In some embodiments, the present disclosure provides an anti- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, comprising an amino acid sequence having at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to an amino acid sequence selected from the group consisting of SEQ ID NO: 159-206 and 415-420 and, e.g., the antibody or fragment selectively binds $\alpha 11\beta 1$.

[0063] In some embodiments, the disclosure provides an antibody or fragment thereof that selectively binds $\alpha 11\beta 1$, wherein the antibody or fragment comprises one or more CDR sequences depicted in the list of exemplary sequences provided herein. For example, in some embodiments, an antibody or fragment thereof comprises one or more CDRs from SEQ ID NOs: 103-114. In some embodiments, the disclosure provides an antibody or fragment thereof that selectively binds $\alpha 11\beta 1$, wherein the antibody or fragment comprises an amino acid sequence that is at least 95%, 96%, 97%, 98%, or 99% identical to one or more CDRs from SEQ ID NOs: 103-114. In some embodiments, an antibody or fragment comprises an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to one of SEQ ID NOs: 103-114, wherein the antibody comprises one or more CDRs depicted in one of SEQ ID NOs: 103-114. For example, the antibody or fragment comprises an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to SEQ ID NO: 103, wherein the antibody comprises one or more CDRs (e.g., 1, 2, or 3 CDRs) depicted in SEQ ID NO: 103.

[0064] In some embodiments, the disclosure provides an antibody or fragment thereof that selectively binds $\alpha 11\beta 1$, wherein the antibody or fragment comprises one or more CDR sequences depicted in the list of exemplary sequences provided herein. For example, in some embodiments, an antibody or fragment thereof comprises one or more CDRs from SEQ ID NOs: 103-207, 209, 211, 213, 216, 218, 220, 223, 225, 228, 233, 234, 236, 240, 241, 245, 247, 253, 255, 257, 259, 261, 265, 267, 269, 271, 275, 277, 279, 281, 283, 287, 289, 291, 293, 296, 300, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 325, 327, 329, 334, 336, 338, 340, 342, 344, 348, 351, 353, 355, 358, 360, 361, 364, 366, 368, 369, 374, 376, 377, 379, 380, 381, 383, 384, 385, 387, 389, 392, 393, 396, 398, 400, 402, 405, 408, 411, or 413-435. In some embodiments, the disclosure provides an antibody or fragment thereof that selectively binds $\alpha 11\beta 1$, wherein the antibody or fragment comprises an amino acid sequence that is at least 95%, 96%, 97%, 98%, or 99% identical to one or more CDRs from SEQ ID NOs: 103-207, 209, 211,

213, 216, 218, 220, 223, 225, 228, 233, 234, 236, 240, 241, 245, 247, 253, 255, 257, 259, 261, 265, 267, 269, 271, 275, 277, 279, 281, 283, 287, 289, 291, 293, 296, 300, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 325, 327, 329, 334, 336, 338, 340, 342, 344, 348, 351, 353, 355, 358, 360, 361, 364, 366, 368, 369, 374, 376, 377, 379, 380, 381, 383, 384, 385, 387, 389, 392, 393, 396, 398, 400, 402, 405, 408, 411, or 413-435. In some embodiments, an antibody or fragment comprises an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to one of SEQ ID NOs: 103-207, 209, 211, 213, 216, 218, 220, 223, 225, 228, 233, 234, 236, 240, 241, 245, 247, 253, 255, 257, 259, 261, 265, 267, 269, 271, 275, 277, 279, 281, 283, 287, 289, 291, 293, 296, 300, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 325, 327, 329, 334, 336, 338, 340, 342, 344, 348, 351, 353, 355, 358, 360, 361, 364, 366, 368, 369, 374, 376, 377, 379, 380, 381, 383, 384, 385, 387, 389, 392, 393, 396, 398, 400, 402, 405, 408, 411, or 413-435, wherein the antibody comprises one or more CDRs depicted in one of SEQ ID NOs: 103-207, 209, 211, 213, 216, 218, 220, 223, 225, 228, 233, 234, 236, 240, 241, 245, 247, 253, 255, 257, 259, 261, 265, 267, 269, 271, 275, 277, 279, 281, 283, 287, 289, 291, 293, 296, 300, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 325, 327, 329, 334, 336, 338, 340, 342, 344, 348, 351, 353, 355, 358, 360, 361, 364, 366, 368, 369, 374, 376, 377, 379, 380, 381, 383, 384, 385, 387, 389, 392, 393, 396, 398, 400, 402, 405, 408, 411, or 413-435. For example, the antibody or fragment comprises an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to SEQ ID NO: 103, wherein the antibody comprises one or more CDRs (e.g., 1, 2, or 3 CDRs) depicted in SEQ ID NO:103.

[0065] The present disclosure provides, among other things, methods of making an anti- α 11 β 1 antibody, or antigen-binding fragment thereof. Methods of making antibodies are known in the art. In some embodiments, the present disclosure provides methods of producing an antibody, or antigen-binding fragment thereof, comprising culturing a host cell comprising a nucleic acid comprising a nucleic acid sequence selected from a group consisting of SEQ ID NO: 1-102 under conditions suitable for expression of the antibody or antigen-binding fragment thereof.

Exemplary Nucleotide Sequences

[0066] The present disclosure includes nucleotide sequences encoding one or more heavy chains, heavy chain variable domains, heavy chain framework regions, heavy chain CDRs, heavy chain constant domains, light chains, light chain variable domains, light chain framework regions, light chain CDRs, light chain constant domains, or other immunoglobulin-like sequences, antibodies, or binding molecules disclosed herein. In some embodiments, such nucleotide sequences may be present in a vector. In some embodiments such nucleotides may be present in the genome of a cell, e.g., a cell of a subject in need of treatment or a cell for production of an antibody, e.g. a mammalian cell for production of a an antibody.

[0067] In some embodiments, the present disclosure provides a nucleic acid comprising a nucleic acid sequence encoding an antibody, or antigen-binding fragment thereof, comprising an amino acid sequence selected from a group consisting of SEQ ID NO: 103-206. In some embodiments, the present disclosure provides a nucleic acid comprising a nucleic acid sequence encoding an antibody, or antigen-binding fragment thereof, comprising an amino acid sequence selected from a group consisting of SEQ ID NO: 103-114. In some embodiments, the present disclosure provides a nucleic acid comprising a nucleic acid sequence selected from a group consisting of SEQ ID NO: 1-102. In some embodiments, the present disclosure provides a vector comprising a nucleic acid comprising a nucleic acid sequence selected from a group consisting of SEQ ID NO: 1-102. In some embodiments, the present disclosure provides a host cell comprising a nucleic acid comprising a nucleic acid sequence selected from a group consisting of SEQ ID NO: 1-102. In some embodiments, the present disclosure provides a vector comprising a nucleic acid comprising a nucleic acid sequence selected from a group consisting of SEQ ID NO: 1-102.

[0068] In some embodiments, the present disclosure provides a nucleic acid comprising a nucleic acid sequence having at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity a nucleic acid sequence selected from a group consisting of SEQ ID NO: 1-102.

Measuring Interactions of Antibodies and $\alpha 11\beta 1$

[0069] The binding properties of an antibody described herein to $\alpha 11\beta 1$ can be measured by methods known in the art, e.g., one of the following methods: BIACORE analysis, Enzyme Linked Immunosorbent Assay (ELISA), x-ray crystallography, sequence analysis and scanning mutagenesis. The binding interaction of an antibody and $\alpha 11\beta 1$ can be analyzed using surface plasmon resonance (SPR). SPR or Biomolecular Interaction Analysis (BIA) detects bio-specific interactions in real time, without labeling any of the interactants. Changes in the mass at the binding surface (indicative of a binding event) of the BIA chip result in alterations of the refractive index of light near the surface. The changes in the refractivity generate a detectable signal, which are measured as an indication of real-time reactions between biological molecules. Methods for using SPR are described, for example, in U.S. Pat. No. 5,641,640; Raether (1988) Surface Plasmons Springer Verlag; Sjolander and Urbaniczky (1991) Anal. Chem. 63:2338-2345; Szabo et al. (1995) Curr. Opin. Struct. Biol. 5:699-705 and on-line resources provide by BIAcore International AB (Uppsala, Sweden). Additionally, a KinExA® (Kinetic Exclusion Assay) assay, available from Sapidyne Instruments (Boise, Id.) can also be used.

[0070] Information from SPR can be used to provide an accurate and quantitative measure of the equilibrium dissociation constant (K_D), and kinetic parameters, including K_{on} and K_{off} , for the binding of an antibody to $\alpha 11\beta 1$. Such data can be used to compare different molecules. Information from SPR can also be used to develop structure-activity relationships (SAR). Variant amino acids at given positions can be identified that correlate with particular binding parameters, e.g., high affinity.

[0071] In certain embodiments, an antibody described herein exhibits high affinity for binding $\alpha 11\beta 1$. In various embodiments, K_D of an antibody as described herein for $\alpha 11\beta 1$ is less than about 10^{-4} , 10^{-5} , 10^{-6} , 10^{-7} , 10^{-8} , 10^{-9} , 10^{-10} , 10^{-11} , 10^{-12} , 10^{-13} , 10^{-14} , or 10^{-15} M. In certain instances, K_D of an antibody as described herein for $\alpha 11\beta 1$ is between 0.001 and 1 nM, e.g., 0.001 nM, 0.005 nM, 0.01 nM, 0.05 nM, 0.1 nM, 0.5 nM, or 1 nM.

Methods of Treatment

[0072] In some embodiments, one or more anti- $\alpha 1 \beta 1$ antibodies described herein are used in a method of treating one or more disorders described herein, e.g., one or more fibrotic disorders and/or one or more cancers. In some embodiments, the method comprises administering to a subject in need thereof a therapeutically effective amount of an antibody, or antigen-binding fragment thereof, described herein. In some embodiments, a fibrotic disorder is or comprises idiopathic pulmonary fibrosis (IPF), chronic kidney disease, diabetic cardiomyopathy, primary sclerosing cholangitis (PSC), primary biliary cirrhosis (PBC), non-alcoholic fatty liver disease (NAFLD/NASH), Crohn's disease, ulcerative colitis, or systemic sclerosis. In some embodiments, a fibrotic disorder is or comprises atrial fibrosis, endomyocardial fibrosis, arthrofibrosis, mediastinal fibrosis, myelofibrosis, progressive massive fibrosis, retroperitoneal fibrosis or skeletal muscle fibrosis.

[0073] In some embodiments, one or more anti- $\alpha 1 \beta 1$ antibodies described herein are used in a method of treating cancer, such as one or more of the following: head and neck squamous cell carcinomas, pancreatic ductal adenocarcinoma, non-small cell lung cancer, adrenocortical carcinoma, acute myeloid leukemia, bladder urothelial carcinoma, invasive breast carcinoma, cervical squamous cell carcinoma, cholangiocarcinoma, colorectal adenocarcinoma, diffuse large B-cell lymphoma, esophageal adenocarcinoma, glioblastoma multiforme, liver hepatocellular carcinoma, lung adenocarcinoma, lung squamous cell carcinoma, skin cutaneous melanoma, mesothelioma, ovarian serous cystadenocarcinoma, pheochromocytoma and paraganglioma, prostate adenocarcinoma, sarcoma, stomach adenocarcinoma, testicular germ cell tumors, thymoma, thyroid carcinoma, uterine corpus endometrial carcinoma, uterine carcinosarcoma, uveal melanoma, kidney renal clear cell carcinoma, kidney chromophobe, and kidney renal papillary cell carcinoma.

Combination Therapy

[0074] In some embodiments, an anti- $\alpha 1 \beta 1$ antibody described herein is administered in combination with one or more additional therapeutic agents, such as a chemotherapeutic agent or an oncolytic therapeutic agent. "Combination therapy", as used herein, refers to those situations in which two or more different pharmaceutical agents are administered in overlapping regimens so that the subject is simultaneously exposed to both agents. When used in combination therapy,

two or more different agents may be administered simultaneously or separately. Administration in combination can include simultaneous administration of the two or more agents in the same dosage form, simultaneous administration in separate dosage forms, and separate administration. That is, two or more agents can be formulated together in the same dosage form and administered simultaneously. Alternatively, two or more agents can be simultaneously administered, wherein the agents are present in separate formulations. In another alternative, a first agent can be administered just followed by one or more additional agents. In the separate administration protocol, two or more agents may be administered a few minutes apart, or a few hours apart, or a few days apart.

[0075] As used herein, the term “chemotherapeutic agent” or “oncolytic therapeutic agent” (e.g., anti-cancer drug, e.g., anti-cancer therapy, e.g., immune cell therapy) has its art-understood meaning referring to one or more pro-apoptotic, cytostatic and/or cytotoxic agents, and/or hormonal agents, for example, specifically including agents utilized and/or recommended for use in treating one or more diseases, disorders or conditions associated with undesirable cell proliferation. In some embodiments, a chemotherapeutic agent and/or oncolytic therapeutic agent may be or comprise platinum compounds (e.g., cisplatin, carboplatin, and oxaliplatin), alkylating agents (e.g., cyclophosphamide, ifosfamide, chlorambucil, nitrogen mustard, thiopeta, melphalan, busulfan, procarbazine, streptozocin, temozolomide, dacarbazine, and bendamustine), antitumor antibiotics (e.g., daunorubicin, doxorubicin, idarubicin, epirubicin, mitoxantrone, bleomycin, mytomycin C, plicamycin, and dactinomycin), taxanes (e.g., paclitaxel and docetaxel), antimetabolites (e.g., 5-fluorouracil, cytarabine, premetrexed, thioguanine, floxuridine, capecitabine, and methotrexate), nucleoside analogues (e.g., fludarabine, clofarabine, cladribine, pentostatin, and nelarabine), topoisomerase inhibitors (e.g., topotecan and irinotecan), hypomethylating agents (e.g., azacitidine and decitabine), proteasome inhibitors (e.g., bortezomib), epipodophyllotoxins (e.g., etoposide and teniposide), DNA synthesis inhibitors (e.g., hydroxyurea), vinca alkaloids (e.g., vincristine, vindesine, vinorelbine, and vinblastine), tyrosine kinase inhibitors (e.g., imatinib, dasatinib, nilotinib, sorafenib, and sunitinib), nitrosoureas (e.g., carmustine, fotemustine, and lomustine), hexamethylmelamine, mitotane, angiogenesis inhibitors (e.g., thalidomide and lenalidomide), steroids (e.g., prednisone, dexamethasone, and prednisolone), hormonal agents (e.g., tamoxifen, raloxifene, leuprolide, bicalutamide, granisetron, and flutamide), aromatase inhibitors (e.g., letrozole and anastrozole),

arsenic trioxide, tretinoin, nonselective cyclooxygenase inhibitors (e.g., nonsteroidal anti-inflammatory agents, salicylates, aspirin, piroxicam, ibuprofen, indomethacin, naprosyn, diclofenac, tolmetin, ketoprofen, nabumetone, and oxaprozin), selective cyclooxygenase-2 (COX-2) inhibitors, or any combination thereof.

[0076] In certain embodiments, chemotherapeutic agents and/or oncolytic therapeutic agents for anti-cancer treatment comprise biological agents such as tumor-infiltrating lymphocytes, CAR T-cells, antibodies, antigens, therapeutic vaccines (e.g., made from a patient's own tumor cells or other substances such as antigens that are produced by certain tumors), immune-modulating agents (e.g., cytokines, e.g., immunomodulatory drugs or biological response modifiers), checkpoint inhibitors or other immunologic agents. In certain embodiments, immunologic agents include immunoglobins, immunostimulants (e.g., bacterial vaccines, colony stimulating factors, interferons, interleukins, therapeutic vaccines, vaccine combinations, viral vaccines) and/or immunosuppressive agents (e.g., calcineurin inhibitors, interleukin inhibitors, TNF alpha inhibitors). In certain embodiments, hormonal agents include agents for anti-androgen therapy (e.g., Ketoconazole, ABiraterone, TAK-700, TOK-001, Bicalutamide, Nilutamide, Flutamide, Enzalutamide, ARN-509).

[0077] Additional chemotherapeutic agents and/or oncolytic therapeutic agents include immune checkpoint therapeutics (e.g., pembrolizumab, nivolumab, ipilimumab, atezolizumab, avelumab, durvalumab, tremelimumab, or cemiplimab), other monoclonal antibodies (e.g., rituximab, cetuximab, panetumumab, tositumomab, trastuzumab, alemtuzumab, gemtuzumab, ozogamicin, bevacizumab, catumaxomab, denosumab, obinutuzumab, ofatumumab, ramucirumab, pertuzumab, nimotuzumab, lambrolizumab, pidilizumab, siltuximab, BMS-936559, RG7446/MPDL3280A, MEDI4736), antibody-drug conjugates (e.g., brentuximab vedotin (ADCETRIS®, Seattle Genetics); ado-trastuzumab emtansine (KADCYLA®, Roche); Gemtuzumab ozogamicin (Wyeth); CMC-544; SAR3419; CDX-011; PSMA-ADC; BT-062; and IMGN901 (see, e.g., Sassoon et al., *Methods Mol. Biol.* 1045:1-27 (2013); Bouchard et al., *Bioorganic Med. Chem. Lett.* 24: 5357-5363 (2014)), or any combination thereof.

[0078] In some embodiments, combined administration of an anti- α 1 β 1 antibody and an additional therapeutic agent results in an improvement in cancer to an extent that is greater than one produced by either the anti- α 1 β 1 antibody or the additional therapeutic agent alone. The

difference between the combined effect and the effect of each agent alone can be a statistically significant difference. In some embodiments, the combined effect can be a synergistic effect. In some embodiments, combined administration of an anti- $\alpha 1 \beta 1$ antibody and an additional therapeutic agent allows administration of the additional therapeutic agent at a reduced dose, at a reduced number of doses, and/or at a reduced frequency of dosage compared to a standard dosing regimen, e.g., an approved dosing regimen for the additional therapeutic agent.

[0079] In some embodiments, treatment methods described herein are performed on subjects for whom other treatments of the medical condition have failed or have had less success in treatment through other means. Additionally, the treatment methods described herein can be performed in conjunction with one or more additional treatments of the medical condition. For instance, the method can comprise administering a cancer regimen, e.g., non-myeloablative chemotherapy, surgery, hormone therapy, and/or radiation, prior to, substantially simultaneously with, or after the administration of an anti- $\alpha 1 \beta 1$ antibody described herein, or composition thereof.

Formulations and Administration

[0080] In various embodiments, an antibody described herein can be incorporated into a pharmaceutical composition. Such a pharmaceutical composition can be useful, e.g., for the prevention and/or treatment of diseases, e.g., fibrotic disorders. Pharmaceutical compositions can be formulated by methods known to those skilled in the art (such as described in Remington's Pharmaceutical Sciences, 17th edition, ed. Alfonso R. Gennaro, Mack Publishing Company, Easton, Pa. (1985)).

[0081] In some embodiments, a pharmaceutical composition can be formulated to include a pharmaceutically acceptable carrier or excipient. Examples of pharmaceutically acceptable carriers include, without limitation, any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like that are physiologically compatible. Compositions of the present invention can include a pharmaceutically acceptable salt, e.g., an acid addition salt or a base addition salt.

[0082] In some embodiments, a composition including an antibody as described herein, e.g., a sterile formulation for injection, can be formulated in accordance with conventional

pharmaceutical practices using distilled water for injection as a vehicle. For example, physiological saline or an isotonic solution containing glucose and other supplements such as D-sorbitol, D-mannose, D-mannitol, and sodium chloride may be used as an aqueous solution for injection, optionally in combination with a suitable solubilizing agent, such as, for example, an alcohol such as ethanol and/or a polyalcohol such as propylene glycol or polyethylene glycol, and/or a nonionic surfactant such as polysorbate 80™ or HCO-50.

[0083] As disclosed herein, a pharmaceutical composition may be in any form known in the art. Such forms include, e.g., liquid, semi-solid and solid dosage forms, such as liquid solutions (e.g., injectable and infusible solutions), dispersions or suspensions, tablets, pills, powders, liposomes and suppositories.

[0084] Selection or use of any particular form may depend, in part, on the intended mode of administration and therapeutic application. For example, compositions containing a composition intended for systemic or local delivery can be in the form of injectable or infusible solutions. Accordingly, compositions can be formulated for administration by a parenteral mode (e.g., intravenous, subcutaneous, intraperitoneal, or intramuscular injection). As used herein, parenteral administration refers to modes of administration other than enteral and topical administration, usually by injection, and include, without limitation, intravenous, intranasal, intraocular, pulmonary, intramuscular, intraarterial, intrathecal, intracapsular, intraorbital, intracardiac, intradermal, intrapulmonary, intraperitoneal, transtracheal, subcutaneous, subcuticular, intraarticular, subcapsular, subarachnoid, intraspinal, epidural, intracerebral, intracranial, intracarotid and intrasternal injection and infusion.

[0085] Route of administration can be parenteral, for example, administration by injection, transnasal administration, transpulmonary administration, or transcutaneous administration. Administration can be systemic or local by intravenous injection, intramuscular injection, intraperitoneal injection, or subcutaneous injection.

[0086] In some embodiments, a pharmaceutical composition of the present invention can be formulated as a solution, microemulsion, dispersion, liposome, or other ordered structure suitable for stable storage at high concentration. Sterile injectable solutions can be prepared by incorporating a composition described herein in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filter

sterilization. Generally, dispersions are prepared by incorporating a composition described herein into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, methods for preparation include vacuum drying and freeze-drying that yield a powder of a composition described herein plus any additional desired ingredient (see below) from a previously sterile-filtered solution thereof. The proper fluidity of a solution can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prolonged absorption of injectable compositions can be brought about by including in the composition a reagent that delays absorption, for example, monostearate salts, and gelatin.

[0087] A pharmaceutical composition can be administered parenterally in the form of an injectable formulation comprising a sterile solution or suspension in water or another pharmaceutically acceptable liquid. For example, the pharmaceutical composition can be formulated by suitably combining the therapeutic molecule with pharmaceutically acceptable vehicles or media, such as sterile water and physiological saline, vegetable oil, emulsifier, suspension agent, surfactant, stabilizer, flavoring excipient, diluent, vehicle, preservative, binder, followed by mixing in a unit dose form required for generally accepted pharmaceutical practices. The amount of active ingredient included in a pharmaceutical preparation is such that a suitable dose within the designated range is provided. Non-limiting examples of oily liquid include sesame oil and soybean oil, and may be combined with benzyl benzoate or benzyl alcohol as a solubilizing agent. Other items that may be included are a buffer such as a phosphate buffer, or sodium acetate buffer, a soothing agent such as procaine hydrochloride, a stabilizer such as benzyl alcohol or phenol, and an antioxidant. A formulated injection can be packaged in a suitable ampule.

[0088] In various embodiments, subcutaneous administration can be accomplished by means of a device, such as a syringe, a prefilled syringe, an auto-injector (e.g., disposable or reusable), a pen injector, a patch injector, a wearable injector, an ambulatory syringe infusion pump with subcutaneous infusion sets, or other device for combining with antibody drug for subcutaneous injection.

[0089] An injection system of the present disclosure may employ a delivery pen as described in U.S. Pat. No. 5,308,341. Pen devices, most commonly used for self-delivery of insulin to patients with diabetes, are well known in the art. Such devices can comprise at least one injection needle (e.g., a 31 gauge needle of about 5 to 8 mm in length), are typically pre-filled with one or more therapeutic unit doses of a therapeutic solution, and are useful for rapidly delivering solution to a subject with as little pain as possible. One medication delivery pen includes a vial holder into which a vial of a therapeutic or other medication may be received. The pen may be an entirely mechanical device or it may be combined with electronic circuitry to accurately set and/or indicate the dosage of medication that is injected into the user. See, e.g., U.S. Pat. No. 6,192,891. In some embodiments, the needle of the pen device is disposable and the kits include one or more disposable replacement needles. Pen devices suitable for delivery of any one of the presently featured compositions are also described in, e.g., U.S. Pat. Nos. 6,277,099; 6,200,296; and 6,146,361, the disclosures of each of which are incorporated herein by reference in their entirety. A microneedle-based pen device is described in, e.g., U.S. Pat. No. 7,556,615, the disclosure of which is incorporated herein by reference in its entirety. See also the Precision Pen Injector (PPI) device, MOLLY™, manufactured by Scandinavian Health Ltd.

[0090] In some embodiments, a composition described herein can be therapeutically delivered to a subject by way of local administration. As used herein, "local administration" or "local delivery," can refer to delivery that does not rely upon transport of the composition or agent to its intended target tissue or site via the vascular system. For example, the composition may be delivered by injection or implantation of the composition or agent or by injection or implantation of a device containing the composition or agent. In certain embodiments, following local administration in the vicinity of a target tissue or site, the composition or agent, or one or more components thereof, may diffuse to an intended target tissue or site that is not the site of administration.

[0091] In some embodiments, a composition can be formulated for storage at a temperature below 0°C (e.g., -20°C or -80°C). In some embodiments, the composition can be formulated for storage for up to 2 years (e.g., one month, two months, three months, four months, five months, six months, seven months, eight months, nine months, 10 months, 11 months, 1 year, 1 1/2 years, or 2 years) at 2-8°C (e.g., 4°C). Thus, in some embodiments, the compositions described herein are stable in storage for at least 1 year at 2-8°C (e.g., 4°C).

[0092] In some embodiments, a pharmaceutical composition can be formulated as a solution. In some embodiments, a composition can be formulated, for example, as a buffered solution at a concentration suitable for storage at 2-8°C (e.g., 4°C).

[0093] Compositions including one or more antibodies as described herein can be formulated in immunoliposome compositions. Such formulations can be prepared by methods known in the art. Liposomes with enhanced circulation time are disclosed in, e.g., U.S. Pat. No. 5,013,556.

[0094] In certain embodiments, compositions can be formulated with a carrier that will protect the compound against rapid release, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Many methods for the preparation of such formulations are known in the art. See, e.g., J. R. Robinson (1978) "Sustained and Controlled Release Drug Delivery Systems," Marcel Dekker, Inc., New York.

[0095] In some embodiments, administration of an antibody as described herein is achieved by administering to a subject a nucleic acid encoding the antibody. Nucleic acids encoding a therapeutic antibody described herein can be incorporated into a gene construct to be used as a part of a gene therapy protocol to deliver nucleic acids that can be used to express and produce antibody within cells. Expression constructs of such components may be administered in any therapeutically effective carrier, e.g. any formulation or composition capable of effectively delivering the component gene to cells in vivo. Approaches include insertion of the subject gene in viral vectors including recombinant retroviruses, adenovirus, adeno-associated virus, lentivirus, and herpes simplex virus-1 (HSV-1), or recombinant bacterial or eukaryotic plasmids. Viral vectors can transfect cells directly; plasmid DNA can be delivered with the help of, for example, cationic liposomes (lipofectin) or derivatized, polylysine conjugates, gramicidin S, artificial viral envelopes or other such intracellular carriers, as well as direct injection of the gene construct or CaPO₄ precipitation (see, e.g., WO04/060407). Examples of suitable retroviruses include pLJ, pZIP, pWE and pEM which are known to those skilled in the art (see, e.g., Eglitis et al. (1985) Science 230:1395-1398; Danos and Mulligan (1988) Proc Natl Acad Sci USA 85:6460-6464; Wilson et al. (1988) Proc Natl Acad Sci USA 85:3014-3018; Armentano et

al. (1990) Proc Natl Acad Sci USA 87:6141-6145; Huber et al. (1991) Proc Natl Acad Sci USA 88:8039-8043; Ferry et al. (1991) Proc Natl Acad Sci USA 88:8377-8381; Chowdhury et al. (1991) Science 254:1802-1805; van Beusechem et al. (1992) Proc Natl Acad Sci USA 89:7640-7644; Kay et al. (1992) Human Gene Therapy 3:641-647; Dai et al. (1992) Proc Natl Acad Sci USA 89:10892-10895; Hwu et al. (1993) J Immunol 150:4104-4115; U.S. Pat. Nos. 4,868,116 and 4,980,286; and PCT Publication Nos. WO89/07136, WO89/02468, WO89/05345, and WO92/07573). Another viral gene delivery system utilizes adenovirus-derived vectors (see, e.g., Berkner et al. (1988) BioTechniques 6:616; Rosenfeld et al. (1991) Science 252:431-434; and Rosenfeld et al. (1992) Cell 68:143-155). Suitable adenoviral vectors derived from the adenovirus strain Ad type 5 dl324 or other strains of adenovirus (e.g., Ad2, Ad3, Ad7, etc.) are known to those skilled in the art. Yet another viral vector system useful for delivery of the subject gene is the adeno-associated virus (AAV). See, e.g., Flotte et al. (1992) Am J Respir Cell Mol Biol 7:349-356; Samulski et al. (1989) J Virol 63:3822-3828; and McLaughlin et al. (1989) J Virol 62:1963-1973.

[0096] In some embodiments, the compositions provided herein are present in unit dosage form, which unit dosage form can be suitable for self-administration. Such a unit dosage form may be provided within a container, typically, for example, a vial, cartridge, prefilled syringe or disposable pen. A doser such as the doser device described in U.S. Pat. No. 6,302,855, may also be used, for example, with an injection system as described herein.

[0097] A suitable dose of a composition described herein, which dose is capable of treating or preventing a disorder in a subject, can depend on a variety of factors including, e.g., the age, sex, and weight of a subject to be treated and the particular inhibitor compound used. For example, a different dose of one composition including an antibody as described herein may be required to treat a subject with a fibrotic disorder as compared to the dose of a different formulation of that antibody. Other factors affecting the dose administered to the subject include, e.g., the type or severity of the disorder. Other factors can include, e.g., other medical disorders concurrently or previously affecting the subject, the general health of the subject, the genetic disposition of the subject, diet, time of administration, rate of excretion, drug combination, and any other additional therapeutics that are administered to the subject. It should also be understood that a specific dosage and treatment regimen for any particular subject can also be adjusted based upon the judgment of the treating medical practitioner.

[0098] A composition described herein can be administered as a fixed dose, or in a milligram per kilogram (mg/kg) dose. In some embodiments, the dose can also be chosen to reduce or avoid production of antibodies or other host immune responses against one or more of the antigen-binding molecules in the composition. Exemplary dosages of an antibody, such as a composition described herein, include, e.g., 0.0001 to 100 mg/kg, 0.01 to 5 mg/kg, 1-1000 mg/kg, 1-100 mg/kg, 0.5-50 mg/kg, 0.1-100 mg/kg, 0.5-25 mg/kg, 1-20 mg/kg, and 1-10 mg/kg of the subject body weight. For example dosages can be 0.1 mg/kg, 0.3 mg/kg, 0.5 mg/kg, 1.0 mg/kg, 2.0 mg/kg, 3.0 mg/kg, 4.0 mg/kg, 5.0 mg/kg, 10 mg/kg or 20 mg/kg body weight or within the range of 1-20 mg/kg body weight. An exemplary treatment regime entails administration once per week, once every two weeks, once every three weeks, once every four weeks, once a month, once every 3 months or once every three to 6 months, or with a short administration interval at the beginning (such as once per week to once every three weeks), and then an extended interval later (such as once a month to once every three to 6 months).

[0099] A pharmaceutical solution can include a therapeutically effective amount of a composition described herein. Such effective amounts can be readily determined by one of ordinary skill in the art based, in part, on the effect of the administered composition, or the combinatorial effect of the composition and one or more additional active agents, if more than one agent is used. A therapeutically effective amount of a composition described herein can also vary according to factors such as the disease state, age, sex, and weight of the individual, and the ability of the composition (and one or more additional active agents) to elicit a desired response in the individual, e.g., amelioration of at least one condition parameter, e.g., amelioration of at least one symptom of a fibrotic disorder. For example, a therapeutically effective amount of a composition described herein can inhibit (lessen the severity of or eliminate the occurrence of) and/or prevent a particular disorder, and/or any one of the symptoms of the particular disorder known in the art or described herein. A therapeutically effective amount is also one in which any toxic or detrimental effects of the composition are outweighed by the therapeutically beneficial effects.

[0100] Suitable human doses of any of the compositions described herein can further be evaluated in, e.g., Phase I dose escalation studies. See, e.g., van Gurp et al. (2008) *Am J Transplantation* 8(8):1711-1718; Hanouska et al. (2007) *Clin Cancer Res* 13(2, part 1):523-531; and Hetherington et al. (2006) *Antimicrobial Agents and Chemotherapy* 50(10): 3499-3500.

[0101] Toxicity and therapeutic efficacy of compositions can be determined by known pharmaceutical procedures in cell cultures or experimental animals (e.g., animal models of any of the fibrotic disorders described herein). These procedures can be used, e.g., for determining the LD₅₀ (the dose lethal to 50% of the population) and the ED₅₀ (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD₅₀/ED₅₀. A composition described herein that exhibits a high therapeutic index is preferred. While compositions that exhibit toxic side effects may be used, care should be taken to design a delivery system that targets such compounds to the site of affected tissue and to minimize potential damage to normal cells and, thereby, reduce side effects.

[0102] Those of skill in the art will appreciate that data obtained from cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. Appropriate dosages of compositions described herein lie generally within a range of circulating concentrations of the compositions that include the ED₅₀ with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For a composition described herein, the therapeutically effective dose can be estimated initially from cell culture assays. A dose can be formulated in animal models to achieve a circulating plasma concentration range that includes the IC₅₀ (i.e., the concentration of the antibody which achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma may be measured, for example, by high performance liquid chromatography. In some embodiments, e.g., where local administration (e.g., to the eye or a joint) is desired, cell culture or animal modeling can be used to determine a dose required to achieve a therapeutically effective concentration within the local site.

[0103] All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting. Unless otherwise defined, 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. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described herein.

[0104] The disclosure is further illustrated by the following examples. The examples are provided for illustrative purposes only. They are not to be construed as limiting the scope or content of the disclosure in any way.

EXAMPLES

Methods

Generation of Novel Antibodies Against $\alpha 11\beta 1$

Rat Immunization

[0105] Wistar rats were immunized with recombinant human $\alpha 11\beta 1$ protein. An enzyme-linked immunosorbent assay (ELISA) was used to test an immune response against target human and mouse proteins. Subsequently, cell fusion (by electro fusion) was performed with animals that produced a good immune response. All fused cells were plated in a 96-well plate and supernatants were screened by ELISA against soluble human and mouse $\alpha 11\beta 1$. Positive clones were counter-screened against human $\alpha 1\beta 1$, $\alpha 2\beta 1$ and $\alpha 10\beta 1$. Clones that specifically bound to human and mouse $\alpha 11\beta 1$ and did not bind to $\alpha 1\beta 1$, $\alpha 2\beta 1$ and $\alpha 10\beta 1$ were selected, subcloned, expanded and cryopreserved. Purified antibodies were then generated from the selected clones and heavy chain and light chain variable domain sequences were obtained from each purified antibody.

Rabbit Immunization

[0106] Rabbits were immunized employing a cell-based monoclonal antibody platform. Two rabbits were immunized with recombinant human $\alpha 11\beta 1$ protein. Splenocytes from the immunized rabbits were sorted and selected against human $\beta 1$, in order to reduce the number of $\beta 1$ -specific B cell clones. Sorted splenocytes were then cultured for approximately 1 week and culture supernatants were screened for binding to human $\alpha 11\beta 1$. Top results were sequenced and subsequently rabbit antibodies were recombinantly produced using a HEK cell system.

Mouse Immunization

[0107] 10 mice from 5 different strains were immunized with an appropriate mixture of human $\alpha 11\beta 1$, mouse $\alpha 11\beta 1$ and tolerance breaking protein. Plasma titers were evaluated by ELISA against a mixture of human and mouse $\alpha 11\beta 1$. Popliteal, inguinal, and iliac lymph nodes

were collected. ELISA-positive anti-human/mouse $\alpha 11\beta 1$ hybridomas were expanded and subjected to a secondary screen against human and mouse $\alpha 11\beta 1$, control HIS protein, and a counter-screen was performed against human $\alpha 11\beta 1$, $\alpha 2\beta 1$ and $\alpha 10\beta 1$. Supernatant IgG concentration was sufficient for functional screening. Selected hybridomas satisfying all the criteria were cloned and clonal hybridomas were confirmed by ELISA against human and mouse $\alpha 11\beta 1$ and subsequently scaled-up and IgGs were purified. Heavy and light chain variable regions of selected hybridomas were then sequenced.

Phage Library Display

[0108] Phage library display was employed for generation of fully human anti- $\alpha 11\beta 1$ antibodies. Fully human anti- $\alpha 11\beta 1$ antibodies were discovered using single chain fragment variable (scFv) antigen-binding fragments displayed on phages (phage display library). Three rounds of selection were performed on purified human and mouse $\alpha 11\beta 1$ antigen as well as deselection against $\alpha 10\beta 1$, to enrich for $\alpha 11$ subunit-specific antibodies. Subsequently, optimal populations were subcloned into a bacterial soluble expression vector, recombinant antibody expression was induced and supernatant was screened for binding via ELISA assays. Antibodies with appropriate binding profiles were sequenced and subsequently converted from scFv to IgG.

ELISA

[0109] 0.25 $\mu\text{g/mL}$ of target antigen (recombinant human or mouse $\alpha 11\beta 1$) was plated in a 96-well plate over night at 4°C. Plates were washed (PBS with 0.1% Tween-20), blocked (PBS with 2% BSA and 0.05% Tween-20) for 1 hour at room temperature and incubated with a range of antibody concentrations for 1 hour at room temperature. Subsequently, plates were washed and incubated with biotinylated anti-rabbit/mouse/human IgG in a 1:1000 dilution buffer and incubated for 1 hour at room temperature. After washing the plates, Streptavidin HRP was added at 1:200 in dilution buffer and incubated for 1 hour at room temperature. Ultra TMB ELISA substrate solution was added and the plates incubated for 5 minutes on a plate shaker. The reaction was stopped by adding stop solution to each well and plates were read at 450 nm.

FACS

Antibody Binding to CHO-K1

[0110] 200,000 cells (wild-type CHO-K1 cells or CHO-K1 cells expressing human $\alpha 11$) were incubated with each antibody at desired concentrations in FACS buffer for 30 min at 4°C. Then, the cells were washed with FACS buffer and incubated with secondary antibody at 1:100 dilution for 30 minutes at 4°C. Cells were then washed and fixed with 1% PFA in PBS for 20 minutes at room temperature; washed again and read on a cytometer in FACS buffer.

Antibody Binding to HPF/MF

[0111] Human Pulmonary Fibroblasts (ScienCell) were cultured in complete Fibroblast Growth Medium (ScienCell) until 80% confluent in T-150 flasks. Cells were washed and harvested using Accutase. Cells were seeded into T-150 flasks at 7,500 cells/cm² in complete FGF and cultured for 72 hours. Cells were then washed and starved in serum reduced medium for 24 hours. After starvation, cells were treated with TGF β -1 (R&D Systems) for 72 hours. Cells were harvested using Accutase and seeded in 96-well conical bottom plates. Cells were blocked with Heat Inactivated Fetal Bovine Serum (Gibco) for 30 minutes at 4°C. Cells were then incubated with anti- $\alpha 11$ antibodies at the doses described in each figure for 30 minutes at 4°C. A human anti- $\alpha 11$ antibody (Creative BioLabs) was included as a positive control as well as the appropriate IgG isotype negative controls. Cells were washed twice and incubated with PE conjugated secondary antibodies specific to the IgG class of the anti- $\alpha 11$ antibodies being tested for 30 minutes at 4°C. Cells were washed twice and fixed in 1% PFA for 30 minutes. Cells were acquired on a FACS Verse (Benton Dickson) binding of each antibody. Data were analyzed by gating on single cells and determining the geometric Mean Fluorescence Intensity (gMFI) in the PE channel for each sample.

Surface Plasmon Resonance (SPR)

[0112] The affinity of antibodies for human $\alpha 11\beta 1$ was measured by surface plasmon resonance assay (SPR). Affinity was measured at pH 7.6 and 25°C with a Biacore T200 instrument. Anti-HIS antibody was immobilized on the SPR sensor surface using EDC/NHS covalent attachment. HIS-tagged human $\alpha 11\beta 1$ was captured on the sensor surface and a single-cycle kinetics assay was used. Increasing concentrations of test antibody were injected in series over the sensor-bound $\alpha 11\beta 1$. Dissociation was monitored for 1000 seconds. A sensor surface with only anti-HIS antibody and a series of blank injections were used to double-reference subtract the data. A 1:1 Langmuir model was fit to the data to estimate the kinetic association

and dissociation constants. The affinity (equilibrium dissociation constant) of the interaction was calculated by dividing the kinetic dissociation constant by the kinetic association constant. Between injection cycles $\alpha 1 \beta 1$ and bound antibody were removed with an injection of 10mM glycine at pH 1.5.

Cell Adhesion Inhibition

[0113] 0.6×10^6 cells/mL were incubated with each antibody at a range of concentrations for 20 minutes at 37°C. E-Plate VIEW 96 PET plate coated with 100 ng/mL type I collagen or PBS overnight at room temperature was blocked in 3% BSA for 1 hour at room temperature. After washing the plate with PBS, cell and antibody mixture was added to the wells and the plate was placed into an xCelligence machine. Cell adhesion was recorded over 6 hours. The time point of maximum cell adhesion was used for comparison relative to control.

Fibroblast-to-Myofibroblasts Transition (FMT)

[0114] Human Pulmonary Fibroblasts (ScienCell) were cultured in complete Fibroblast Growth Medium (ScienCell) until 80% confluent. Cells were washed and harvested using Accutase. Cells were seeded onto tissue culture-treated 96 well plates at 20,000 cells/well in complete Fibroblast Growth Medium. After 24 hours, cells were washed and starved in serum reduced medium for an additional 24 hours. After starvation, cells were treated with TGF β -1 (R&D Systems) with or without anti- $\alpha 1 \beta 1$ antibodies. A polyclonal rabbit anti-human $\alpha 1 \beta 1$ antibody was used as a positive control. Appropriate IgG isotype controls were also included. After 48 hours, cells were harvested, fixed, permeabilized and stained with AlexaFluor488 Labeled Anti- α SMA (α -smooth muscle actin) (Invitrogen). Cells were acquired on a FACS Verse (Benton Dickson) to determine expression levels of α SMA. Data were analyzed by gating on single cells and determining the geometric Mean Fluorescence Intensity (gMFI) in the FITC channel for each sample. gMFI for each sample was normalized to the untreated control and presented as % inhibition.

Collagen Gel Contraction Assay

[0115] 24-well plates were blocked with 2% BSA in PBS overnight at 37°C. The following day, the plates were washed 3 times with PBS before being used in the assay. Human

CHO cell lines expressing $\alpha 11$ were harvested and resuspended at 1.25×10^6 in ExpiCHO Expression Medium (Gibco™ Cat# A2910002). The collagen gel solution was prepared by diluting 3 mg/mL stock collagen type I (Gibco™ Collagen I Rat Protein, Tail Cat# A1048301) to 1 mg/mL in the media containing the CHO cells. Sodium hydroxide was added to the solution to neutralize the pH and 400 μ L of the collagen solution was added to each well of the 24-well plates. For the wells where the antibodies were included in the collagen gel solution, CHO cells were prepared at 2.5×10^6 and the antibodies were prepared at 2x final concentration in ExpiCHO media. The cells and antibodies were then combined 1:1 before the addition of the stock collagen type 1. The gels were allowed to polymerize for 60 minutes at 37°C. Antibodies were added to the ExpiCHO media, which was then layered on top of the polymerized gel (400 μ L/well). The gels were incubated for 6 days at 37°C before gel contraction was quantified. Images of each well were analyzed using Image J and gel contraction was determined as a percentage of the initial gel area.

Tumor Xenograft Model

[0116] Fifty-six female C.B-17 SCID mice were inoculated with A549 cells (5×10^6 cells/mouse) subcutaneously in the flank. Once tumor volume reached $\sim 100 \text{ mm}^3$, animals were randomized amongst 7 groups of 8 mice each. Mice were then treated intraperitoneally every 3 days for a total of 7 doses with isotype controls or novel mAbs 79E3E3, 16E10 and 9G04 (2 and 20 mg/kg) or with docetaxel at 10 mg/kg every 4 days for a total of 6 doses. Tumor volumes and body weights were recorded twice a week with a gap of 2-3 days in between two measurements until any of the following conditions defined were observed: loss of 20% or more body weight; tumors that inhibit normal physiological function such as eating, drinking, and mobility; ulcerated tumors; tumor size greater than 2000 mm^3 and clinical observations of prostration, paralysis, seizures and hemorrhages.

Precision-Cut Liver Slices (PCLS)

[0117] Precision-Cut Liver Slices (PCLS) were prepared from resected liver tissue and rested for 24 hours to allow the post-slicing stress period to elapse before experiments began. PCLS were cultured without exogenous challenge (Group 1), with 100 μ g/mL control antibodies (Groups 2 and 3 – either mouse IgG2a or rabbit IgG), or with a combination of TGF- β 1 (3

ng/mL) and PDGF- $\beta\beta$ (50 ng/mL) (Groups 2-10). PCLS were cultured in the presence or absence of 10 μ M Alk5i (Group 4) as a positive control or novel inhibitors (16E10, 79E3E3, and 9G05) at 2 escalating doses (10 and 100 μ g/mL) in Groups 5-10. Each of the 10 groups included n=6 human PCLS prepared from a single human liver. PCLS culture media, including all stimuli and compounds, was refreshed and harvested at 24 hour intervals. Cell culture supernatant (n=2/3 paired wells) was collected every 24 hours and snap frozen for quantification of soluble outputs. All PCLS were harvested at 96 hours.

[0118] Tissue culture levels of markers of liver damage (lactate dehydrogenase (LDH) and aspartate transaminase (AST)) and hepatocyte function/viability (albumin) were quantified on all PCLS at all time points. Albumin secretion was quantified by ELISA as a marker of PCLS integrity and function. Levels of collagen 1a1, IL-6, hyaluronic acid and Timp-1 in the cell culture supernatants were quantified using R&D DuoSet ELISA kits.

[0119] Total RNA extraction from PCLS was performed on all samples. RNeasy Mini kits (Qiagen) were used for RNA extraction. RNA was reverse-transcribed to cDNA and used in qPCR to measure transcript levels of Col1a1, α SMA, TIMP-1, TGF- β 1, IL-6 and β -actin/GAPDH.

Example 1. Generation of Novel Monoclonal Antibodies Against α 11 β 1 and Determination of Binding Affinity

[0120] Antibody discovery was performed by immunizing rats and rabbits with recombinant human α 11 β 1, and by immunizing mice with both human and mouse α 11 β 1. 51 novel anti-human α 11 β 1 monoclonal antibodies were generated (24 rabbit, 7 rat and 20 mouse). Heavy chain and light chain variable region sequences were determined for the mouse and rat antibodies, while full heavy chain and light chain sequences were determined for the rabbit antibodies.

[0121] ELISA results illustrating exemplary binding of selected mouse monoclonal antibodies to recombinant human α 11 β 1 are shown in **Figure 2A**. Three of those mAbs also bound to mouse α 11 β 1, as shown in **Figure 2B**.

[0122] Data was also collected to determine whether antibodies of interest bind to the I domain of $\alpha 11\beta 1$. An in-house generated I domain of $\alpha 11\beta 1$ was used. The rat clones 79E3E3, 8H8E9 and 6E5C11 exhibited high, medium, and low binding, respectively, as determined by ELISA. Mouse antibodies 10-F23, 10-L15, 7-O8, 6-A12, 9-G05 and 9-E16 and rabbit antibodies 7-H12 and 2-D3 were also tested for binding against the in-house generated $\alpha 11\beta 1$ I domain.

Figures 3A and 3B show graphs illustrating binding data from exemplary mAbs.

[0123] $\alpha 11\beta 1$ belongs to a family of collagen receptors and has a relatively high homology to them. Therefore, the novel antibodies of this invention were counter-screened against $\alpha 1\beta 1$, $\alpha 2\beta 1$ and/or $\alpha 10\beta 1$. **Table 2** includes results of cross-reactivity to the other receptors.

Table 2. Data summary of tested monoclonal antibodies

	Clone ID	Human $\alpha 11\beta 1$ ELISA	Murine $\alpha 11\beta 1$ ELISA	Off Target	I Domain binding	CHO-K1 FACS	HPF FACS	MF FACS	Inhibition of CHO-K1 adhesion to collagen	Inhibition of FMT	Inhibition of CHO-K1 gel contraction
MOUSE	10-L15	Yes	Yes	No	Yes	No	No	No	No	No	
	8-I14	Yes	Yes	No	No	Yes	No	Yes	No	Yes	No
	3-G5	Yes	Yes/Low	No	No	No	No	No	No	No	
	2-A3	Yes	Yes/Low	No	No	No	No	No	No	No	
	8-G15	Yes	No	No	No	Yes	No	Yes	Yes	Yes	
	8-P20	Yes	No	No	No	Yes	No	Yes	No	No	
	10-F23	Yes	Yes/Low	No	Yes	Yes	No	Yes	Yes	No	
	7-O8	Yes	Yes/Low	Yes ($\alpha 10\beta 1$)	Yes	Yes	No	Yes	No	No	
	8-J17	Yes	No	Yes (at high doses)	No	Yes	No	Yes	No	Yes	
	9-E16	Yes	Yes	No	Yes	Yes	Low	Yes	Yes	Yes	
	9-G05	Yes	Yes	No	Yes	Yes	No	Yes	Yes	Yes	Yes
	10-K10	Yes	Yes/Low	No	No	No	No	Yes	No	No	
	6-O12	Yes	No	No	No	No	No	No	No	No	
	6-A15	Yes	Yes/Low	No	No	No	No	No	No	No	
	6-B21	Yes	Yes/Low	No	No	No	No	No	No	No	
	6-A12	Yes	Yes/Low	No	Yes	Yes	No	Yes	Yes	No	
	6-M8	Yes	No	No	No	No	No	No	No	No	
	6-P20	Yes	No	No	No	Yes	No	No	No	No	

	6-O17	Yes	Yes/Low	No	No	Yes	No	Yes	No	No	
	9-B11	Yes	No	No	Yes	Yes	No	Yes	Yes	Yes	No
	7-H14	Yes	Yes/Low	No	No	Yes	No	Yes	No	No	
RAT	24E4G6	Yes	No/Low	No	No	Yes	No	Yes	No	Yes	Yes
	40G10H11	Yes	Yes	Yes (all)	No	Yes	N/A	N/A	Yes	Yes	
	18E10F10	Yes	No	No	No	Yes	N/A	N/A	Yes	Yes	
	8H8E9	Yes	No	No	No	Yes	N/A	N/A	Yes	Yes	
	6E5C11	Yes	No	No	No	Yes	N/A	N/A	No	Yes	
	7D8B10	Yes	No	No	No	Yes	No	Yes	No	Yes	
	79E3E3	Yes	Yes	No	Yes	Yes	No	Yes	Yes	No	Yes
RABBIT	16E10	Yes	No	No	No	Yes	No	Yes	Yes	Yes	Yes
	6F9	Yes	No	No	No	Yes	No	Yes	Yes	No	
	6G4	Yes	No	No	No	Yes	No	Yes	Yes	No	
	4E1	Yes	No	No	No	Yes	No	Yes	Yes	No	
	6C7	Yes	No	No	No	Yes	No	Yes	Yes	No	
	5D7	Yes	No	No	No	Yes	No	Yes	Yes	No	
	5A7	Yes	No	No	No	Yes	No	Yes	Yes	No	
	3B1	Yes	No	No	No	Yes	No	Yes	Yes	No	
	16G7	Yes	Yes	No	No	Yes	No	Yes	No	Yes	No

N/A = not tested

[0124] Since integrins are large, transmembrane receptors that exist in different conformational shapes, experiments were performed to confirm that the novel antibodies also bound cell-expressed $\alpha 11\beta 1$. A CHO-K1 cell line that endogenously expressed high levels of the $\beta 1$ subunit was engineered to stably express human $\alpha 11$ (CHO-K1 hu $\alpha 11$).

[0125] **Figures 4A and 4B** show selected rat and mouse mAbs that bound human $\alpha 11\beta 1$ (as tested by ELISA) and also demonstrated binding ability to $\alpha 11\beta 1$ expressed on the surface of CHO-K1 cells. **Figures 11A and 11B** show selected rabbit, rat, mouse and human mAbs that demonstrated binding ability to $\alpha 11\beta 1$ expressed on the surface of CHO cells. Additionally, **Figure 14** shows selected fully human mAbs that demonstrated binding ability to $\alpha 11\beta 1$ expressed on the surface of CHO cells. However, as shown in **Table 1**, there were several mAbs that were shown to bind $\alpha 11\beta 1$ by ELISA, but did not bind cell-expressed $\alpha 11\beta 1$.

[0126] Binding EC_{50} was estimated using data from Fluorescence-activated cell sorting (FACS) performed with CHO-K1 hu $\alpha 11\beta 1$ cells. The results are shown in **Table 3**. Four out of

six mAbs tested had EC₅₀ results in the low nanomolar range (8-P20, 8-G15, 8-J17, 8-I14), while the remaining two mAbs were not as potent (9-G05 and 9-E16; both I domain binders).

Table 3. Estimated CHO-K1 binding EC₅₀ for mouse mAbs

mAb	Conc. (µg/mL)	Molarity (nM)
9-G05	21.03	140.2
8-P20	0.12	0.8
8-G15	0.22	1.5
8-J17	0.33	2.2
8-I14	1.22	8.1
9-E16	42.80	285.3

[0127] As shown in **Figure 9**, when antibodies 16E10, 79E3E3, 9G05 and 1994_01_C07 were tested for their affinity to human $\alpha 11\beta 1$ via surface plasmon resonance (SPR), they exhibited KDs of 48 pM, 10pM, 2.85 nM and 0.77 nM, respectively. Interestingly, 16E10 and 1994_01_C07 do not bind either the I domain or the headpiece domain of $\alpha 11\beta 1$, which indicates that both might act as allosteric inhibitors by not binding to the ligand binding domain but still inhibiting $\alpha 11\beta 1$ function. 9G05 and 79E3E3 do bind to the I domain (the ligand binding domain) and therefore might directly inhibit the ligand binding site. The binding affinity of antibodies for the $\alpha 11\beta 1$ Headpiece and $\alpha 11\beta 1$ I Domain as measured by SPR is shown in **Figure 10A** and **Figure 10B**, respectively.

[0128] Binding to a physiologically relevant primary human cell type was also tested. Human pulmonary fibroblasts (HPF) and TGF β treatment were used to induce a fibroblast-to-myofibroblast transition (FMT), giving rise to myofibroblasts (MF). While HPFs do not express $\alpha 11\beta 1$, significant expression of $\alpha 11\beta 1$ is exhibited by MFs. Additionally, HPFs express $\alpha 1\beta 1$ and $\alpha 2\beta 1$, other collagen binding receptors, which means that HPFs can be to test cross-reactivity of antibodies of interest. Selected mAbs were assessed for binding to HPFs and MFs, and as shown in **Figure 5**, **Figure 12**, and **Figure 13**, it is apparent that the tested antibodies bound MFs strongly while not binding HPFs, with the exception of 9-E16, which showed some HPF binding, indicative of off-target binding.

Example 2. Biological activity of Novel Monoclonal Antibodies Against $\alpha 11\beta 1$

[0129] Myofibroblasts are responsible for secreting fibrotic matrix, so blocking and/or reducing MF accumulation is an important step for treating and/or preventing fibrosis. This can be achieved by using anti- $\alpha 11\beta 1$ antibodies to inhibit the fibroblast-to-myofibroblast transition. Typical functional inhibitors of a receptor block ligand binding, and while preventing the binding of $\alpha 11\beta 1$ to type I collagen is a desired feature of anti- $\alpha 11\beta 1$ antibodies, it may not be necessary for therapeutic efficacy. Unlike many other receptors, integrins are able to perform both “outside-in” (canonical, ligand-mediated) signaling and also “inside-out” signaling. Therefore, it might be possible for an antibody to bind $\alpha 11\beta 1$ in a way that affects the structure of $\alpha 11\beta 1$ in a way that prevents inside-out signaling and FMT, but does not affect the ability of $\alpha 11\beta 1$ to bind type I collagen. For this reason, both mAbs that block ligand binding and those that do not were included these studies.

[0130] A CHO-K1 hu $\alpha 11$ cell line was used to assess the ability of mAbs to block $\alpha 11\beta 1$ -mediated binding to type I collagen. As shown in **Figure 6A**, out of three rat mAbs tested, two significantly inhibited adhesion of CHO-K1 hu $\alpha 11$ cells to type I collagen-coated plates. In the “Untreated” condition, cells were plated on type I collagen but no antibody was added and in the “Uncoated” condition, cells were seeded onto BSA-coated wells containing no type I collagen. Statistics were performed using one-way ANOVA followed by Dunnett’s multiple comparisons test. 79E3E3, which is an I-domain binder, was able to block cell adhesion with an IC₅₀ of 9.4 nM. However, 40G10H11 strongly inhibited cell adhesion but was not found to be an I-domain binder, though it does cross-react with other collagen receptors ($\alpha 1\beta 1$, $\alpha 2\beta 1$ and $\alpha 10\beta 1$). 24E4G6 did not bind to the I-domain nor did it inhibit cell adhesion to collagen. When rabbit mAbs were tested, eight of the nine mAbs strongly and significantly inhibited cell adhesion and none of those mAbs were found to be I-domain binders (**Figure 6B**). Therefore, it is possible that these mAbs bind on an $\alpha 11\beta 1$ domain that keeps the integrin in a low or intermediate affinity state. **Figure 6C** shows the activity of selected mouse mAbs. Three of six mAbs significantly blocked cell adhesion, and two of those mAbs were found to be I-domain binders (9-G05 and 9-E16). 8-G15, however, is a strong blocker of cell adhesion but was not found to bind the I-domain. 8-P20, 8-J17 and 8-I14 did not block cell adhesion to type I collagen. Nine human mAbs were also tested for their ability to inhibit the binding of human CHO- $\alpha 11$ cells to type I collagen. As shown in **Figures 15A** and **15B**, all of the human Abs

inhibited cell adhesion relative to the control, with 1994-01-C07 having an IC₅₀ of 3.3 nM. As illustrated by these data (and summarized in **Table 1**), some anti- $\alpha 11\beta 1$ mAbs were found to strongly bind human $\alpha 11\beta 1$ when tested by ELISA and FACS, but not all of those antibodies were able to block ligand interaction. Furthermore, binding to the I-domain (ligand binding domain on $\alpha 11\beta 1$) was found to not be necessary for blocking the interaction of $\alpha 11\beta 1$ with type I collagen.

[0131] In addition to the binding abilities described above, it is important for an anti- $\alpha 11\beta 1$ antibody to inhibit the fibroblast-to-myofibroblast transition (FMT). It is now appreciated that myofibroblasts are a heterogeneous cell population, existing in different activation states, with the main function of producing and contracting collagen extracellular matrix (ECM). FMT is a multi-step event that is controlled by a changing mechanical environment in tissues undergoing repair. TGF β is one of the potent factors that potentiates this process and alpha smooth muscle actin (α SMA) is one of the main markers that becomes overexpressed when fibroblasts are undergoing the transition to becoming myofibroblasts. The presence of α SMA enhances fibroblast contraction and guides myofibroblast activation through an intracellular feedback loop. Because α SMA is the main molecular marker of myofibroblasts, the ability of the novel anti- $\alpha 11\beta 1$ mAbs to inhibit α SMA expression in TGF β -induced FMT was tested.

[0132] As shown in **Figure 7A**, two rat mAbs (40G10H11 and 24E4G6) significantly inhibited α SMA expression compared to control, but neither of the antibodies was found to be an I-domain binder. Statistics were performed using one-way ANOVA followed by Dunnett's multiple comparisons test. Furthermore, only 40G10H11 inhibited cell adhesion to type I collagen. Interestingly, the 79E3E3 mAb was found to be an I-domain binder and strongly inhibited cell adhesion to collagen but failed to decrease α SMA expression (a surrogate for myofibroblast generation). As shown in **Figure 7B**, two rabbit mAbs significantly inhibited α SMA expression compared to control, but neither of the antibodies was found to be an I-domain binder. 16E10 was found to inhibit both ligand binding and FMT (% inhibition of α SMA upregulation), but 16G7 was found to inhibit FMT but didn't have an effect on cell adhesion to collagen. Finally, as shown in **Figure 7C**, five of the six tested mouse mAb significantly inhibited α SMA expression compared to control. Three of the FMT inhibitors (9-G05, 8-G15, 9-E16) were also found to decrease cell adhesion to collagen and two of those (9-G05, 9-E16) also

bound the I domain. Mouse antibodies 8-J17 and 8-I14 only inhibited FMT and had effect on ligand binding.

Example 3. Ability of selected antibodies to inhibit cell-mediated contraction of collagen gels

[0133] Cell-mediated contraction of CD collagen I gels is a process previously shown to be $\alpha 11\beta 1$ -mediated, and a more recent study showed that $\alpha 11\beta 1$ -mediated downstream signaling was indispensable for gel contraction to occur. Selected exemplary antibodies were tested for the ability to inhibit cell-mediated 3D gel contraction because this ability is directly linked to the functionality of the exemplary antibodies.

[0134] As can be seen in **Figure 8**, rat 79E3E3, mouse 9E16, 9G05 and 8I14, rabbit 16E10, and human 1994_01_C07, 2004_04_B03, 2004_04_C12, and 1994_01_D12 antibodies all inhibited CHO-hu $\alpha 11$ -mediated collagen gel contraction. Of note, CHO-hu $\alpha 11$ cells were able to contract collagen gel without the addition of TGF β , as shown in the UT (untreated) condition. In the untreated condition, cells were embedded in the collagen gel but no antibody was added. Statistics were performed using one-way ANOVA followed by Dunnett's multiple comparisons test; each treatment conditions was compared to untreated condition. Asterisks indicate statistical significance and "ns" indicates that the difference was not statistically significant.

Example 4. Assessing Effect of selected antibodies on Tumor Xenograft Growth

[0135] Previous studies have shown growth of A549 cell xenografts in $\alpha 11$ knockout SCID mice to be significantly impeded compared to wild-type mice. In this example, studies were performed to determine if inhibition of $\alpha 11\beta 1$ function with mAb results in xenograft growth inhibition. As shown in **Figure 16** and **Table 4**, blocking $\alpha 11\beta 1$ on mouse CAFs impeded xenograft growth in SCID mice. Specifically, 79E3E3, an effectorless mAb that cross-reacts with mouse $\alpha 11\beta 1$, significantly inhibited tumor growth compared to isotype control, while 16E10, a mAb that does not bind mouse $\alpha 11\beta 1$, showed no significant inhibition of tumor growth. Inhibition of tumor-expressed $\alpha 11\beta 1$ did not affect tumor growth as 16E10 did not show any effect.

Table 4. Days to volume doubling after treatment with mAbs

Treatment	Days to Volume Doubling (ave, 95% CI)
Mouse IgG2a	7.6 (7.3, 8.0)
Docetaxel	11.0 (10.0, 12.0)
79E3E3 2mpk	8.5 (8.0, 9.0)
79E3E3 20mpk	8.5 (8.0, 9.0)
16E10 2mpk	7.9 (7.5, 8.3)
16E10 20mpk	7.9 (7.5, 8.3)

Example 5. Effect of anti- α 11 β 1 antibodies on human Precision-Cut Liver Slices (PCLS)

[0136] Precision-Cut Liver Slices (PCLS) from human liver tissue are physiologically and structurally representative of the tissue architecture and testing therapeutic targets in human PCLS allow for assessment of their effectiveness and relevance to the clinical situation, overcoming the limitations of *in vivo* rodent models and *in vitro* 2D cell culture methods. Tissue bioreactor technology maintains viability and functionality of PCLS from human liver tissue for at least 6 days *in vitro*.

[0137] As shown in **Figures 17A-17C**, all anti- α 11- β 1 antibodies that were tested provided partial inhibition of soluble pro-fibrogenic markers (COL1A1, hyaluronic acid and TIMP1) either in a dose-dependent manner or at the highest dose tested. No toxicity was observed after treatment with any of the antibodies (i.e., no elevation in ALT, AST, or albumin; data not shown).

EXEMPLARY SEQUENCES**DNA sequences of anti- α 11 β 1 monoclonal antibodies*****Rat mAb sequences***

Signal sequence-FR1-**CDR1**-FR2-**CDR2**-FR3-**CDR3**-FR4

79E3E3 Heavy Chain Variable Region

Signal sequence-FR1-**CDR1**-FR2-**CDR2**-FR3-**CDR3**-FR4

ATGGATTGGTTGTGGAAGTCTGCTATTCCTGATGGTAGTTGCCCAAAGTGCTCAAGCACAG
ATCCAGTTGGTACAGTCTGGACCTGAAGTAAAGAAGCCTGGAGAGTCAGTGAAGAT

CTCCTGCAAGGCCTCTGGGTATACCTTCACAGACTATGCAATGAACTGGGTGAAAC
AGGCTCCAGGAAATGGCCTGAAGTGGATGGGCTGGATCAACACCCAAACTGGAAA
GCCAACATATGCGGATGATTTCAAACAACGGTTTGTCTTCTCTTTGGAAACTTCTG
CCAGAACTACATATTTGCAGATCAACAACCTCAATATTGAAGACACAGCTACATATT
TCTGTACGAGATTGGGTACAGGTAATACGAAGGGGTTTGCTTACTGGGGCCAAG
GCACTCTGGTCACTGTCTCTTCA (SEQ ID NO: 1)

79E3E3 Light Chain Variable Region

ATGGAATCACAGACGCATGTCCTCATTTCCCTTCTGCTCTGTGTATCAGGTACCTGTGGGG
ACATTTTGATAAACCAGTCTCCAGCCTCTCTGACTGTGTCAGCAGGAGAGAGGGTCA
CTATGAGCTGCAAGTCCAGTCAGAGTCTTCTATACAGTGAAAACAACCAGGACT
ATTTGGCTTGGTACCAGCAGAAACCAGGACAGTTTCCTAAATTGCTTATCTATGGG
GCATCCAACCGGCACACTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGA
CAGACTTCACTCTGACCATCAGCAGTGTGCAGGCTGAAGACCTGGCTGATTATTATT
GTGAGCAGACCTACAGATATCCATTACGTTCCGGCTCAGGGACGAAGTTGGAAAT
AAAA (SEQ ID NO: 2)

24E4G6 Heavy Chain Variable Region

ATGGAGTTGGAATTGAGCTTAATTTTTATTTTTCTCTTTTAAAAGATGTCCAGTGTGAAGT
ACAGCTGGTGGAGTCTGGAGGAAGCTTGGTTCAACCTGGGGGTTCTCTGAAACTCTC
CTGTGTAGCCTCAGGATACACTTTCAGTAACTACTGGATGGACTGGGTTCCGGCAGT
CTCCTGGAAAGTCCCTGGAATGGATTGGAGAGATTAAACACGGATGGCAGAAGGAC
CAACTATGCACCATCCATAAAGGATCGATTCAATCTCCAGAGACAATGCCAAG
AGCACCTGTATCTGCAGATGAGCAATGTGAAATCAGATGACACAGCCATTTATTAC
TGTACCATACTACGGGTATACCCCCACTACTTTGATTACTGGGGCCAAGGAGTCA
TGGTCACAGTCTCCTCA (SEQ ID NO: 3)

24E4G6 Light Chain Variable Region

ATGATGAGTCCTGCCCAGTTCCTGTTTCTGCTAATGCTCTGGATCCAGGAAGCCCGC
GGAGATGTTGTGATGACCCAGACACCACCGTCTTTGTGCGTTGCCATTGGACAATCA
GTCTCCATCTCTTGCAAGTCAAGTCAGAGCCTCGTATATAGTGATGGAGAGACAT
ATTTGCATTGGTTTTTACAGAGTCCTGGCAGGTCTCCGAAGCGCCTAATTTATCAGG
TGTCTAATCTGGGCTCTGGAGTCCCTGACAGGTTCACTGGCACTGGATCACTGACA
GATTTTACACTTAGAATCAGCAGAGTGGAGGCTGAGGATTTGGGAGTTTATTACTGC
GCGCAAACCTACACATTTTCCTCCACGTTTGGAGCTGGGACCAAGCTGGAAGTGA
AA (SEQ ID NO: 4)

8H8E9 Heavy Chain Variable Region

ATGGCTGTCCTGGTGCTGTTGCTCTGCCTGGTGACATTTCCAAGCTGTGCCCTGTCCCAG
GTGCAGTTGAAGGAGTCAGGACCTGGTCTGGTGCAGCCCTCACAGACCCTGTCCCTC
ACCTGCACTGTCTCTGGGTTCTCATTAACCAGCAATAGTGTTAGCTGGGTTTCGCCA
GGCTCCGGGAAAGGGTCTGGAGTGGATGGGAGCAATATGGAGTGGTGGAAAGCAC
AGATTATAATTCAGCTCTCAAATCCCGACTGAGCATCAGCAGGGACACCTCCAAG
AGCCAAGTTTCTTAAAAATGAACAGTCTGCAAACCTGAAGACACAGCCATTTACTTC
TGTACCAGATCTCACTGGGAGCCCTTTGATTACTGGGGCCAAGGAGTCATGGTCA
CAGTCTCCTCA (SEQ ID NO: 5)

8H8E9 Light Chain Variable Region

ATGGAATCACAAACTCAGGCCCTCATATCCCTGCTGCTCTGGGTATATGGTACCTGTGGG
GACATTGTGATGACCCAGTCTCCATTCTCCCTGGCTGTGTCAGAAGGAGAGATGGTC
ACTATAAACTGCAAGTCCAGTCAGGGTCTTTTATCCAGTGGAACCAAAAGAAC
TACTTGGCCTGGTACCAGCAGAGACCAGGGCAGTCTCCTAACTACTGATCTACTA
TGCATCCACTAGGCAATCAGGGGTCCCTGATCGCTTCATAGGCGGTGGATCTGGGA
CAGACTTCACTCTGACCATCAGCGATGTGCAGGCTGAAGACCTGGCAGATTATTACT
GCCTGCAGCATTACAGCTATCCTCCCACGTTTCGGTTCTGGGACCAAGCTGGAGAT
CAAA (SEQ ID NO: 6)

6E5C11 Heavy Chain Variable Region

ATGGCTGTCCTGGTGCTGTTGCTCTGCCTGGTGACATTTCCAAGCTGTGCCCTGTCCAG
GTGCAGCTGAGGGAGTCAGGACCTGGTCTGGTGCAGCCCTCACAGACCCTGTCCCTC
ACCTGCACTGTCTCTGGGTTCTCATTGACCAGCAATAGTGTGACCTGGGTTTCGCCA
GCCTCCGGGAAAGGGTCTGGAGTGGATGGGAGCGATATGGAGTGATGGAAGCAC
AGATTATAATTCAACTCTCAAATCCCGACTGAGCATCAGTAGGGACACCTCCAAG
AGCCAAGTTTCTTAAAAATGAGCAGTCTGCAAACTGAAGACACAGCCATTTACTTC
TGTACCAGATCCCCTGGGAGCCCTTTGATTACTGGGGCCAAGGAGTCATGGTCA
CAGTCTCCTCA (SEQ ID NO: 7)

6E5C11 Light Chain Variable Region

ATGGAATCACAAACTCAGGCCCTCATATCCCTGCTGCTCTGGGTATATGGTACCTGTGGG
GACATTGTGATGACCCAGTCTCCACTCTCCCTGGCTGTGTCAGAAGGAGAGACGGTC
ACTATGAACTGCAAGTCCAGTCAGAGTCTTTTTTCCAGTGGAATCAAAAGAAC
TACTTGGCCTGGTACCAGCAGAAACCAGGGCAGTCTCCTAACTACTGATCTACTA
TGCATCCACTAGGCAATCAGGGGTCCCTGATCGCTTCATAGGCAGTGGATCTGGGA
CAGACTTCACTCTGACCATCAGCGATGTGCAGACTGAAGACCTGGCAGATTATTACT
GCCTGCAGCATTACAACCTATCCTCCCACGTTTCGGTTCTGGGACCAAGCTGGAGA
(SEQ ID NO: 8)

7D8B10 Heavy Chain Variable Region

ATGGACTTGCGACTGACTTATGTCTTTATTGTTGCTATTTTAAAAGGTGTCTTGTGTGAGGT
GAAACTGGAGGAATCTGGGGGAGGTTTGGTGCACCTGGAATGTCCGTGAACTCT
CTTGTGCAACCTCTGGATTCAATTTTCACTGACTACTGGATGGAATGGGTCCGCCAG
GCTCCAGGGAAGGGGCTAGAATGGGTAGCCGAAATTAGAAACAAAGCTAATAATT
ATGCAACATACTATGGGAAGTCTATGAAAGGCAGATTCACCATCTCAAGAGATGA
TTCCAAAAGTATAGTCTACCTACAAGTGAACAGCATAAGATCTGAAGATACTGCTAT
TTATTACTGTGCACCGAATTTTGATTACTGGGGCCAAGGAGTCATGGTCACGGTCTC
CTCA (SEQ ID NO: 9)

7D8B10 Light Chain Variable Region

ATGAGTCCCTGTCCAGTCCCTGTTTTTGCTATTGCTTTGGATTCTGGGAACCCATGGTGATG
TTGTGCTGACCCAGACTCCACCCACTTTATCGGCTACCATTTGGACAATCAGTCTCTAT
CTCTTGCAAGTCAAGTCAGAGTCTTTACATAGTACTGGAAACACCTATTTAAAT

TGGTTGCTACAGAGGCCAGGCCAACCTCCGCAACTTCTAATTTATTTGGTTTCCAG
ACTGGAATCTGGGGTCCCCAACAGGTTTCAGTGCCAGTGGGTCAGGAACTGATTTC
CACTCAAAATCAGTGGAATAGAGGCTGAGGATTTGGGGGTTTATTACTGCGTGCAA
AGTTCCCATACTCCGTACACGTTTGGGACTGGGACCAAGCTGGAAGTGAAG (SEQ
ID NO: 10)

18E10F10 Heavy Chain Variable Region

ATGGACATCAGGCTCAGCTTGGTTTTTCCTTGTCCTTTTTATGAAAGGTGTCCAGTGTGAGG
TGCAGTTGGTGGAGTCTGGGGGAGGCTTAGTGACAGCTGGAAGGTCCCTGAAACTCT
CCTGTGCAGCCTCACGATTCACCTTTTAGTGACTATAACATGGCCTGGGTCCGCCAG
GCTCCAAAGAAGGGTCTGGAGTGGGTCGCAACCATTATCATGATGATAGTGGTT
CTTACTATCGAGACTCCGTGAAGGGCCGATTACCATCTCCAGAAATAATGCAAA
AAGCACTCTGTACCTGCAGATGGACAGTCTGAGGTCTGAGGACATGGCCACTTATTA
CTGTGCAAGACATAACAATGGCTTTGATTACTGGGGCCAAGGAGTCATGGTCACA
GTCGCCTCA (SEQ ID NO: 11)

18E10F10 Light Chain Variable Region

ATGAAGTGGCCTGTAGGCTGTTGGTGCTGTTCTTCTGGATTCTGCTTCCGGGGGTGAT
GTTGTGATGACACAACTCCAGTCTCCCTGCCTGTCCGCCTTGGAGGTCAAGCCTCT
ATCTCTTGCCGGTCAAGTCAGAGCCTGGTACACAGTAATGGAAACACCTACTTG
CATTGGTACCTACAGAAGCCAGGCCAGTCTCCACAGCTCCTCATCAATCGGGTTTC
CAACAGATTTTCTGGGGTGCCAGACAGGTTTCAGTGGCAGTGGGTCAGGGACAGATT
TCACCTCAAGATCAACAGAGTAGAGCCTGAGGACTTGGGAGATTATTACTGCTTA
CAAAGTACACATTTTCCACTCACGTTTCGGTCTGAGGACCAAGCTGGAGACCAA
(SEQ ID NO: 12)

40G10H11 Heavy Chain Variable Region

ATGGACATCAGGCTCAGCTTGGGTTTTCTTGTCCTTTTCATAAAAGGTGACCAGTGTGCGG
TGCAACTGGTGGAGTCTGGGGGAGGCTTAGTGACAGCTGGAAGGTCCCTGAAACTC
TCCTGTGCAGCCTCAAGAATCACTTTCACTGACTATTACATGGCCTGGGTCCGCCA
GGCTCCAACGAAGGGTCTGGAGTGGGTCGCAACCATTAGTTCTGATGGTGGTGAC
ACTTTCTATCGAGACTCCGTGAAGGGCCGATTTACTATCTCCAGAGACAATGCAA
AAAGCACCTATATTTGCAAATGGTCAGTCTGAGGTCTGAGGACACGGCCACTTATT
ACTGTTCAACAGATCGGGGAGCTCAGTTTGGTTACTGGGGCCAAGGCACTCTGGT
CACTGTCTCTTCA (SEQ ID NO: 13)

40G10H11 Light Chain Variable Region

ATGGCTCCAGTCCAGCTCTTAGGGCTGCTGCTGATTGGCTCCAGCCATGAGATGTGAC
ATCCAGATGACCCAGTCTCCTTCATTCTGTCTGCATCTGTGGGAGACAGAGTCTCT
ATCAACTGCAAAGCAAGTCAGAATGTTTCACGAGAACCTAACTGGTATCAGCAAA
AGCTTGGAGAAGCTCCCAAACGCCTGATATATAATACAAACAATTTGCAAACAGG
CATCCCATCAAGGTTTCAGTGGCAGTGGATCTGGTGCAGATTACACACTCACCATCAG
CAGCCTGCAGCCTGAAGATTTTGCCACATATTTCTGTTTGCAGCATAATGCTTTTC
CGTACACGTTTGGACCTGGGACGAAGCTGGAAGTGAAG (SEQ ID NO: 14)

Mouse mAb sequences

9-G05 Heavy Chain Variable Region

GAGGTCCAGCTGCAACAGTCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAA
GATACCCTGCAAGGCTTCTGGATACACATTCCCTGACTACAACATGGACTGGGTGAA
GCAGAGCCATGGAAAGAGCCTTGAGTGGATTGGATATATTAATCCTGACAATGGTG
GTACTATCTACAACCAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAGTCC
TCCAGCACAGCCTACATGGAGCTCCGCAGCCTGACATCTGAGGACACTGCAGTCTAT
TACTGTGCAAGATTAGACAGCTCAGGCTACGGTACTATGCTATGGACTACTGGGGT
CAAGGAACCTCAGTCACCGTCTCCTCA (SEQ ID NO: 15)

9-G05 Light Chain Variable Region

GACATTGTGCTGACCCAATCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCC
ACCATCTCCTGCAGAGCCAGCGAAAGTGTTGATAATTATGGCATTAGTTTTATGCAC
TGGTACCAGCAGAAACCAGGACAGCCACCCAACTCCTCATCTATCGTGCATCCAA
CCTAGACTCTGAGATCCCTGCCAGGTTCAAGTGGCAGTGGGTCTAGGACAGACTTCAC
CCTCACCATTGATCCTGTGGAGACTGATGATGTTGCAACCTATTACTGTCAGCAAAG
TTATAAGGATCCTCGGACGTTCCGTGGAGGCACCAAGCTGGAAATCAAA (SEQ ID
NO: 16)

8-P20 Heavy Chain Variable Region

AAAGTGATGCTGGTGGAGTCTGGGGGAGCCTTAGTGAAGCCTGGAGGGTCCCTGAA
ACTCTCCTGTGTAGCCTCTGGATTCACTTTCAGTAACTATGCCATGTCTTGGGTTCGC
CAGACTCCAGAGAAGAGGCTGGAGTGGGTCGCAACCATTAGTAGTGGTGGTTATTA
CACTTACTATCCAGACAGTGTGAAGGGTCGATTACCATCTCCAGAGACAATGCCAG
GAACACCCTGTTCTGCAAATGAGCAGTCTGAGGTCTGAGGACACGGCCATGTTTTA
CTGTGCAAGAGAGGATGATTACGGAAGATATTCCTATACTATGGACTACTGGGGTCA
AGGAACCTCAGTCACCGTCTCCTCA (SEQ ID NO: 17)

8-P20 Light Chain Variable Region

GATGTTGTGATGACCCAACTCCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGTC
TCCATCTCTTGCAGATGTAGTCAGAGCCTTGACACAGTAATGGAAACACCTATTTA
CATTGGTACCTGCAGAAGCCAGGCCAGTCTCCACAGCTCCTGATCTACAAAATTTCC
AACCGATTTTCTGGGGTCCCAGACAGGTTCAAGTGGCAGTGGATCAGGGACAGATTTC
ACACTCAAGATCAGCAGAGTGGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAA
AGTACACATGTTCCGTACACGTTCCGAGGGGGGACCGAGCTGGAAATAAAA (SEQ
ID NO: 18)

8-G15 Heavy Chain Variable Region

GAGGTCCAGCTGCAGCAGTCTGGACCTGAGCTGGTAAAGCCTGGGGCTTCAGTGAG
GATATCCTGCAAGGCTTCTGGATACACATTCACTGACTACTACATACTGGGTGAA
GCAGAAGCCTGGGCAGGGCCTTGAATGCATTGGAGAGATTTATCCTGGAAGTATA
ATACTTACTACAGTAAAAAATTCAGGGGCAAGGCCACACTGACTGCAGACAAATCC
TCCGACACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCAGTCTAT
TTCTGTGCAAGAGGAGACTACTATAGGGGGTACTTCGATGTCTGGGGCGCAGGGAC
CACGGTCACCGTCTCCTCA (SEQ ID NO: 19)

8-G15 Light Chain Variable Region

GATGTTGTGATGACTCAGACCTCACTCACTTTGTCTGGTTACCATTGGACAACCAGCC
TCCATCTCTTGCAAGTCAAGTCAGAGCCTCTTACATAGTAATGGAAAGACATATTTG
AATTGGTTATTACAGAGGCCAGGCCAGTCTCCAAAGTTCCTAATCTATCTGGTGTCT
AAACTGGAATCTGGAGTCCCTGACAGGTTCAAGTGGCAGTGGATCAGGGACAGATTT
CACACTGAAAATCAGCAGAGTGGAGGCTGAGGATTTGGGGGTTTATTACTGCTTGCA
ATCTACACATTTTCCTTGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA (SEQ
ID NO: 20)

8-I14 Heavy Chain Variable Region

GAGGTCCAGCTGCAGCAGTCTGGACCTGAGCTGGTAAAGCCTGGGGCTTCAGTGAA
GAAATCCTGCAAGGCTTCTGGATACACATTCAGTACTACTACATGCACTGGGTGAA
GCAGAAAGCCTGGGCAGGGCCTTGAGTGGATTGGAAAGATTTATCCTGGAAGTGGTA
ATACTCACTACAATGAGAAGTTCAAGGGCAAGGCCCACTGACTGCAGACAAATCC
TCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCAGTCTAT
TTCTGTGCAACCAATTACTACGGCTACAGGGCAATGAACTATTGGGGTCAAGGATCC
TCAGTCACCGTCTCCTCA (SEQ ID NO: 21)

8-I14 Light Chain Variable Region

GACATCCATTTGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAATC
AGTCTCACTTGCCGGGCAAGTCAGGACATTTATATTAGCTTAAACTGGTTTCAGCAG
AAACCAGATGGAATATTAAGCTCCTGATCTACGGCACATCCAGTTTAGATTCTGGT
GTCCCCAAAAGGTTCAAGTGGCAGTAGGTCTGGGTGAGATTATTCTCTACCATCAGC
AGCCTTGAGTCTGAAGATTTTGCAGACTATTACTGTCTACAATATGCTAGTTCTCCGT
ACACGTTCCGAGGGGGGACCAAGCTGGAAATAAAA (SEQ ID NO: 22)

9-E16 Heavy Chain Variable Region

GAGGTCCAGCTGCAGCAGTCTGGACCTGAGCTGGTAAAGCCTGGGGCTTCAGTGAA
GATATCCTGCAAGGCTTCTGGATACACATTCAGTACTACTACATGCACTGGGTGAA
GCAGAAAGCCTGGGCAGGGCCTTGAGTGGATTGGAGAGATTTATCCTGGAAGTGGTA
ATCCTTACTACAATGAGAAGTTCAAGGGCAAGGCCCACTGACTGCAGACAAATCA
TCCAGCTCAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCAGTCTAT
TTCTGTGCAAGAACCTCCTACGGTAGAGTAGGGACAGGGTTTGCTTACTGGGGCCAA
GGGACTCTGGTCACTGTCTCTGCA (SEQ ID NO: 23)

9-E16 Light Chain Variable Region

AATTTTGTGATGACCCAAACTCCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCCT
CCATCTCTTGCAAGTCTAGTCAGAGCCTTCTACACAGTAACGGAAACACCTATTTAC
ATTGGTACCTGCAGAAGCCAGGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCA
ACCGATTTTCTGGGGTCCCAGACAGGTTCAAGTGGCAGTGGATCAGGGACAGATTTCA
CACTCAAGATCAACAGAGTGGAGACTGAGGATCTGGGAATTTATTTCTGCTCTCAAA
GTTACATGTTCCACGTTCGGTGCTGGGACCAAGCTGGAGCTGAAA (SEQ ID NO:
24)

8-J17 Heavy Chain Variable Region

CAGGTCCAGCTGCAGCAGTCTGGGGCTGAACTGGCAAAACCTGGGGCCTCAGTGAA
GATGTCCTGCAAGGCTTCTGGCTACACCTTTACTAACTACTGGATGCACTGGGTAAA
ACAGAGGCCTGGACAGGGTCTGGAATGGATTGGATACATTAATCCTAACAATGGTT
ATACTGAGTACAATCAGCGATTCAAGGACAAGGCCACATTGACTGCAGACAGATCC
TCCACCACAGCCTACATGCAACTAAGCAGCCTGACATCTGAGGACTCTGCAGTCTAT
TACTGTGCAAGATCCGATATCATTACGACAGACTACTGGGGCCAAGGCACCACTCTC
ACAGTCTCCTCA (SEQ ID NO: 25)

8-J17 Light Chain Variable Region

GATGTTGTGATGACCCAACTCCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCC
TCCATCTCTTGCAGATCTAGTCAGAGCCTTGTATATAGTAATGGAAATACCTATTTAC
ATTGGTACCTGCAGAAGCCAGGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCA
ACCGATTTTCTGGGGTCCCAGACAGGTTCAAGTGGCAGTGGATCAGGGACAGATTTCA
CACTCAAGATAAGCAGAGTGGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAA
GTACACATGTTCCGTGGACGTTCCGGTGGAGGCACCAAGCTGGAAATCAAA (SEQ ID
NO: 26)

6-O12 Heavy Chain Variable Region

GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAA
ACTCTCTTGTGCTGCCTCTGGATTCACTTTTAGTGACGCCTGGATGGACTGGGTCCGC
CAGTCTCCAGAGGCGGGGCTTGAGTGGGTTGCTGAAATTAGAAACAAAGCTCATAA
TCCTGCAACATACTATGCTGAGTCTGTGAAAGGGAGATTCACCATCTCAAGAGATGA
TTCCAAAAGTAGTGTCTACCTGCAAAATGAACAGCTTAAGAGCTGAAGACACTGGCA
TTTATTACTGTACCTTAGTAGCCCTGATGCTATGGACTACTGGGGTCAAGGAACCT
CAGTCACCGTCTCCTCA (SEQ ID NO: 27)

6-O12 Light Chain Variable Region

GACATTGTGATGTCACTGTCTCCATCCTCCCTAGCTGTGTCAGTTGGAGAGAAGGTT
ACTATGAGCTGCAAGTCCAGTCAGAGCCTTTTATATAGTCGCAATCAAAAGAACTAC
TTGGCCTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATTTACTGGGCA
TCCACTAGGGCATCTGGAGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGAT
TTCCTCTCACCATCAGCAGTGTGAAGGCTGAAGACCTGGCAGTTTATTACTGTGAG
CAATATTATAGCTATCCGTACACGTTCCGGAGGGGGGACCAAGCTGGAAATAAAA
(SEQ ID NO: 28)

10-L15 Heavy Chain Variable Region

CAGGTCCAACTGCAGCAGTCTGGGCCTGAGCTGGTGAGGCCTGGGGCTTCAGTGAA
GATGTCCTGCAAGGCTTCAGGCTATACCTTCACCAGCTACTGGATGCACTGGGTGAA
ACAGAGGCCTGGACAAGGCCTTGAGTGGATTGGCATGATTGATCCTTCCAATAGTGA
AACTTGGTTAAATCAGAAGTTCAAGGACAAGGCCACATTGAATGTAGACAAATCCT
CCAACACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCAGTCTATT
ACTGTGCAAGATATGATGGTTACTACGACTACTGGGGCCAAGGCACCACTCTCACAG
TCTCCTCA (SEQ ID NO: 29)

10-L15 Light Chain Variable Region

AACATTGTGCTGACCCAATCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCC
ACCATATCCTGCAGAGCCAGTGAAAGTGTTGATAGTTATGGCAATAGTTTTATGCAC
TGGTACCAGCAGAAACCAGGACAGCCACCCAACTCCTCATCTATCTTGCATCCAAC
GTAGAATCTGGGGTCCCTGCCAGGTTTCAGTGGCAGTGGGTCTAGGACAGACTTCACC
CTCACCATTGATCCTGTGGAGGCTGATGATGCTGCAACCTATTACTGTCAGCAAAAT
AATGAGGATCCGTGGACGTTTCGGTGGAGGCACCAAGCTGGAAATCAAA (SEQ ID
NO: 30)

7-H14 Heavy Chain Variable Region

CAGGTCCAAGTGCAGCAGCCTGGGGCTGAGCTGGTGAGGCCTGGGGCTTCAGTGAA
GCTGTCCTGCAAGCCTTCTGGCTACACCTTCACCAGCTACTGGATGAACTGGGTGAA
GCAGAGGCCTGGACAAGGCCTTGAATGGATTGGTATGATTGATCCTTCAGACAGTG
AACTCACTACAATCAAATGTTCAAGGACAAGGCCACATTGACTGTTGACAAATCCT
CCAACACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATT
ACTGTGCGCAGATCTACTATGCTTACGACAAGGCTTACTGGGGCCAAGGGACTCTGG
TCACTGTCTCTGCA (SEQ ID NO: 31)

7-H14 Light Chain Variable Region

GACATTGTGATGTACAGTCTCCATCCTCCCTAGCTGTGTTCAGTTGGAGAGAAGGTT
ACTATGAGCTGCAAGTCCAGTCAGAGCCTTTTATATAGTAGCCATCAAAAGAACTAC
TTGGCCTGGTACCAGCAGAAACCAGGGCAGTCTCCTAACTGCTGATTTACTGGGCA
TCCACTAGGGAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGAT
TTCAGTCTCACCATCAGCAGTGTGAAGGCTGAAGACCTGGCAGTTTATTACTGTCAG
GAATATTATAGCTGGACGTTTCGGTGGAGGCACCAAGCTGGAAATCAAA (SEQ ID
NO: 32)

6-B21 Heavy Chain Variable Region

GAGGTCCAGCTGCAACAATCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAA
GATATCCTGTAAGGCTTCTGGATACACGTTCACTGACTACTACATGAACTGGGTGAA
GCAGAGCCATGGAAAGAGCCTTGAGTGGATTGGAGATATTAATCCTCACAATGGTG
GTACTAGCTTCATCCAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAGTCCT
CCAGCACAGCCTACATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCAGTCTATT
ATTGTGCCCTCTGGGACGAAAGGAGGGGTTTGCTTACTGGGGCCAAGGGACTCTG
GTCACTGTCTCTGCA (SEQ ID NO: 33)

6-B21 Light Chain Variable Region

GACACTGTGCTGACACAGTCTCCTGCTTCCTTAGTTGTATCTCTGGGGCAGAGGGCC
ACCATCTCATGCAGGGCCAGCAAAAGTGTCAGTACATCTGGCTATAGTTATATGCAC
TGGTACCAACAGAAACCAGGACAGCCACCCAACTCCTCATCTATCTTGCATCCAAC
CTAGAATCTGGGGTCCCTGCCAGGTTTCAGTGGCAGTGGGTCTGGGACAGCCTTCACC
CTCAACATCCATCCTGTGGAGGAGGAGGATGCTGCAACCTATTACTGTCAGCACAGT
AGGGAGCTTCCGTACACGTTTCGGAGGGGGGACCAAGCTGGAAATAAAA (SEQ ID
NO: 34)

10-F23 Heavy Chain Variable Region

CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCCAGACCCTCAGT
CTGACTTGTTCTTTCTCTGGGTTTTCACTGAGCACTTTTGCTATGGGTGTAGGCTGGA
TTCGTCAGCCTTCAGGGAAGGGTCTGGAGTGGCTGGCACACATTTGGTGGGATGATG
ATAAGTACTATAACCCAGCCCTGAAGAGCCGGCTCACAATCTCCAAGGATACCTCC
AAAAACCATGTATTCCTCAAGATCGCCAATGTGGACACTGCAGATACTGCCACATAC
TACTGTGCTCGAATGCCGCTAACTTTCTACTTTGACTACTGGGGCCAAGGCACCACT
CTCACAGTCTCCTCA (SEQ ID NO: 35)

10-F23 Light Chain Variable Region

GATGTTTTGCTGACCCAACTCCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCCT
CCATCTCTTGAGATCTAGTCAGAGCATTGTACATAGTAATGGACACACCTATTTAG
AATGGTACCTGCAGAAACCAGGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCA
ACCGATTTTCTGGGGTCCCAGACAGGTTCAAGTGGCAGTGGATCAGGGACAGATTTCA
CACTCAAGATCAGCAGAGTGGAGGCTGAGGATCTGGGAGTTTATTACTGCTTTCAAG
GTTACATGTTCCGTTACGTTTCGGAGGGGGGACCAAGCTGGAAATAAAA (SEQ ID
NO: 36)

6-A12 Heavy Chain Variable Region

CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCCAGACCCTCAGT
CTGACTTGTTCTTTCTCTGGGTTTTCACTGAGAACTTTTGCTATGGGTGTAGGCTGGA
TTCGTCAGCCTTCAGGGAAGGGTCTGGAGTGGCTGGCACACATTTGGTGGGATGATG
ATAAGTACTATAACCCAGCCCTGAAGAGCCGGCTCACAATCTCCAAGGATACCTCC
AAAAACCAAGGTATTCCTCAAGATCGCCAATGTGGACACTGCAGATACTGCCACATA
CTACTGTGCTCGAATGCCGCTAACTTTCTACTTTGACTACTGGGGCCAAGGCACCAC
TCTCACAGTCTCCTCA (SEQ ID NO: 37)

6-A12 Light Chain Variable Region

GATGTTTTGATGACCCAACTCCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCCT
CCATCTCTTGAGATCTAGTCAGAGCATTGTACATAGTAATGGAAACACCTATTTAG
AATGGTACCTGCAGAAACCAGGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCA
CCCGATTTTCTGGGGTCCCAGACAGGTTCAAGTGGCAGTGGATCAGGGACAGATTTCA
CACTCAAGATCAGCAGAGTGGAGGCTGAGGATCTGGGAGTTTATTACTGCTTTCAAG
GTTACATGTTCCGTTACGTTTCGGAGGGGGGACCAAGCTGGAAATAAAA (SEQ ID
NO: 38)

6-M8 Heavy Chain Variable Region

CAGGTCCAACTGCAGCAGCCTGGGGCTGAACTTGTGATGCCTGGGGCTTCAGTGAA
GCTGTCCTGCAAGGCTTCTGGCTACACCTTACCAACTACTGGATGCACTGGGTGAA
ACAGAGGCCTGGACAAGGCCTTGAGTGGATCGGAGAGATTGATCCTTCTGATAGTT
ATACTAACTACAATCAAAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAATCC
TCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTAT
TACTGTACAAGACAGGGTAGTACCTACGCGTGGGGTCAAGGAACCTCAGTCACCGT
CTCCTCA (SEQ ID NO: 39)

6-M8 Light Chain Variable Region

GATATTGTGATGACGCAGGCTGCATTCTCCAATCCAGTCACTCTTGGAACATCAGCT
TCCATCTCCTGCAGGTCTAGTAAGAGTCTCCTACATAGTAATGGCATCACTTATTTGT
ATTGGTATCTGCAGAAGCCAGGCCAGTCTCCTCAGCTCCTGATTTATCAGATGTCCA
ACCTTGCCTCAGGAGTCCCAGACAGGTTTCAGTAGCAGTGGGTCAGGAACTGATTTCA
CACTGAGAATCAGCAGAGTGGAGGCTGAGGATGTGGGTGTTTATTACTGTGCTCAA
AATCTAGAACTTCTCCGACGTTTCGGTGGAGGCACCAAGCTGGAAATCAAA (SEQ ID
NO: 40)

2-A3 Heavy Chain Variable Region

GAGGTCCAGCTGCAACAATCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAA
GATGTCCTGTAAGGCTTCTGGATACACATTCAGTACTACTACATGATGTGGGTGAA
GCAGAGTCATGGAAAGAGCCTTGAGTGGATTGGAGATATTAATCCTTACAATGGTG
GTTCTAGCTACAACCCGAAGTTCAAGGGCAGGGCCACATTGACTGTAGACAAATCCT
CCAGCACAGCCTACATGCAGCTCAACAGCCTGACATCTGAGGACTCTGCAGTCTATT
ACTGTGCAAGAGGGACTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCA (SEQ
ID NO: 41)

2-A3 Light Chain Variable Region

GATGTTGTGATGACCCAGACTCCACTCACTTTGTTCGGTTACCATTGGACAACCAGCC
TCCATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGCTGGAAAGACATATTTG
AATTGGTTGTTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATGTATCTGGTGTCT
AAACTGGACTCTGGAGTCCCTGACAGGTTCACTGGCAGCGGATCAGGGACAGATTT
CACACTGAAAATCAGCAGAGTGGAGGCTGAGGATTTGGGAGTTTATTATTGCTGGC
AAGGTACACATTTTCCGTACACGTTTCGGAGGGGGGACCAAGCTGGAAATAAAA
(SEQ ID NO: 42)

6-O17 Heavy Chain Variable Region

CAGGTCCAACCTGCAGCAGCCTGGGGCTGAGCTTGTGAAGCCTGGGGCTTCAGTGAA
GTTGTCCTGCAAGGCTTCTGGCTACACCTTACCAGCTACTGGATGCACTGGATAAA
GCAGAGACCTGGACAAGGCCTTGAGTGGATTGGAGAGATTAACCCTAGCAATGGTG
GTTCTAACTACAATGAGAAGTTCAAGAGCAAGGCCCACTGACTGTAGACAAATCC
TCCAGCACAGCCTACATGCAACTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTAT
CACTGTAAAAGCAGAGGCTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA
(SEQ ID NO: 43)

6-O17 Light Chain Variable Region

GATGTTGTGATGACCCAGACTCCACTCACTTTGTTCGGTTACCATTGGACAACCAGCC
TCCATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTTATGGAAAGACATATTTG
AATTGGTTGTTACAGCGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGGTGTCT
AAATTGGACTCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTT
ACACTGAAAATCAGCAGAGTGGAGGCTGAGGATTTGGGAATTTATTATTGCTGGCA
AGGTACACATTTTCTCACACGTTTCGGCTCGGGGACAAAGTTGGAAATAAAA (SEQ
ID NO: 44)

3-G5 Heavy Chain Variable Region

CAGGTTTCAGCTGCAGCAGTCTGGAGCTGAGCTGGCGAGGCCTGGGGCTTCAGTGAA
ACTGTCCTGCAAGGCTTCTGGCTACACCTTCACAAGCTATGGTATAAGCTGGGTGAA
ACAGAGAACTGGACAGGGCCTTGAGTGGATTGGAGAGATTTTTCCTAGAAGTAGTA
ATACTTACTATAATGAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGACAAGTCC
TCCAGCACAGTGTACATGGAGTTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTAT
TTCTGTGCAAGAGAGGGGGGCCTGGCCTGGTTTGCTTACTGGGGCCAAGGGACTCTG
GTCACTGTCTCTGCA (SEQ ID NO: 45)

3-G5 Light Chain Variable Region

GATGTTGTGATGACCCAGACTCCACTCACTTTGTGCGTTACCATTGGACAACCAGCT
TCCATCTCTTGCAAGTCAAGTCAGAGCCTCTTATATACTAATGGAAACACCTATTTG
AATTGGTTATTACAGAGGCCAGGCCAGTCTCCAAAACGCCTAATCTATCTGGTGTCT
AAATTGGACTCTGGAATCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTC
ACACTGAGAATCAGCAGAGTGGAGGCTGAGGATTTGGGAGTTTATTACTGCTTGCA
GAGTACACATTTTCATTACGTTTCGGCTCGGGGACAAAGTTGGAAATAAAA (SEQ
ID NO: 46)

6-A15 Heavy Chain Variable Region

GAGGTCCAGCTGCAACAATCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAA
GATGTCCTGTAAGGCTTCTGGATACACAATCACTGACTACTACATGATGTGGTTGAA
GCAGAGTCATGGAAAGAGCCTTGAATGGATTGGAGATATTAATCCTTACACTGGTG
GTACTAGCTACAACCAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAATCC
TCCAGCACAGCCTACCTGCAGCTCCACAGCCTGACATCTGAGGACTCTGCAGTCTAT
TACTGTGCAAGAGGGGCCTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA
(SEQ ID NO: 47)

6-A15 Light Chain Variable Region

GATGTTGTGATGACCCAGACTCCACTCACTTTGTGCGTTACCATTGGACAACCAGCC
TCCATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGATGGAAAGACATATTTG
AATTGGTTGTTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGGTGTCT
AAACTGGACTCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTC
ACACTGAAAATCAGCAGAGTGGAGGCTGAGGATTTGGGAGTTTATTATTGCTGGCA
AGGTACACATTTTCGTACACGTTTCGGAGGGGGGACCAAGCTGGAAATAAAA (SEQ
ID NO: 48)

10-K10 Heavy Chain Variable Region

GAGGTCCAGCTGCAACAATCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAA
GATGTCCTGTAAGGCTTCTGGATACACAATCACTGACTACTACATGATGTGGTTGAA
GCAGAGTCATGGAAAGAGCCTTGAATGGATTGGAGATATTAATCCTTACACTGGTG
GTACTAGCTACAACCAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAATCC
TCCAGCACAGCCTACATGCAGCTCAACAGCCTGACATCTGAGGACTCTGCAGTCTAT
TACTGTGCAAGAGGGGCCTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA
(SEQ ID NO: 49)

10-K10 Light Chain Variable Region

GATGTTGTGATGACCCAGACTCCACTCACTTTGTCTGGTTACCATTGGACAACCAGCC
TCCATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGATGGAAAGACATATTTG
AATTGGTTGTTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGGTGTCT
AAACTGGACTCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTT
ACACTGAAAATCAGCAGAGTGGAGGCTGAGGATTTGGGAGTTTATTATTGCTGGCA
AGGTACACATTTTCCGTACACGTTCTGGAGGGGGGACCAAGCTGGAAATAAAA (SEQ
ID NO: 50)

6-P20 Heavy Chain Variable Region

GAGGTCCAGCTGCAACAATCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAA
GATATCCTGTAAGGCTTCTGGATACACGTTCACTGACTACTACATGAAGTGGGTGAA
GCAGAGCCATGGCAGGAGCCTTGAGTTGATTGGAGATATTAATCCTAACAATGGTG
GTTCTAACTTCAACCAGAAGTTCAGGGGCAAGGCCACATTGACTGTAGACAAGTCCT
CCAGCACAGCCTATATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCAATCTATT
ACTGTGCAAGAATGGGTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCA (SEQ
ID NO: 51)

6-P20 Light Chain Variable Region

GATGTTGTGATGACCCAGACTCCACTCACTTTGTCTGGTTACCATTGGACAACCAGCC
TCCATCTCTTGCAAGTCAAGTCAGAGCCTCTTACATAGTGATGGAAAGACATATTTG
AATTGGATGTTCCAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGGTGTCT
AAACTGGACTCTGGAGTCCCTTACAGGTTCACTGGCAGTGGATCAGGGACAGATTTT
ACACTGCAAATCAGCAGAGTGGAGACTGAGGATTTGGGAGTTTATTATTGCTGGCA
AGGTACACATTTTCTCGGACGTTCTGGTGGAGGCACCAAGCTGGAAATCAAA (SEQ
ID NO: 52)

7-O8 Heavy Chain Variable Region

GAGGTCCAGCTGCAGCAGTCTGGACCTGAACTGGTCAAGCCTGGGGCTTCAGTGAA
GATGTCCTGCAAGGCTTCTGGATACACATTCAGTACTACTACATACTGGGTGAA
GCAGAAAGCCTGGGCAGGGCCTTGAGTACATTGGAGAGATTTATCCTGGAAGTGGTA
ATACTTACTACAATGGGAAGTTCAGGGGCAAGGCCACACTGACTGCAGACAAGTCC
TCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCAGTCTAT
TTCTGTGGTAGTGGCTACTTTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCC
TCA (SEQ ID NO: 53)

7-O8 Light Chain Variable Region

GATGTTGTGATGACCCAGACTCCACTCACTTTGTCTGTTACCATTGGACAGCCAGCTT
CCATTTCTTGCAAGTCAAGTCAGAGCCTCTTATATAGTAATGGAAAAACCTATTTGA
ATTGGTTATTACAGAGTCCAGGCCAGTCTCCAAAGCTCCTAATCTATCTGGTGTCTA
AACTGGAATCTGGAGTCCCTGACAGATTCACTGGCAGTGGATCAGGGACAGATTTT
ACACTGAAACTCAGCAGAGTGGAGGCTGAGGATTTGGGAGTATATTACTGCGTGCA
AGGTACACATTTCCATTACGTTCTGGCTCGGGGACAAAGTTGGAAATAAAA (SEQ
ID NO: 54)

Rabbit mAb sequences

A11B1_16G7 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGTTCAAAGGTGTCCAGTGT
CAGGAGCAACTGGTGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGAC
ACTCACCTGCACAGCCTCTGGATTCTCCTTCAATAAGAATTATTGGATGTGCTGGGT
CCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGATGCATTTATAATGGTGATG
GCAACACATACTACGCGAGCTGGGTGAATGGCCGATTACCATCTCCAAAACCTCGT
CGACCACGGTGACTCTGCAAATGACCAGTCTGACAGTCGCGGACACGGCCATCTATT
TCTGTGCGAGACTACTTAATATGTGGGGCCCAGGCACCCTGGTCACCGTCTCCTCAG
GGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCTGCTGCGGGGACACACCCA
GCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCTCCCGGAGCCAGTGACC
GTGACCTGGAACCTCGGGCACCCCTACCAATGGGGTACGCACCTTCCCGTCCGTCCGG
CAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCAGCCA
GCCCCGTACCTGCAACGTGGCCACCCAGCCACCAACACCAAAGTGAGACAAGACCG
TTGCGCCCTCGACATGCAGCAAGCCCATGTGCCACCCCCCTGAACTCCCGGGGGGAC
CGTCTGTCTTCATCTTCCCCCAAAAACCCAAGGACACCCTCATGATCTCACGCACCC
CCGAGGTACATGCGTGGTGGTGGACGTGAGCCAGGATGACCCCGAGGTGCAGTTC
ACATGGTACATAAAACAACGAGCAGGTGCGCACCCGCCCGCCGCTACGGGAGCA
GCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCCTCCCCATCGCGCACCAAGGACT
GGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAGGCACTCCCGGCCCCC
ATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCCTGGAGCCGAAGGTCTACAC
CATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTGCGTCAGCCTGACCTGCATGA
TCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAGAAGAACGGGAAGGCA
GAGGACAACTACAAGACCACGCCGACCGTGCTGGACAGCGACGGCTCCTACTTCT
CTACAGCAAGCTCTCAGTGCCACGAGTGAGTGGCAGCGGGGCGACGTCTTCACT
GCTCCGTGATGCACGAGGCCTTGACACAACCACTACACGCAGAAGTCCATCTCCCGCT
CTCCGG GTAAATAG (SEQ ID NO: 55)

A11B1_16G7 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTACTGCTCTGGCTCCCAGGT
GCCAGATGTGCTGACATTGTGATGACCCAGACTCCAGCCTCCGTGGAGGCAGCTGTG
GGAGGCACAGTCACCATCAAGTGCCAGGCCAGTGAGAGCATTGGCAATGCATTAGC
CTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTATACTGCAGCCAC
TCTGGCATCTGGGGTCCCATCGCGGTTACGCGGCAGTGGATCTGGGACAGAGTTCAC
TCTACCATCAGTGGCGTGCAGTGTGACGATGCTGCCACTTACTACTGTCAAAGCTA
TTATTTTACTAGTGTTAGTAGTTATGGCAATGCTTTCGGCGGAGGGACCGAGGTGGT
GGTCAAAGGTGATCCAGTTGCACCTACTGTCTCATCTTCCCACCAGCTGCTGATCA
GGTGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGT
CACCGTCACCTGGGAGGTGGATGGCACCACCCAAACAACCTGGCATCGAGAACAGTA
AAACACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGA
CCAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACG
ACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 56)

A11B1_16E10 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACT

CACCTGCAGAGTCTCTGGATTCTCCTTCAGTAGCAGTTATTATATGTGTTGGGTCCGC
CAGGCTCCAGGGAAGGGGCTGGAATGGATCGCATGTATTGGTACTACTCGTGGTAG
CACTTACTACGCGACCTGGGCGAAAGGCCGATTACCATTTCTAAAATCTCGTCGAC
CACGGTGACTCTACAAATGACCAGTCTGACAGACGCGGACACGGCCACCTATTTCTG
TGCGAGAGATGCTACTGGTTATAGGATTAACACGATTGGCCTCTATTTTAATTTGTG
GGGCCCAGGCACCTGGTCACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTT
CCCCTGGCCCCCTGCTGCGGGGACACACCCAGCTCCACGGTGACCTGGGCTGCCT
GGTCAAAGGCTACCTCCCGGAGCCAGTGACCGTGACCTGGAACCTCGGGCACCTCA
CCAATGGGGTACGCACCTTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGA
GCAGCGTGGTGAGCGTGACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGCCAC
CCAGCCACCAACACCAAAGTGGACAAGACCGTTGCGCCCTCGACATGCAGCAAGCC
CATGTGCCCACCCCTGAACTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCCAA
ACCCAAGGACACCTCATGATCTCACGCACCCCGAGGTACATGCGTGGTGGTGG
ACGTGAGCCAGGATGACCCCGAGGTGCAGTTCACATGGTACATAAACACGAGCAG
GTGCGCACCGCCCGGCCCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGT
GGTCAGCACCTTCCCATCGCGCACCAAGGACTGGCTGAGGGGCAAGGAGTTCAAGT
GCAAAGTCCACAACAAGGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCC
AGAGGGCAGCCCCTGGAGCCGAAGGTCTACACCATGGGCCCTCCCGGGAGGAGCT
GAGCAGCAGGTCGGTCAGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACAT
CTCGGTGGAGTGGGAGAAGAACGGGAAGGCAGAGGACAACCTACAAGACCACGCCG
ACCGTGCTGGACAGCGACGGCTCCTACTTCCTCTACAGCAAGCTCTCAGTGCCACG
AGTGAGTGGCAGCGGGGCGACGTCTTCACCTGCTCCGTGATGCACGAGGCCTTGCA
CAACCACTACACGCAGAAGTCCATCTCCCGCTCTCCGGGTAAATAG (SEQ ID NO:
57)

A11B1_16E10 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCAGATGTGCGTTTGAATTGACCCAGACTCCATCCTCCGTGGAGGCTGCTGTGGGA
GGCACGCCACCATCAAGTGCCAGGCCAGTCAGACCATTTACAGTTACTTATCTGG
TATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTATGAAGCGTCCAACT
GGCCTCTGGGGTCCCATCGCGGTTACGCGGCAGTGGATCTGGGACAGACTACACTCT
CACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTACTACTGTCAAAGCTATCA
TGGTACTGCTAGTACTGAATATAATACTTTTCGGCGGGGGGACCGAGGTGGTGGTCAG
AGGTGATCCAGTTGCACCTACTGTCTCATCTTCCCACCAGCTGCTGATCAGGTGGC
AACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTACCGT
CACCTGGGAGGTGGATGGCACCAACCAAACTGGCATCGAGAACAGTAAACAC
CGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAGCA
CACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACCTCA
GTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 58)

A11B1_15G10 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGCAGCAGCTGGTGGAGTCCGGGGGAGGCCTGGTCAAGCCTGGGGCAGCCCTGAC
ATTCACCTGCACAGCCTCTGGATTCTCCTTCAGTGGCAATTATTGGATATGCTGGGTC
CGCCAGGCTCCAGGGAAGGGGTTGGAGTGGATCGCGTGCATTGGTACTATTACTAGT
AGGACATACTACGCGAGCTGGGCGAAAGGCCGATTACCATTTCCAAAACCTCGTC

GACCACGGTGACTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACGTATT
TCTGTGCGAGAGGTGCGGTTGTTAGTAGTGGTAATGCTCCCTACTACTTTACCTTGTG
GGGCCCAGGCACCTTGGTCACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTT
CCCACTGGCCCCCTGCTGCGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCT
GGTCAAAGGCTACCTCCCGGAGCCAGTGACCGTGACCTGGAACCTCGGGCACCTCA
CCAATGGGGTACGCACCTTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGA
GCAGCGTGGTGAGCGTGACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGCCAC
CCAGCCACCAACACCAAAGTGGACAAGACCGTTGCGCCCTCGACATGCAGCAAGCC
CATGTGCCCCACCCCTGAACTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCCAAA
ACCCAAGGACACCTCATGATCTCACGCACCCCGAGGTACATGCGTGGTGGTGG
ACGTGAGCCAGGATGACCCCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAG
GTGCGCACCGCCCGGCCGCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGT
GGTCAGCACCTTCCCATCGCGCACCAAGGACTGGCTGAGGGGCAAGGAGTTCAAGT
GCAAAGTCCACAACAAGGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCC
AGAGGGCAGCCCTGGAGCCGAAGGTCTACACCATGGGCCCTCCCGGGAGGAGCT
GAGCAGCAGGTGCGTCAGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACAT
CTCGGTGGAGTGGGAGAAGAACGGGAAGGCAGAGGACAACCTACAAGACCACGCCG
ACCGTGCTGGACAGCGACGGCTCCTACTTCCTCTACAGCAAGCTCTCAGTGCCACG
AGTGAGTGGCAGCGGGGCGACGTCTTCACCTGCTCCGTGATGCACGAGGCCTTGCA
CAACCACTACACGCAGAAGTCCATCTCCCGCTCTCCGGGTAAATAG (SEQ ID NO:
59)

A11B1_15G10 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCAGATGTGCATTGCAATTGACGCAGACTCCATCCTCCGTGGAGGCAGCTGTGGGA
GGCACAGTCACCATCAAGTGCCAGGCCAGTCAGAGCATTAGTAGTTACTTATCCTGG
TATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTACAGGGCATCCACTCTG
GAATCTGGGGTCCCATCGCGGTTTAAAGGCAGTGGATCTGGGACAGAGTTCACTCTC
ACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTACTTCTGTCAAAGCTATTAT
GGTGTTACTTTTAGTGTTTGTCTTCGGCGGAGGGACCGAGGTGGTGGTCAAAGGT
GATCCAGTTGCACCTACTGTCTCATCTTCCCACCAGCTGCTGATCAGGTGGCAACT
GGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCACCGTCACC
TGGGAGGTGGATGGCACCACCAAACAACCTGGCATCGAGAACAGTAAAACACCGCA
GAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAGCACACA
GTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACCTCAGTCG
TCCAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 60)

A11B1_14H1 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACT
CACCTGCAAAGCCTCTGGAATCGACTTCAATAACTATTGGATAACCTGGGTCCGCCA
GGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATTTATGTTGGAATTACCGGCC
GCACATGGTACGCGAACTGGGCGAAAGGCCGATTACCATCTCCAAGGCCTCGAGC
ACGGTGGATCTGAAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATTTCTGT
GCGAGGAATGGTGTGTTGGTATTTATGCTCTTAACCTTGTGGGGCCCAGGCACCCTG
GTCACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCTGC

TGCGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCT
CCCGGAGCCAGTGACCGTGACCTGGAACCTCGGGCACCCCTACCAATGGGGTACGCA
CCTTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCG
TGACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGCCACCCAGCCACCAACACC
AAAGTGGAACAAGACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCACCCCC
TGAACCTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCCAAAACCAAGGACACCCT
CATGATCTCACGCACCCCCGAGGTCACATGCGTGGTGGTGGACGTGAGCCAGGATG
ACCCCGAGGTGCAGTTACATGGTACATAAACAACGAGCAGGTGCGCACCGCCCGG
CCGCCGTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCCTCCC
CATCGCGCACCCAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACA
AGGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCTG
GAGCCGAAGGTCTACACCATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTGCGT
CAGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGA
GAAGAACGGGAAGGCAGAGGACAACACTACAAGACCACGCCGACCGTGCTGGACAGC
GACGGCTCCTACTTCTCTACAGCAAGCTCTCAGTGCCACGAGTGAGTGGCAGCGG
GGCGACGTCTTACCTGCTCCGTGATGCACGAGGCCTTGACAACCACTACACGCAG
AAGTCCATCTCCCGCTCTCCGGGTAAATAG (SEQ ID NO: 61)

A11B1_14H1 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCACATTTGCACAAGTGCTGACCCAGACTGCATCGTCCGTGTCTGCAGCTGTGGGA
GGCACAGTCACCATCAGTTGCCAGTCCAGTCAGAGTGTTTATAATAATAATTGGTTA
GCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTACAGGGCATC
CACTCTGACATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACACAGTT
CACTCTCACCATCAGCGACCTGGAGTGTGACGATGCTGCCACTTACTACTGTGCAGG
CGGTTATAGTGGTAATATTTACGTAAATGATTTCCGCGGAGGGACCGAGGTGGTGGT
CAAAGGTGATCCAGTTGCACCTACTGTCTCATCTTCCCACCAGCTGCTGATCAGGT
GGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCAC
CGTCACCTGGGAGGTGGATGGCACCACCCAAACAACCTGGCATCGAGAACAGTAAAA
CACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCA
GCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACC
TCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 62)

A11B1_13G4 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGGAGCAGCTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGGATCCCTGAC
ACTCACCTGCAAAGCCTCTGGATTCTCCTTCAAGTAATACCTACTGGGCATGCTGGGT
CCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATGAATCCTGCTAGTA
GTGGTAGCTCTTACTACGCGAGCTGGGCGAAAGGCCGATTACCATCTCCAAAACCT
CGTCGACCACGGTGACTCTGCACATGCCAGTCTGACAGCCGCGGACACGGCCACC
TATTTCTGTGCGAAATGGGATACTGCTTTCGATGTGTGGGGCCAGGCACCCTGGTC
ACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCCTGCCCCCTGCTGC
GGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCTCCC
GGAGCCAGTGACCGTGACCTGGAACCTCGGGCACCCCTACCAATGGGGTACGCACCT
TCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTGA
CCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGCCACCCAGCCACCAACACCAAA

GTGGACAAGACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCCACCCCCTGA
ACTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCCAAACCCAAGGACACCCTCAT
GATCTCACGCACCCCGAGGTACATGCGTGGTGGTGGACGTGAGCCAGGATGACC
CCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAGGTGCGCACCGCCCGGCCG
CCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCTCCCCAT
CGCGCACCAAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAG
GCACTCCCGGGCCCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCTGGA
GCCGAAGGTCTACACCATGGGCCCCTCCCGGGAGGAGCTGAGCAGCAGGTTCGGTCA
GCCTGACCTGCATGATCAACGGCTTCTACCTTCCGACATCTCGGTGGAGTGGGAGA
AGAACGGGAAGGCAGAGGACAACATAAGACCACGCCGACCGTGCTGGACAGCGA
CGGCTCCTACTTCTCTACAGCAAGCTCTCAGTGCCACGAGTGAGTGGCAGCGGGG
CGACGTCTTCACCTGCTCCGTGATGCACGAGGCCTTGACAACCACTACACGCAGAA
GTCCATCTCCCGCTCTCCGGGTAAATAG (SEQ ID NO: 63)

A11B1_13G4 Light Chain

ATGGACACGAGGGCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCAGATGTGCCGATGTTGTGATGACCCAGACTCCATCCTCCGTGGAGGCAGCTGTG
GGAGGCACAGTCACCATCAAGTGCCAGGCCAGTCAGAGCATTAGTAGCTACTTAGC
CTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTATGGTGCATCCAA
TCTGGAGTCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGAGTACA
CTCTACCATCAGCGGCGTGACGTGTGACGATGCTGCCACTTACTACTGTCAAACT
ATTATGCTATTGATACTTATGGTCATGCTTTCGGCGGAGGGACCGAGGTGGTGGTCA
AAGGTGATCCAGTTGCACCTACTGTCTCATCTTCCCACCAAGCTGCTGATCAGGTGG
CAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAAATACTTCCCAGATGTCACCG
TCACCTGGGAGGTGGATGGCACCACCAAACAACACTGGCATCGAGAACAGTAAAACA
CCGCAGAAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAGC
ACACAGTACAACAGCCACAAGAGTACACCTGCAAGGTGACCCAGGGCACGACCTC
AGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 64)

A11B1_13C3 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGGAGCAGCTGGAGGAGTCCGGGGGAGACCTGGTCAAAGCCTGGGGCATCCCTGAC
ACTCACCTGCACAGCCTCTGGATTCTCCTTTAGTAGCAACTATCACATCTGCTGGGTC
CGCCAGGCTCCAGGAAAGGGGCTGGAGTTGATCGCATGCATTTATGTTGGTGATGGC
AGCACATACTACGCGAGCTGGGCGAAAGGCCGATTACCATCTCCAAATCCTCGTC
GACCACGGTAGCTCTGCAAATGACCAAGTCTGACAGCCGCGGACACGGCCACCTATT
TCTGTGGGAGAATGTTTAACTTGTGGGGCCCAGGCACCCTGGTCACCGTCTCCTCAG
GGCAACCTAAGGCTCCATCAGTCTTCCCCTGACCCCTGCTGCGGGGACACACCCA
GCTCCACGGTGACCTGCGGCTGCCTGGTCAAAGGCTACCTCCCGGAGCCAGTGACC
GTGACCTGGAACCTCGGGCACCTCACCAATGGGGTACGCACCTTCCCGTCCGTCCGG
CAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAAGCTGACCTCAAGCAGCCA
GCCCCGTACCTGCAACGTGGCCACCCAGCCACCAACACCAAAGTGGAACAAGACCG
TTGCGCCCTCGACATGCAGCAAGCCCATGTGCCACCCCCCTGAACCTCCCGGGGGGAC
CGTCTGTCTTCATCTTCCCCCAAACCCAAGGACACCCTCATGATCTCACGCACCC
CCGAGGTACATGCGTGGTGGTGGACGTGAGCCAGGATGACCCCGAGGTGCAGTTC
ACATGGTACATAAACAACGAGCAGGTGCGCACCGCCCGGCCGCGCTACGGGAGCA

GCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCCTCCCCATCGCGCACCCAGGACT
GGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAGGCACTCCCGGGCCCCC
ATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCTGGAGCCGAAGGTCTACAC
CATGGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTCGGTCAGCCTGACCTGCATGA
TCAACGGCTTCTACCTTCCGACATCTCGGTGGAGTGGGAGAAGAACGGGAAGGCA
GAGGACAACTACAAGACCACGCCGACCGTGCTGGACAGCGACGGCTCCTACTTCT
CTACAGCAAGCTCTCAGTGCCACGAGTGAGTGGCAGCGGGGCGACGTCTTCACCT
GCTCCGTGATGCACGAGGCCTTGACACAACCACTACACGCAGAAGTCCATCTCCCGCT
CTCCGGGTAAATAG (SEQ ID NO: 65)

A11B1_13C3 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCATATGTGACCCTGTGCTGACCCAGACTCCATCCTCCGTGTCTGCGGGCTGTGGGA
GTCACAGTCACCATCAACTGCCAGTCCAGTCCGAGTGTTTATAGTAACTACTTATCC
TGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTCATCTATCTGGCATCTACT
CTGGCATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACACAGTTCCT
CTCACCATCAGCGACGTGCAGTGTGACGATGCTGCCACTTACTACTGTGCAGGCACT
TATAGTGGTAATATTTGGTCTTTCGGCGGAGGGACCGAGGTGGTGGTCAAAGGTGAT
CCAGTTGCACCTACTGTCCTCATCTTCCCACCAGCTGCTGATCAGGTGGCAACTGGA
ACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCACCGTCACCTGG
GAGGTGGATGGCACCACCCAAACAACCTGGCATCGAGAACAGTAAAACACCGCAGA
ATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAGCACACAGT
ACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACCTCAGTCGTC
CAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 66)

A11B1_12F2 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGCAGCAGCTGGTGGAGTCCGGGGGAGGCCTGGTCAAGCCTGGGGCATCCCTGAC
ACTCACCTGCACAGCCTCTGGATTCTCCTTCAGTAGCGGCTATCACATGTGCTGGGT
CCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCTTTGGTGTTTATACTGG
TACCACTACCTACGCGAGCTGGGCGAAAGGTCGATTACCATCTCCAAAACCTCGTC
GACCACGGTGACTCTACAAATGACCAGTCTAACAGTCGCGGACACGGCCACCTATTT
CTGTGCGAGAATCAGTGCTGAAAATGGTGGGGACTTGTGGGGCCCAGGCACCCTGG
TCACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCCTGCCCCCTGCT
GCGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCTC
CCGGAGCCAGTGACCGTGACCTGGAACCTCGGGCACCCCTACCAATGGGGTACGCAC
CTTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGT
GACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGCCCACCCAGCCACCAACACCA
AAGTGGAACAAGACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCCACCCCT
GAACTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCCAAACCCAAGGACACCCTC
ATGATCTCACGCACCCCGAGGTACATGCGTGGTGGTGGACGTGAGCCAGGATGA
CCCCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAGGTGCGCACCGCCCGGC
CGCCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCCTCCCC
ATCGCGCACCAAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAA
GGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCTGG
AGCCGAAGGTCTACACCATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTGCGTC

AGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAG
AAGAACGGGAAGGCAGAGGACAACCTACAAGACCACGCCGACCGTGTGGACAGCG
ACGGCTCCTACTTCCTCTACAGCAAGCTCTCAGTGCCACGAGTGAGTGGCAGCGGG
GCGACGTCTTCACCTGCTCCGTGATGCACGAGGCCTTGACACAACCACTACACGCAGA
AGTCCATCTCCCGCTCTCCGGGTAAATAG (SEQ ID NO: 67)

A11B1_12F2 Light Chain

ATGGACACGAGGGCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCAGATGTGATGTTGTGATGACCCAGACTCCAGCCTCCGTGGAGGCAGCTGTGGG
AGGCACAGTCACCATCAAGTGCCAGGCCAGTCAGAGCATTAGCAACTACTTTTCTTG
GTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTACAGGGCGTCCACTCT
GGCATCTGGGGTCCCATCGCGGTTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCT
CACCATCAGCGACCTGGAGTGTGCCGATTCTGCCACTTACTACTGTCACTGCACTTA
TGGTAGTAGTAGTACTGGTTTTGGTTTCGGCGGAGGGACCGAGGTGGTGGTCAAAG
GTGATCCAGTTGCACCTACTGTCCCCATCTTCCACCAGCTGCTGATCAGGTGGCAA
CTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCACCGTCA
CCTGGGAGGTGGATGGCACCACCCAAACAACCTGGCATCGAGAACAGTAAAACACCG
CAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAGCACA
CAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACCTCAGT
CGTCCAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 68)

A11B1_11D10 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACT
CACCTGCATGGCCTCTGGAATCGACTTCAGTAGCGGCTACGGCATGTGGTGGGTCCG
CCAGGCTCCAGGGAAGGGACTGGAGTATATCGGATACATTGATACTGGTGATGATA
ACACATACTACGCGAACTGGGCGAAAGGCCGATTACCATCTCCAAAACCTCGTCG
ACCACGGTGACTCTGCAAAATGACCAGTCTGACAGTCGCGGACACGGCCACCTATTTT
TGTGCGAAAGGGGGCGCCATAGACCTCTGGGGGCCAGGGACCTCGTCACCGTCTC
TTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCTGCTGCGGGGACAC
ACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCTCCCGGAGCCAGT
GACCGTGACCTGGAACCTCGGGCACCTCACCAATGGGGTACGCACCTTCCCGTCCGT
CCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCA
GCCAGCCCGTCACCTGCAACGTGGCCACCCAGCCACCAACACCAAAGTGGACAAG
ACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCCACCCCTGAACTCCCGGGG
GGACCGTCTGTCTTCATCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCACGC
ACCCCGAGGTACATGCGTGGTGGTGGACGTGAGCCAGGATGACCCCGAGGTGCA
GTTACATGGTACATAAACAACGAGCAGGTGCGCACCGCCCGGCCCGCTACGGG
AGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCTCCCCATCGCGCACCAAG
GACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAGGCACTCCCGGC
CCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCCTGGAGCCGAAGGTCT
ACACCATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTTCGGTCAGCCTGACCTGC
ATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAGAAGAACGGGAA
GGCAGAGGACAACCTACAAGACCACGCCGACCGTGTGGACAGCGACGGCTCCTACT
TCCTCTACAGCAAGCTCTCAGTGCCACGAGTGAGTGGCAGCGGGGCGACGTCTTCA

CCTGCTCCGTGATGCACGAGGCCTTGCACAACCACTACACGCAGAAGTCCATCTCCC
GCTCTCCGGGTAAATAG (SEQ ID NO: 69)

A11B1_11D10 Light Chain

ATGGACACGAGGGCCCCACTCAGCTGCTGGGACTCCTACTGCTCTGGCTCCCAGGT
GCCAGATGTGCTGACATTGTGATGACCCAGACTCCAGCCTCCGTGGAGGCAGCTGTG
GGAGGCACAGTCACCATCAAGTGCCAGGCCAGTCAGAGCATTAGTAGTTACTTAGC
CTGGTATCAGCAGAAACCAGGGCAGCGTCCCAAGCTCCTGATCTACAGGGCATCCA
CTCTAAAATCTGGGGTCCCATCGCGTTCAAAGGCAGTGGATCTGGGACAGAGTAC
ACTCTCACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTATTATTGTCAAGCG
TATTATCTTAGTAGTAGTATCAGTTATGGTAATACTTTCGGCGGAGGGACCGAGGTG
GTGGTCAAAGGTGATCCAGTTGCACCTACTGTCTCATCTTCCCACCAGCTGCTGAT
CAGGTGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGAT
GTCACCGTCACCTGGGAGGTGGATGGCACCACCCAAACAACCTGGCATCGAGAACAG
TAAACACCCGAGAAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACT
GACCAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGC
ACGACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 70)

A11B1_10F9 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCGTCCCTGACACT
CACCTGCACAGCCTCTGGATTCTCCCTCAGTAGCGGGTATGGCATGTGCTGGGTCCG
CCAGGCTCCAGGGAAGGGACTGGAGTGGATCGGATACACTGATACTGCTACTGGTA
CCATTCACTACGCGAGCTGGGCGAAAGGCCGATTACCATCTCCAAAACCTCGTCGA
CCACGGTGACTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATTTCT
GTGCGAAAGGGGGCGCCATGGACCTCTGGGGCCAGGGACCCTCGTCACCGTCTCT
TCAGGGCAACCTAAGGCTCCATCAGTCTTCCCCTGAGCCCCCTGCTGCGGGGACACA
CCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCTCCCGGAGCCAGTG
ACCGTGACCTGGAACCTCGGGCACCCCTACCAATGGGGTACGCACCTTCCCGTCCGTC
CGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCAG
CCAGCCCCTCACCTGCAACGTGGCCCCACCCAGCCACCAACACCAAAGTGAGACAAGA
CCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCACCCCTGAACTCCCGGGGG
GACCGTCTGTCTTCATCTTCCCCCAAAAACCCAAGGACACCCTCATGATCTCACGCA
CCCCCGAGGTACATGCGTGGTGGTGGACGTGAGCCAGGATGACCCCGAGGTGCAG
TTCACATGGTACATAAACAACGAGCAGGTGCGCACCGCCCGGCCGCGCTACGGGA
GCAGCAGTTCAACAGCACGATCCGCGTGGTCAAGCACCCTCCCCATCGCGCACCAAGG
ACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAGGCACTCCCGGCC
CCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCCTGGAGCCGAAGGTCTA
CACCATGGGGCCCTCCCGGGAGGAGCTGAGCAGCAGGTGCGTCAGCCTGACCTGCA
TGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAGAAGAACGGGAAG
GCAGAGGACAACCTACAAGACCACGCCGACCGTGCTGGACAGCGACGGCTCCTACTT
CCTCTACAGCAAGCTCTCAGTGCCACGAGTGAGTGGCAGCGGGGCGACGTCTTCA
CCTGCTCCGTGATGCACGAGGCCTTGCACAACCACTACACGCAGAAGTCCATCTCCC
GCTCTCCGGGTAAATAG (SEQ ID NO: 71)

A11B1_10F9 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTACTGCTCTGGCTCCCAGGT
GCCAGATGTGCTGACATTGTGATGACCCAGACTCCAGCCTCCGTGGAGGCAGCTGTG
GGAGGCACAGTCACCATCAAGTGCCAGGCCAGTCAGAGCATTAGTAGCTACTTAGC
CTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTACAGGACATCCA
CTCTGGCATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGAGTAC
ACTCTCACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTACTATTGTCAAAGC
TATGCTTATAGTAGTAGTAGCAGTTATGGTAATGCTTTCGGCGGAGGGACCGAGGTG
GTGGTCAAAGGTGATCCAGTTGCACCTACTGTCTCATCTTCCCACCAGCTGCTGAT
CAGGTGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGAT
GTCACCGTCACCTGGGAGGTGGATGGCACCACCCAAACAACCTGGCATCGAGAACAG
TAAAACACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACT
GACCAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGC
ACGACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 72)

A11B1_7H12 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACT
CACCTGCACAGGCTCTGGAATCGACTTCAGTAGCAGCTACTGGATATGCTGGGTCCG
CCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATCGATGGTAGTGATGGTA
ACACTTACTACGCGAGCTGGGCGAGAGGCCGATTACCATCTCCAAAACCTCGTCG
ACCACGGTGACTCTGCAAATGGCCAGTCTGACAGCCGCGGACACGGCCACCTATTTC
TGTACGAGAGATCTCAGGTTGTGGGGCCCAGGCACCCTGGTCACCGTCTCCTCAGGG
CAACCTAAGGCTCCATCAGTCTTCCCCTGAGCCCCCTGCTGCGGGGACACACCCAGC
TCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCTCCCGGAGCCAGTGACCGTG
ACCTGGAACCTCGGGCACCTCACCAATGGGGTACGCACCTTCCCGTCCGTCCGGCAG
TCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCAGCCAGCCC
GTCACCTGCAACGTGGCCCCACCCAGCCACCAACACCAAAAGTGGACAAGACCGTTGC
GCCCTCGACATGCAGCAAGCCCATGTGCCACCCCCTGAACTCCCGGGGGGACCGT
CTGTCTTCATCTTCCCCC AAAACCAAGGACACCCTCATGATCTCACGCACCCCCG
AGGTCACATGCGTGGTGGTGGACGTGAGCCAGGATGACCCCGAGGTGCAGTTTACA
TGGTACATAAACAACGAGCAGGTGCGCACCCGCGCCGCGCTACGGGAGCAGCA
GTTCAACAGCACGATCCGCGTGGTCAGCACCTCCCCATCGCGCACCCAGGACTGGCT
GAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAGGCACTCCCGGCCCCCATCG
AGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCTGGAGCCGAAGGTCTACACCATG
GGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTTCGGTCAGCTGACCTGCATGATCAA
CGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAGAAGAACGGGAAGGCAGAGG
ACAACCTACAAGACCACGCCGACCGTGCTGGACAGCGACGGCTCCTACTTCTCTACA
GCAAGCTCTCAGTGCCACGAGTGAGTGGCAGCGGGGCGACGTCTTCACCTGCTCC
GTGATGCACGAGGCCTTGACACAACCACTACACGCAGAAAGTCCATCTCCCGCTCTCCG
GGTAAATAG (SEQ ID NO: 73)

A11B1_7H12 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCAGATGTGCTGACATTGTGCTGACCCAGACTCCAGCCTCCGTGTCTGCAGCTGTG
GGAGGCACAGTCACCATCAACTGCCAGGCCAGTCAGAATGTTTATAGTAACAATGC
CTTAGCCTGGCATCAGCAGAAACCAGGGCAGCGTCCCAACCTCCTGATCTACAAGG

CTTCCACTCTGGCATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACAC
AGTTTACTCTCACCATCAGCGACGTGCAGTGTGACGATGCTGCCACTTACTACTGTC
TAGGCGAATTTAGTTGTAGTAGTGGTGATTGTTTTGTTTTTCGGCGGAGGGACCGAGG
TGGTGGTCAAAGGTGATCCAGTTGCACCTACTGTCTCATCTTCCCACCAGCTGCTG
ATCAGGTGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCG
ATGTCACCGTCACCTGGGAGGTGGATGGCACCACCCAAACAAGTGGCATCGAGAAC
AGTAAACACCCGCAGAAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGAC
ACTGACCAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGG
GCACGACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTAG (SEQ ID NO: 74)

A11B1_7G12 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACT
CACCTGCATGGCCTCTGGAATCGACTTCAGTAGCGGCTACGGCATGTGGTGGGTCCG
CCAGGCTCCAGGGAAGGGACTGGAGTATATCGGATACATTGATACTGGTGATGATA
ACACATACTACGCGAACTGGGCGAAAGGCCGATTACCATCTCCAAAACCTCGTCG
ACCACGGTGACTCTGCAAATGACCAGTCTGACAGTCGCGGACACGGCCACCTATTTT
TGTGCGAAAGGGGGCGCCATAGACCTCTGGGGCCCAGGGACCCTCGTCACCGTCTC
TTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCCTGCCCCCTGCTGCGGGGACAC
ACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCTCCCGGAGCCAGT
GACCGTGACCTGGAACCTCGGGCACCCCTACCAATGGGGTACGCACCTTCCCGTCCGT
CCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCA
GCCAGCCCGTCACCTGCAACGTGGCCCACCCAGCCACCAACACCAAAGTGGACAAG
ACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCACCCCCCTGAACCTCCCGGG
GGACCGTCTGTCTTCTATCTTCCCCCAAAACCCAAAGGACACCCTCATGATCTCACGC
ACCCCCGAGGTCACATGCGTGGTGGTGGACGTGAGCCAGGATGACCCCGAGGTGCA
GTTACATGGTACATAAACAACGAGCAGGTGCGCACCCGCCCGGCCGCTACGGG
AGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCCTCCCCATCGCGCACCA
GACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAGGCACTCCCGGC
CCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCTGGAGCCGAAGGTCT
ACACCATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTTCGGTCAGCCTGACCTGC
ATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAGAAGAACGGGAA
GGCAGAGGACAACCTACAAGACCACGCCGACCGTGCTGGACAGCGACGGCTCCTACT
TCCTCTACAGCAAGCTCTCAGTGCCCACGAGTGAGTGGCAGCGGGGCGACGTCTTCA
CCTGCTCCGTGATGCACGAGGCCTTGCAACCACTACACGCAGAAGTCCATCTCCC
GCTCTCCGGGTAAATAG (SEQ ID NO: 75)

A11B1_7G12 Light Chain

ATGGACACGAGGGCCCCCTCAGCTGCTGGGACTCCTACTGCTCTGGCTCCCAGGT
GCCAGATGTGCTGACATTGTGATGACCCAGACTCCAGCCTCCGTGGAGGCAGCTGTG
GGAGGCACAGTCACCATCAAGTGCCAGGCCAGTCAGAGCATTAGTAGTTACTTAGC
CTGGTATCAGCAGAAACCAGGGCAGCGTCCCAAGCTCCTGATCTACAGGGCATCCA
CTCTAAAATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGAGTAC
ACTCTCACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTATTATTGTCAAGCG
TATTATCTTAGTAGTAGTATCAGTTATGGTAATACTTTTCGGCGGAGGGACCGAGGTG

GTGGTCAAAGGTGATCCAGTTGCACCTACTGTCTCATCTTCCCACCAGCTGCTGAT
CAGGTGGCAACTGGAACAGTCAACCATCGTGTGTGTGGCGAATAAATACTTTCCCGAT
GTCACCGTCACCTGGGAGGTGGATGGCACCACCCAAACAACCTGGCATCGAGAACAG
TAAACACCCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACT
GACCAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGC
ACGACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 76)

A11B1_6G4 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGCAGCAGCTGGAGGAGTCCGGGGGAGGCCTGGTCAAGCCTGGAGGAACCCTGAC
ACTCACCTGCAAAGCCTCTGGAGTCGCCCTCAATCCCTACTACTATATGTGCTGGGT
CCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCGTGGATGCTGATAGTA
GTGGTAGCACTTACTACGCGAGCTGGGCGAAAGGCCGATTACCATCTCCAAAACC
TCGTCGACCACGGTGACTCTGAAAATGACCAGTCTGACAGCCGCGGACACGGCCAC
CTATTTCTGTGCGAGAGAATCGGTTGACTATAGTTCTGTTGGTATTGGCTATGTACAT
GGTACGGATGGCTTGTGGGGGCCAGGCACCCTGGTCACCGTCTCCTCAGGGCAACCT
AAGGCTCCATCAGTCTTCCCACTGGCCCCCTGCTGCGGGGACACACCCAGCTCCACG
GTGACCCTGGGCTGCCTGGTCAAAGGCTACCTCCCGGAGCCAGTGACCGTGACCTG
GAACTCGGGCACCTCACCAATGGGGTACGCACCTTCCCGTCCGTCCGGCAGTCCTC
AGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCAGCCAGCCCGTCA
CCTGCAACGTGGGCCACCCAGCCACCAACACCAAAGTGGAACAAGACCGTTGCGCCC
TCGACATGCAGCAAGCCCATGTGCCACCCCCCTGAACTCCCGGGGGGACCGTCTGTC
TTCATCTTCCCCC AAAACCCAAGGACACCTCATGATCTCACGCACCCCCGAGGTC
ACATGCGTGGTGGTGGACGTGAGCCAGGATGACCCCGAGGTGCAGTTCACATGGTA
CATAACAACGAGCAGGTGCGCACCGCCCGGCCGCGCTACGGGAGCAGCAGTTCA
ACAGCACGATCCGCGTGGTCAGCACCTCCCCATCGCGCACCCAGGACTGGCTGAGG
GGCAAGGAGTTCAAGTGCAAAGTCCACAACAAGGCACTCCCGGCCCCCATCGAGAA
AACCATCTCCAAAGCCAGAGGGCAGCCCTGGAGCCGAAGGTCTACACCATGGGCC
CTCCCCGGGAGGAGCTGAGCAGCAGGTGCGTCAGCCTGACCTGCATGATCAACGGC
TTCTACCTTCCGACATCTCGGTGGAGTGGGAGAAGAACGGGAAGGCAGAGGACAA
CTACAAGACCACGCCGACCGTGCTGGACAGCGACGGCTCCTACTTCTCTACAGCAA
GCTCTCAGTGCCACGAGTGAGTGGCAGCGGGGCGACGTCTTACCTGCTCCGTGAT
GCACGAGGCCTTGACAACCACTACACGCAGAAGTCCATCTCCCGCTCTCCGGGTAA
ATAG (SEQ ID NO: 77)

A11B1_6G4 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCAGATGTGCCGACATCGTGGTGACCCAGACTCCATCCTCCGTGTCTGCAGCTGTG
GGAGGCACAGTCACCATCAAGTGCCAGGCCAGTCAGAGCATTAGCAACTACTTTTCT
TGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTACAGGGCGTCCAC
TCTGGCATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGAGTTCAC
TCTACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTACTACTGTCAATGCAC
TTACGGTAGAAGTAATAGTAATTTTTTTTATGGTTTCGGCGGAGGGACCGAGGTGGT
GGTCAAAGGTGATCCAGTTGCACCTACTGTCTCATCTTCCCACCAGCTGCTGATCA
GGTGGCAACTGGAACAGTCAACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGT
CACCGTCACCTGGGAGGTGGATGGCACCACCCAAACAACCTGGCATCGAGAACAGTA

AAACACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGA
CCAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACG
ACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTAG (SEQ ID NO: 78)

A11B1_6F9 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCCGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCCTCCCTGACACT
CACCTGCACAGCCTCTGGATCCTCCTTCAGTAGTACCTACTGGAACCTGCTGGGTCCG
CCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATTAATGCTGGTAGTGTA
CCACTTACTACGCGAGCTGGGCGAAAGGCCGATTACCGTCTCCAAAACCTCGTCGA
CCACGGTGACTCTGCAAATGACCACTCTGACAGCCGCGGACACGGCCACCTATTTCT
GTACGAGAGATAGTGATGGTCGTTTTAGTAGTGGCTACTATTTTAACTTGTGGGGCC
CAGGCACCCTGGTCACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTTCCAC
TGGCCCCCTGTGCGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCA
AAGGCTACCTCCCGGAGCCAGTGACCGTGACCTGGAACCTCGGGCACCCCTACCAAT
GGGGTACGCACCTTCCCGTCCGTCCGGCAGTCTCAGGCCTCTACTCGCTGAGCAGC
GTGGTGAGCGTGACCTCAAGCAGCCAGCCCGTCACTGCAACGTGGCCACCCAGC
CACCAACACCAAAGTGGACAAGACCGTTGCGCCCTCGACATGCAGCAAGCCCATGT
GCCCCCCCCCTGAACTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCCAAAACCCA
AGGACACCCTCATGATCTCACGCACCCCCGAGGTCACATGCGTGGTGGTGGACGTG
AGCCAGGATGACCCCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAGGTGCG
CACCGCCCGGCCGCCGTACGGGAGCAGCAGTTC AACAGCACGATCCGCGTGGTCA
GCACCTTCCCCATCGCGCACCAAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAA
GTCCACAACAAGGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAGAGG
GCAGCCCCTGGAGCCGAAGGTCTACACCATGGGCCCTCCCCGGGAGGAGCTGAGCA
GCAGGTGCGTCAGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACATCTCGG
TGGAGTGGGAGAAGAACGGGAAGGCAGAGGACA ACTACAAGACCACGCCGACCGT
GCTGGACAGCGACGGCTCTACTTCTCTACAGCAAGCTCTCAGTGCCCACGAGTGA
GTGGCAGCGGGGCGACGTCTTACCTGCTCCGTGATGCACGAGGCCTTGACAAACC
ACTACACGCAGAAGTCCATCTCCCGTCTCCGGGTAAATAG (SEQ ID NO: 79)

A11B1_6F9 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCACATTTGCCAAGTGCTGACCCAGACTGCATCCCCTGTGTCTGCAGCTGTGGGA
GGCACAGTCACCATCAATTGTCAAGTCCAGTCAGAGTGTTTATGATAACA ACTGGTTA
GCCTGGTATCAGCAAAAACCAGGGCAGCCTCCCAAACCTTTGATCGACGATGCATC
CAAATTGACATCTGGGGTCTCATCGCGTTCAAAGGCAGTGGATCTGGGACGCAGTT
CACTCTCACCATCAGCGGCGTGCAGTGTGACGATGCTGCCACTTACTACTGTCAAGG
CGTTATTATAGTAGTGTTGGTACTGGGCTTTCGGCGGAGGGACCGAGGTGGTGGT
CAAAGGTGATCCAGTTGCACCTACTGTCTCATCTTCCCACCAGCTGCTGATCAGGT
GGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCAC
CGTCACCTGGGAGGTGGATGGCACCACCCAAACA ACTGGCATCGAGAACAGTAAAA
CACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCA
GCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACC
TCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTAG (SEQ ID NO: 80)

A11B1_6C7 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGCAGCAGCTGGAGGAGTCCGGGGGAGGCCTGGTCAAGCCTGGAGGAACCCTGAC
ACTCACCTGCAAAGCCTCTGGAATCGACTTCAGTAGCTACTACTACATGTGTTGGGT
CCGCCAGGCTCCAGGGAAGGGGCTGGAGTTGATCGTATGTATTTATACTAGTAGTGG
TGGCACATGGTACGCGAGCTGGGTGAATGGCCGACTCACCATCTCCAGAAGCACCA
GCCTAAACACGGTGGATCTGAAAATGACCAGTCTGACAGCCGCGGACACGGCCACC
TATTTCTGTGCCAGAGGGGTTTATTCTGGTAGTAGTGATTATCCAACCTCGGTTGGATC
TCTGGGGCCAGGGCACCCCTGGTCACCGTCTCCTTAGGGCAACCTAAGGCTCCATCAG
TCTTCCCACTGGCCCCCTGCTGCGGGGACACACCAGCTCCACGGTGACCCTGGGCT
GCCTGGTCAAAGGCTACCTCCCGGAGCCAGTGACCGTGACCTGGAACCTCGGGCACC
CTCACCAATGGGGTACGCACCTTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCG
CTGAGCAGCGTGGTGAGCGTGACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGC
CCACCCAGCCACCAACACCAAAGTGGACAAGACCGTTGCGCCCTCGACATGCAGCA
AGCCCATGTGCCCACCCCTGAACTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCC
CAAAACCCAAGGACACCCTCATGATCTCACGCACCCCCGAGGTACATGCGTGGTG
GTGGACGTGAGCCAGGATGACCCCGAGGTGCAGTTCACATGGTACATAAACAACGA
GCAGGTGCGCACCGCCCGGCCGCTACGGGAGCAGCAGTTCAACAGCAGCATCC
GCGTGGTCAGCACCCCTCCCCATCGCGCACCAAGGACTGGCTGAGGGGCAAGGAGTTC
AAGTGCAAAGTCCACAACAAGGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAA
AGCCAGAGGGCAGCCCTGGAGCCGAAGGTCTACACCATGGGGCCCTCCCCGGGAGG
AGCTGAGCAGCAGGTGCGTCAAGCTGACCTGCATGATCAACGGCTTCTACCCTTCCG
ACATCTCGGTGGAGTGGGAGAAGAACGGGAAGGCAGAGGACAACTACAAGACCAC
GCCGACCGTGCTGGACAGCGACGGCTCCTACTTCTCTACAGCAAGCTCTCAGTGCC
CACGAGTGAGTGGCAGCGGGGCGACGTCTTACCTGCTCCGTGATGCACGAGGCCT
TGCACAACCACTACACGCAGAAGTCCATCTCCCGCTCTCCGGGTAAATAG (SEQ ID
NO: 81)

A11B1_6C7 Light Chain

ATGGACACGAGCACCTCCACTGCGCTCCTGGGGCTCCTGCTGCTCTGGCTCACAGGT
GCCAGATGTGCCATCGAGATGACCCAGTCTCCACCCTCCCTGTCTGCATCTGTGGGA
GAAACTGTCAGGATTAGGTGCCTGGCCAGTGAGGACATTTACAGTGGTATATCCTGG
TACCAACAGAAGCCAGAGAAACCTCCTACACTCCTGATCTCTGGTGCATCCAATTTA
GAATCTGGGGTCCCACCACGGTTCAGTGGCGGTGGATCCGGGACAGATTACACCCT
CACCATCGGCGGCGTGCAGGCTGAAGATGTTGCCACCTACTACTGTCTAGGCGGTTA
TAGTTTCAGTAGTACCGGTTTGACTTTTGAGCTGGCACCAAGGTGGAAATCAAACG
TGATCCAGTTGCGCCTTCTGTCTCCTCTTCCCACCATCTAAGGAGGAGCTGACAAC
TGGAACAGCCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCACCGTCAC
CTGGGAGGTGGATGGCACCAACCAAACTGGCATCGAGAACAGTAAACACCCGC
AGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAGCACAC
AGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACCTCAGTC
GTCCAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 82)

A11B1_6B6 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGCAACATCTGGTGGAGTCCGGGGGAGGCCTGGTCAAGCCTGGGGCATCCCTGAC

ACTCACCTGCACAGCCTCTGGATTCTCCTTCACTACCGGCTATCACATGTGCTGGGTC
CGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGTTTTGGTGTATACTAGT
ACCACTACCTACGCGAGCTGGGCGAAAGGTCGATTACCATCTCCAAAACCTCGTCG
ACCACGGTGACTCTACAAATGACCAGTCTAACAGTCGCGGACACGGCCACCTATTTT
TGTGCGAGAATCAGTGCTGAAGATGGTGGGGACTTGTGGGGCCCAGGCACCCTGGT
CACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCTGCTG
CGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCTCC
CGGAGCCAGTGACCGTGACCTGGAACCTCGGGCACCCCTACCAATGGGGTACGCACC
TTCCCGTCCGTCCGGCAGTCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTG
ACCTCAAGCAGCCAGCCGTCACCTGCAACGTGGCCCACCCAGCCACCAACACCAA
AGTGGACAAGACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCACCCCCCTG
AACTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCC AAAACCCAAGGACACCTCA
TGATCTCACGCACCCCCGAGGTACATGCGTGGTGGTGGACGTGAGCCAGGATGAC
CCCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAGGTGCGCACCGCCCCGGCC
GCCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCTTCCCCA
TCGCGCACCCAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAG
GCACTCCCGGGCCCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCTGGA
GCCGAAGGTCTACACCATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTCCGTCA
GCCTGACCTGCATGATCAACGGCTTCTACCTTCCGACATCTCGGTGGAGTGGGAGA
AGAACGGGAAGGCAGAGGACAACCTACAAGACCACGCCGACCGTGCTGGACAGCGA
CGGCTCCTACTTCTCTACAGCAAGCTCTCAGTGCCACGAGTGAGTGGCAGCGGGG
CGACGTCTTACCTGCTCCGTGATGCACGAGGCCTTGCAACAACCTACACGCAGAA
GTCCATCTCCCGCTCTCCGGGTAAATAG (SEQ ID NO: 83)

A11B1_6B6 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCAGATGTGATGTTGTGATGACCCAGACTCCAGCCTCCGTGGAGGCAGCTGTGGG
AGGCACAGTCACCATCACGTGCCAGGCCAGTCAGAGCATTAGCAACTACTTTTCTTG
GTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTACAGGGCGTCCACTCT
GGCATCTGGGGTCCCATCGCGGTTACGCGGCAGTGGATCTGGGACACAGTTCCTCT
CACCATCAGCGACCTGGAGTGTGCCGATTCTGCCACTTACGCCTGTGAGTGCACTTA
TGGTAGTAGTAGTACTGGTTTTGGTTTTCGGCGGAGGGACCGAGGTGGTGGTCAAAG
GTGATCCAGTTGCACCTACTGTCCTCATCTTCCCAACAGCTGCTGATCAGGTGGCAA
CTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCACCGTCA
CCTGGGAGGTGGATGGCACCACCCAAACAACCTGGCATCGAGAACAGTAAAACACCG
CAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAGCACA
CAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACCTCAGT
CGTCCAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 84)

A11B1_5F7 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACT
CACCTGCAAAGCCTCTGGATTCTCCTTCAGTAGTTACTTCTGGATATGCTGGGTCCGC
CAGGCTCCAGGGAAGGGGCTGGAGTGGAGCGCATGCATCTATGGTGATAGTAGTGG
TAGTAGTTACTACGCGAGCTGGGCGAAAGGCCGATTACCATCTCCAAAACCTCGTC
GACCACGGTGACTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATT

TCTGTGCGAGTTATGGTAGTAGTAGTTATTACTACTCTAATTTATGGGGCCCAGGCA
CCCTGGTCACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCCTGGCCC
CCTGCTGCGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGC
TACCTCCCGGAGCCAGTGACCGTGACCTGGAACCTCGGGCACCTCACCAATGGGGT
ACGCACCTTCCCCTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGT
GAGCGTGACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGCCCAACCCAGCCACCA
ACACCAAAGTGAGACAAGACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCCCA
CCCCCTGAACTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCCCTCAACCAAGGAC
ACCCTCATGATCTCACGCACCCCCGAGGTCACATGCGTGGTGGTGGACGTGAGCCA
GGATGACCCCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAGGTGCGCACCG
CCCGGCCGCGCTACGGGAGCAGCAGTTC AACAGCACGATCCGCGTGGTCAGCACC
CTCCCCATCGCGCACCCAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCA
CAACAAGGCACTCCCGGCCCTTCGAGAAAACCATCTCCAAAGCCAGAGGGCAGC
CCCTGGAGCCGAAGGTCTACACCATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGG
TCGGTCAGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAG
TGGGAGAAGAACGGGAAGGCAGAGGACAACACTACAAGACCACGCCGACCGTGCTGG
ACAGCGACGGCTCCTACTTCCTCTACAGCAAGCTCTCAGTGCCACGAGTGAGTGGC
AGCGGGGCGACGTCTTACCTGCTCCGTGATGCACGAGGCCTTGACACAACCACTACA
CGCAGAAGTCCATCTCCCGCTCTCCGGGTAAATAG (SEQ ID NO: 85)

A11B1_5F7 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCATATGTGACCCTGTGATGACCCAGACTCCATCTTCCACGTCTGCGGCTGTGGGA
GGCACAGTCACCATCAGTTGCCAGTCCAGTCAGAGTGTTATAATAACAACACTACTTA
GCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAACGCCTGATCTACGAATCATC
CAAACCTGGCATCTGGGGTCCCATCGCGGTTTCAGAGGCAGTGGATCTGGGGCACAGT
TCACTCTCACCATCAGCGACCTGGAGTGTGACGATGCTGCCACTTACTACTGTCTAG
GCGCATATTATACTACTCTTGATTTTCGGCGGAGGGACCGAGGTGGTGGTCAGAGGTG
ATCCAGTTGCACCTACTGTCTCATCTTCCCACCAGCTGCTGATCAGGTGGCAACTG
GAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTACCGTCACT
GGGAGGTGGATGGCACCACCCAAACAACCTGGCATCGAGAACAGTAAACACCGCA
GAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAGCACACA
GTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACCTCAGTCG
TCCAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 86)

A11B1_5D7 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGGAGCAGTTGGTGGAGTCCGGGGGAGGCCTGGTCCAGCCTGAGGGATCCCTGAC
ACTCACCTGCAAAGCCTCTGGATTCGACTTCAGTAGCAATGCAATGTGCTGGGTCCG
CCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATTTATAATGGTGATGGCA
GCACATACTACGCGAGCTGGGTGAATGGCCGATTCACCATCTCCAAGACCTCGTCGA
CCACGGTGACTCTGCAAATGACCACTGACAGCCGCGGACACGGCCACCTATTTCT
GTGCGAGAGGTCTCTTAATTGGAATAGGGATAACTTATGGGGCCCTGGCACCTGG
TCACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCCTGGCCCCCTGCT
GCGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCTC
CCGGAGCCAGTGACCGTGACCTGGAACCTCGGGCACCTCACCAATGGGGTACGCAC

CTTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGT
GACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGCCACCCAGCCACCAACACCA
AAGTGGACAAGACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCACCCCT
GAACTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCCAAAACCCAAGGACACCCTC
ATGATCTCACGCACCCCGAGGTCACATGCGTGGTGGTGACGTGAGCCAGGATGA
CCCCGAGGTGCAGTTCACATGGTACATAAAACAACGAGCAGGTGCGCACCGCCCGG
CGCCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCCTCCCC
ATCGCGCACCAAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAA
GGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCTGG
AGCCGAAGGTCTACACCATGGGCCCTCCCGGGAGGAGCTGAGCAGCAGGTGCGTC
AGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAG
AAGAACGGGAAGGCAGAGGACAACCTACAAGACCACGCCGACCGTGCTGGACAGCG
ACGGCTCCTACTTCTCTACAGCAAGCTCTCAGTGCCACGAGTGAGTGGCAGCGGG
GCGACGTCTTCACCTGCTCCGTGATGCACGAGGCCTTGACACAACCACTACACGCAGA
AGTCCATCTCCCGCTCTCCGGGTAAATAG (SEQ ID NO: 87)

A11B1_5D7 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCACATTTGCCCAAGTGCTGACCCAGACTCCATCCTCCGTGTCTGCAGCTGTGGGA
GGCACAGCCACCATCAACTGCCAGGCCAGTCAGAGTCTTTATAGTCCCAAGAATTTA
GCCTGGTATCAGCAGACACCAGGGCAGCCTCCCAAGCTCCTGATCTATTCTGCATCG
AAACTGGCATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACACAGTT
CACTCTCACCATCAGCGGCGTGAGTGTGACGATGCTGCAATTTACTACTGTCAAGG
CGAATTTAGTTGTACTACTGCTGCTTGTGTTTGGTGGGAGGGACCGAGGTGGT
GGTCAAAGGTGATCCAGTTGCACCTACTGTCCTCATCTTCCCACCAGCTGCTGATCA
GGTGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGT
CACCGTCACCTGGGAGGTGGATGGCACCACCCAAACAACCTGGCATCGAGAACAGTA
AAACACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGA
CCAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACG
ACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 88)

A11B1_5A7 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCTTTGGAGGAGTCCGGGGGAGGCCTGGTCCAGCCTGAGGGATCCCTGACACT
CGCCTGCACAGCTTCGGGATTCTCCTTCAGTAGCTACTACTACATCTGCTGGGTCCG
CCAGGCTCCAGGGACGGGGCTGGAGTGGATCGGATGCATTAATACTGGTAGTGATG
ACACTCACTACGCGAGCTGGTTGAAAGGCCGATTACCTTCTCCAAGGCCTCGTCGA
CCACGTTGACTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATTTCT
GTGCGAGATCATCTGGTAGTAGTGATGATGCTTATGATCTCTGGGGCCCAGGCACCC
TGGTCACTGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCCTGGCCCCCT
GCTGCGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTAC
CTCCCGGAGCCAGTGACCGTGACCTGGAACCTCGGGCACCTCACCAATGGGGTACG
CACCTTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAG
CGTGACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGCCACCCAGCCACCAACA
CCAAAGTGGACAAGACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCACCC
CCTGAACTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCCAAAACCCAAGGACACC

CTCATGATCTCACGCACCCCCGAGGTCACATGCGTGGTGGTGGACGTGAGCCAGGA
TGACCCCCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAGGTGCGCACCGCCC
GGCCGCCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCCTC
CCCATCGCGCACCAAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAA
CAAGGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCC
TGGAGCCGAAGGTCTACACCATGGGCCCTCCCGGGAGGAGCTGAGCAGCAGGTGCG
GTCAGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGG
GAGAAGAACGGGAAGGCAGAGGACAACACTACAAGACCACGCCGACCGTGCTGGACA
GCGACGGCTCCTACTTCCTCTACAGCAAGCTCTCAGTGCCCACGAGTGAGTGGCAGC
GGGGCGACGTCTTCACCTGCTCCGTGATGCACGAGGCCTTGACACAACCACTACACGC
AGAAGTCCATCTCCCGCTCTCCGGGTAAATAG (SEQ ID NO: 89)

A11B1_5A7 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCAGATGTGATGTTGTGATGACCCAGACTCCAGCCTCCGTGTCTGAACCTGTGGGA
GGCGCAGTCACCATCAAGTGCCAGGCCAGTCAGAGCATTGGTAGTAATTTAGCCTG
GTATCAGCACAAACCAGGGCAGCCTCCCAAGCTCCTGATCTATTTTGCATCCAGCCT
GGCATCTGGGGTCTCGTCGCGGTTCAAGGGCGGTAGATCTGGGACACAGTTCCTCT
CACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTACTACTGTCACTGTACTTA
TTATCCTCTTAGTTATGTTACTTTTCGGCGGAGGGACCGAGGTGGTGGTCAAAGGTGA
TCCAGTTGCACCTACTGTCCTCATCTTCCCACCAGCTGCTGATCAGGTGGCAACTGG
AACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCACCGTCACCTG
GGAGGTGGATGGCACCACCCAAACAACCTGGCATCGAGAACAGTAAACACCCGAG
AATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAGCACACAG
TACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCAGCAGCTCAGTCGT
CCAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 90)

A11B1_4E1 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGACATCCCTGACACT
CTCCTGCACAGCCTCTGGATTCTCCTTCGGTAGCTATTATTATATGTGCTGGGTCCGC
CAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATTGATGTTGGTAGTAGTGG
TGACACATACTACGCGAGCTGGGTGAATGGCCGATTACCATCTCCAAAACCTCGTC
GACCACGGTGACTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATT
TCTGTGCGAGAGATGATACTGCTGCTGGTGGTTTTGGTAATTTGGAATTGTGGGGCC
CAGGCACCCTGGTCACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCAC
TGGCCCCCTGCTGCGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCA
AAGGCTACCTCCCGGAGCCAGTGACCGTGACCTGGAACCTCGGGCACCCCTACCAAT
GGGGTACGCACCTTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGC
GTGGTGAGCGTGACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGCCACCCAGC
CACCAACACCAAAGTGGACAAGACCGTTGCGCCCTCGACATGCAGCAAGCCCATGT
GCCCCACCCCTGAACTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCCAAAAACCCA
AGGACACCCCTCATGATCTCACGCACCCCCGAGGTCACATGCGTGGTGGTGGACGTG
AGCCAGGATGACCCCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAGGTGCG
CACCGCCCCGGCCCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTGGTCA
GCACCTCCCCATCGCGCACCAAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAA

GTCCACAACAAGGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAGAGG
GCAGCCCCTGGAGCCGAAGGTCTACACCATGGGCCCTCCCGGGAGGAGCTGAGCA
GCAGGTTCGGTCAGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACATCTCGG
TGGAGTGGGAGAAGAACGGGAAGGCAGAGGACAACACTACAAGACCACGCCGACCGT
GCTGGACAGCGACGGCTCCTACTTCCTCTACAGCAAGCTCTCAGTGCCCACGAGTGA
GTGGCAGCGGGGCGACGTCTTCACCTGCTCCGTGATGCACGAGGCCTTGACAAACC
ACTACACGCAGAAGTCCATCTCCCGCTCTCCGGGTAAATAG (SEQ ID NO: 91)

A11B1_4E1 Light Chain

ATGGACACGAGGGCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCAGGT
GCCAGATGTGCATTTCGAATTGACCCAGACTCCATCCTCCGTGTCTGAACCTGTGGGA
GGCACAGTCACCATCAAGTGCCAGGGCCAGTCAGAGCATTTACAGCTACTTTTCCTGG
TATCAGCAGAAACCAGGGCAGCCTCCCAAGCGCCTGATTTACCAGGCATCCACTCTG
GCTTCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGATTTCACTCTC
ACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTACTACTGTCAAAACAATTAT
GGTAGGGGTAGTGGTAGTTATTTTTTTGGTTTCGGCGGAGGGACCGAGGTGGTGGTC
AAAGGTGATCCAGTTGCACCTACTGTCTCATCTTCCCACCAGCTGCTGATCAGGTG
GCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCACC
GTCACCTGGGAGGTGGATGGCACCAACCAAACTGGCATCGAGAACAGTAAAC
ACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAG
CACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACCT
CAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 92)

A11B1_3H9 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACT
CACCTGCAAAGCCTCTGGAATCGACTTCAGTAGCGGCTACGGCATGTGGTGGGTCCG
CCAGGCTCCAGGGAAGGGACTGGAGTATATCGGATACATTGATACTGGTAGTGGTA
GCACTTACTACGCGAACTGGGCGAAAGGCCGATTACCATCTCCAAAACCTCGTCG
ACCATGGTGACTCTGCAAATGACCAGTCTGACAGTCGCGGACACGGCCACCTATTTTC
TGTGCGAAAGGGGGCGCCATAGACCTCTGGGGCCCAGGGACCCTCGTCACCGTCTC
TTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCTGCTGCGGGGACAC
ACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCTCCCGGAGCCAGT
GACCGTGACCTGGAACCTCGGGCACCCCTACCAATGGGGTACGCACCTTCCCGTCCGT
CCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCA
GCCAGCCCGTCACCTGCAACGTGGCCACCCAGCCACCAACACCAAAGTGGACAAG
ACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCACCCCTGAACTCCCGGGG
GGACCGTCTGTCTTCATCTTCCCCCAAAACCAAGGACACCCTCATGATCTCACGC
ACCCCCGAGGTACATGCGTGGTGGTGGACGTGAGCCAGGATGACCCCGAGGTGCA
GTTACATGGTACATAAACAACGAGCAGGTGCGCACCGCCCGGCCCGCTACGGG
AGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCCTCCCCATCGCGCACCA
GACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAGGCACTCCCGGC
CCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCTGGAGCCGAAGGTCT
ACACCATGGGCCCTCCCGGGAGGAGCTGAGCAGCAGGTCGGTCAGCCTGACCTGC
ATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAGAAGAACGGGAA
GGCAGAGGACAACACTACAAGACCACGCCGACCGTGCTGGACAGCGACGGCTCCTACT

TCCTCTACAGCAAGCTCTCAGTGCCACGAGTGAGTGGCAGCGGGGCGACGTCTTCA
CCTGCTCCGTGATGCACGAGGCCTTGCACAACCACTACACGCAGAAGTCCATCTCCC
GCTCTCCGGGTAAATAG (SEQ ID NO: 93)

A11B1_3H9 Light Chain

ATGGACACGAGGGCCCCACTCAGCTGCTGGGACTCCTACTGCTCTGGCTCCCAGGT
GCCAGATGTGCTGACATTGTGATGACCCAGACTCCAGCCTCCGTGGAGGCAGCTGTG
GGAGGCACAGTCACCATCAAGTGCCAGGCCAGTCAGAGCATTAGTAGTTACTTAGC
CTGGTATCAGCAGAAACCAGGGCAGCGTCCCAAGCTCCTGATCTACAGGGCATCCA
CTCTGGCATCTGGGGTCCCATCGCGTTCAAAGGCAGTGGATCTGGGACAGACTACA
CTCTCACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTATTATTGTCATACCTA
TTATCTTAGTAGTAGTATCAGTTATGGTAATACTTTCGGCGGAGGGACCGAGGTGGT
GGTCAAAGGTGATCCAGTTGCACCTACTGTCTCATCTTCCCACCAGCTGCTGATCA
GGTGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCGGATGT
CACCGTCACCTGGGAGGTGGATGGCACCACCAAACTGGCATCGAGAACAGTA
AAACACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGA
CCAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACG
ACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 94)

A11B1_3G2 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGGAGCAGCTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGAGGGATCCCTGAC
ACTCACCTGCAAAGCCTCTGGATTCTCCTTCAGTAGCATCTACTGGATTTGCTGGGTC
CGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCACTACTGTTGTCAAAAG
TGGTAGAACTTACTACGCGAACTGGGCGAAAGGCCGATTACCATCTCCAAAACCT
CGTCGACCACGGTGACTCTGCAATGACCAGTCTGACAGCCGCGGACACGGCCACC
TATTTCTGTGCGAGAGAATTTGTTGATGGTGGTGGTAGTAGTGGTAGGGACTTGTGG
GGCCAGGCACCCTGGTCACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTTC
CCACTGGCCCCCTGCTGCGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTG
GTCAAAGGCTACCTCCCGGAGCCAGTGACCGTGACCTGGAACTCGGGACCCCTCAC
CAATGGGGTACGCACCTTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGAG
CAGCGTGGTGAGCGTGACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGCCCACC
CAGCCACCAACACCAAAGTGGAACAGACCGTTGCGCCCTCGACATGCAGCAAGCCC
ATGTGCCCACCCCCTGAACTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCCAAAA
CCCAAGGACACCCTCATGATCTCACGCACCCCGAGGTCACATGCGTGGTGGTGGGA
CGTGAGCCAGGATGACCCCGAGGTGCAGTTACATGGTACATAAACAACGAGCAGG
TGCGCACCGCCCGGCCGCGCTACGGGAGCAGCAGTTCAACAGCAGCATCCGCGTG
GTCAGCACCTCCCCATCGCGCACCAAGGACTGGCTGAGGGGCAAGGAGTTCAAGTG
CAAAGTCCACAACAAGGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCA
GAGGGCAGCCCCTGGAGCCGAAGGTCTACACCATGGGCCCCCTCCCGGGAGGAGCTG
AGCAGCAGGTCTGGTCAGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACATC
TCGGTGGAGTGGGAGAGAAGACGGGAAGGCAGAGGACAACCTACAAGACCACGCCGA
CCGTGCTGGACAGCGACGGCTCCTACTTCTCTACAGCAAGCTCTCAGTGCCACGA
GTGAGTGGCAGCGGGGCGACGTCTTACCTGCTCCGTGATGCACGAGGCCTTGAC
AACCCTACACGCAGAAGTCCATCTCCCGCTCTCCGGGTAAATAG (SEQ ID NO: 95)

A11B1_3G2 Light Chain

ATGGACACGAGGGCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCAGATGTGCCTATGATATGACCCAGACTCCAGCCTCCGTGGAGGCAGCTGTGGG
AGGCACAGTCACCATCAAGTGCCAGGCCAGTCAGAGCATTAGTAGGGACTTATCCT
GGTATCAGCAGAAACCTGGACAGCCTCCCAAGCGCCTAATCTACAAGGCATCCACT
CTGGCATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGATTTCACT
CTCACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTACTACTGTCAACAGGGT
TATAGTAGTATTGATGTTGATAATGATTTCGGCGGAGGGACCGAGGTGGTGGTCAAA
GGTGATCCAGTTGCACCTACTGTCCTCATCTTCCCACCAGCTGCTGATCAGGTGGCA
ACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCACCGTC
ACCTGGGAGGTGGATGGCACCCCAAACAACCTGGCATCGAGAACAGTAAACACC
GCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAGCAC
ACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACCTCAG
TCGTCCAGAGCTTCAATAGGGGTGACTGTAG (SEQ ID NO: 96)

A11B1_3B1 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGGAGCAGCTGGAGGAGTCCGGGGGAGGCCTGGTCAAGCCTGAGGGATCCCTGAC
ACTCACCTGCAAAGCCTCTGGATTCGACCTCAGTAGCGGCTATGACATGTGCTGGGT
CCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATTTATGCTGATTATA
GTGGTAGCACATACTACGCGAGCTGGGTGAATGGCCGATTCACCATCTCCAGCAGC
ACCAGCCTAAACACGGTGGATCTGAAAATGACCAGTCTGACAGCCGCGGACACGGC
CACCTATTTCTGTGCCAGAGGGGCTACTGGTAATGGTGGTTATGGATACTACTTTAA
CTTGTGGGGGCCAGGCACCTTGGTCACCGTCTCCTCAGGGCAACCTAAGGCTCCATC
AGTCTTCCCCTGAGCCCCCTGCTGCGGGGACACACCCAGCTCCACGGTGACCCTGGG
CTGCCTGGTCAAAGGCTACCTCCCGGAGCCAGTGACCGTGACCTGGAACCTCGGGCA
CCCTCACCAATGGGGTACGCACCTTCCCGTCCGTCCGGCAGTCCCTCAGGCCTCTACT
CGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCAGCCAGCCGTCACCTGCAACGTG
GCCCCACCCAGCCACCAACACCAAAGTGGACAAGACCGTTGCGCCCTCGACATGCAG
CAAGCCCATGTGCCCACCCCTGAACTCCCGGGGGGACCGTCTGTCTTCATCTTCCC
CCCAAAACCCAAGGACACCCTCATGATCTCACGCACCCCCGAGGTCACATGCGTGG
TGGTGGACGTGAGCCAGGATGACCCCGAGGTGCAGTTCACATGGTACATAAACAAC
GAGCAGGTGCGCACCCGCGCCGCGCTACGGGAGCAGCAGTTCAACAGCACGAT
CCGCGTGGTCAGCACCTCCCCATCGCGCACCAAGGACTGGCTGAGGGGCAAGGAGT
TCAAGTGCAAAGTCCACAACAAGGCACTCCCGGCCCCATCGAGAAAACCATCTCC
AAAGCCAGAGGGCAGCCCCTGGAGCCGAAGGTCTACACCATGGGCCCTCCCCGGGA
GGAGCTGAGCAGCAGGTTCGGTCAGCCTGACCTGCATGATCAACGGCTTCTACCCTTC
CGACATCTCGGTGGAGTGGGAGAAGAACGGGAAGGCAGAGGACAACCTACAAGACC
ACGCCGACCGTGCTGGACAGCGACGGCTCCTACTTCTCTACAGCAAGCTCTCAGTG
CCCACGAGTGAGTGGCAGCGGGGCGACGTCTTACCTGCTCCGTGATGCACGAGGC
CTTGACAACCACTACACGCAGAAGTCCATCTCCCGCTCTCCGGGTAAATAG (SEQ
ID NO: 97)

A11B1_3B1 Light Chain

ATGGACACGAGGGCCCCACTCAGCTGCTGGGGCTCCTACTGCTCTGGCTCCCAGGT
GCCAGATGTGCTGACATTGTGATGACCCAGACTCCAGCCTCCGTGTCTGAACCTGTG

GGAGGCACAGTCACCATCAAGTGTGTCAGGCCAGTCAGAACATTAATAGCGGCTTAGC
CTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTACAAGGCATCCA
CTCTGGCATCTGGGGTCTCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGAATTCA
CTCTACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTACTACTGTCAAACCT
ATTATTATAGTAGTAGTAGTAGTGATAATGCTTTTCGGCGGAGGGACCGAGGTGGTGG
TCAAAGGTGATCCAGTTGCACCTACTGTCTCATCTTCCCACCAGCTGCTGATCAGG
TGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCA
CCGTCACCTGGGAGGTGGATGGCACCACCCAAACAACCTGGCATCGAGAACAGTAAA
ACACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACC
AGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGA
CCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTAG (SEQ ID NO: 98)

A11B1_2D3 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACT
CACCTGCACAGCTTCTGGATTCTCCTTCAGTAGCAGTTATTGGATATGCTGGGTCCGC
CAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGTATTTATGGTGGTAGTAGTGG
TAACATTGCCTACGCGAGCTGGGCGAAAGGCCGATTACCATCTCCAAAACCTCGTC
GACCACGGTGACTCTACAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATT
TCTGTGCGAGAGATATTCCTAGTGATGCTTTCACCTTAGACTTGTGGGGGCCAGGCA
CCCTGGTCACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCCTGGCCC
CCTGCTGCGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGC
TACCTCCCGGAGCCAGTGACCGTGACCTGGAACCTCGGGCACCTCACCAATGGGGT
ACGCACCTTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGT
GAGCGTGACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGCCCCACCCAGCCACCA
ACACCAAAGTGGACAAGACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCCA
CCCCCTGAACCTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCC AAAACCCAAGGAC
ACCCTCATGATCTCACGCACCCCCGAGGTCACATGCGTGGTGGTGGACGTGAGCCA
GGATGACCCCGAGGTGCAGTTACATGGTACATAAACAACGAGCAGGTGCGCACCG
CCCGGCCGCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACC
CTCCCCATCGCGCACCCAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCA
CAACAAGGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGC
CCCTGGAGCCGAAGGTCTACACCATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGG
TCGGTCAGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAG
TGGGAGAAGAACGGGAAGGCAGAGGACAACCTACAAGACCACGCCGACCGTGCTGG
ACAGCGACGGCTCCTACTTCTCTACAGCAAGCTCTCAGTGCCCACGAGTGAGTGGC
AGCGGGGCGACGTCTTACCTGCTCCGTGATGCACGAGGCCTTGCACAACCACTACA
CGCAGAAGTCCATCTCCCGCTCTCCGGGTAAATAG (SEQ ID NO: 99)

A11B1_2D3 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCACATTTGCCAAGTGCTGACCCAGACTCCATCCTCCGTGTCTGCAGCTGTGGGA
AGCACAGTCACCATCAATTGCCAGGCCAGTCAGAGTGTTTATAAAGACAACAATTTA
GCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTACAAGGCTTCC
ACTCTGGCATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACACAGTTC
ACTCTACCATCAGCGGCGTGCAGTGTGAAGATGCTGCCACTTACTACTGTCAAGGC

GAATTCAGTTGTGGTAGTGCTGATTGTATTGCTTTCGGCGGAGGGACCGAGGTGGTG
GTCAAAGGTGATCCAGTTGCACCTACTGTCTCATCTTCCCACCAGCTGCTGATCAG
GTGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTC
ACCGTCACCTGGGAGGTGGATGGCACCACCCAAACAACCTGGCATCGAGAACAGTAA
AACACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGAC
CAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACG
ACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 100)

A11B1_2A7 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACT
CACCTGCAAAGGCTCTGGAATCGACTTCAGTAGCGGCTACGGCATGTGGTGGGTCCG
CCAGGCTCCAGGGAAGGGACTGGAGTATATCGGATACATTGATACTGGTTATGGTA
GCACTTACTACGCGAGCTGGGCGAAAGGCCGATTACCATCTCCAAGACCTCGTCG
ACCACGGTGACTCTGCAAATGACCAGTCTGACAGTCGCGGACACGGCCACCTATTTT
TGTGCGAAAGGGGGCGCCATAGACCTCTGGGGCCCAGGGACCCTCGTCACCGTCTC
TTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCCTGGCCCCCTGCTGCGGGGACAC
ACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCTCCCGGAGCCAGT
GACCGTGACCTGGAACCTCGGGCACCTCACCAATGGGGTACGCACCTTCCCGTCCGT
CCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCA
GCCAGCCCGTCACCTGCAACGTGGCCCACCCAGCCACCAACACCAAAGTGGACAAG
ACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCACCCCCCTGAACTCCCGGGG
GGACCGTCTGTCTTCATCTTCCCCCAAAACCCAAAGGACACCCTCATGATCTCACGC
ACCCCCGAGGTACATGCGTGGTGGTGGACGTGAGCCAGGATGACCCCGAGGTGCA
GTTACATGGTACATAAACAACGAGCAGGTGCGCACCGCCCGGCCCGCTACGGG
AGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCTCCCCATCGCGCACCA
GACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAGGCACTCCCGGC
CCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCCTGGAGCCGAAGGTCT
ACACCATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTTCGGTCAGCCTGACCTGC
ATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAGAAGAACGGGAA
GGCAGAGGACAACCTACAAGACCACGCCGACCGTGTGGACAGCGACGGCTCCTACT
TCCTCTACAGCAAGCTCTCAGTGCCCACGAGTGAGTGGCAGCGGGGCGACGTCTTCA
CCTGCTCCGTGATGCACGAGGCCTTGCAACAACCTACACGCAGAAGTCCATCTCCC
GCTCTCCGGGTAAATAG (SEQ ID NO: 101)

A11B1_2A7 Light Chain

ATGGACACGAGGGCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCACATTTGCAGCCGTGCTGACCCAGACTCCGGCTTCCACGTCTGCAGCTGTGGGA
GGCACAGTCACCATCAATTGTCAAGTCCAGTCAGAGCGTGTATCGTAGCAACTGGTTA
GCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTATGATGATTT
AATTTGGCATCTGGGGTCCCATCCCGGTTCAAGGGCAGTGGATCTGGGACACAGTTC
ACTCTCACCATCAGCGGCGTGCAGTGTGCCGATGCTGCCACTTACTACTGTCAAGGC
AGTTATTATAGTGGTAATTGGTACAGTGCTTTCGGCGGAGGGACCGAGGTGGTGGTC
AAAGGTGATCCAGTTGCACCTACTGTCTCATCTTCCCACCAGCTGCTGATCAGGTG
GCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCACC
GTCACCTGGGAGGTGGATGGCACCACCCAAACAACCTGGCATCGAGAACAGTAAAC

ACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAG
CACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACCT
CAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 102)

Protein sequences of anti- $\alpha 11\beta 1$ monoclonal antibodies

Rat mAb sequences

Signal peptide-FR1-**CDR1**-FR2-**CDR2**-FR3-**CDR3**-FR4

79E3E3 Heavy Chain Variable Region

MDWLWNLFLMVVAQSAQAQIQLVQSGPEVKKPGESVKISCKASGYTFTDYAMNWVKQ
APGNGLKWMGWINTQTGKPTYADDFKQRFVFSLETSARTTYLQINNLIENEDTATYFCT
RLGTGNTKGFAYWGQGLTVTVSS (SEQ ID NO: 145)

79E3E3 Light Chain Variable Region

MESQTHVLISLLCVSGTCGDILINQSPASLTVSAGERVTMSCKSSQSLLYSENNQDYLA
WYQQKPGQFPKLLIYGASNRHTGVPDRFTGSGSGTDFTLTISVQAEDLADYYCEQTY
RYPFTFGSGTKLEIK (SEQ ID NO: 146)

24E4G6 Heavy Chain Variable Region

MELESLIFIFSLKDVQCEVQLVESGGSLVQPGGSLKLSCLVASGYTFSNYWMDWVRQSP
GKSLEWIGEINTDGRRTNYAPSIKDRFTISRDNASTLYLQMSNVKSDDTAIYYCTILR
VYPHYFDYWGQGVMTVSS (SEQ ID NO: 147)

24E4G6 Light Chain Variable Region

MMSPAQFLFLLMLWIQEARGDVVMTQTTPPSLSVAIGQSVSISCKSSQSLVYSDGETYLH
WFLQSPGRSPKRLIYHVSNLGSGVPDRFSGTGSITDFTLRISRVEAEDLGVIYCAQTTH
FPPTFGAGTKLEIK (SEQ ID NO: 148)

8H8E9 Heavy Chain Variable Region

MAVLVLLLCLVTFPSCALSQVQLKESGPGLVQPSQTLSTCTVSGFSLTSNSVSWVRQAPG
KGLEWMGAIWSDGSTDYNSALKSRLSISRDTSKSQVFLKMNSLQTEDTAIYFCTRSHW
EPFDYWGQGVMTVSS (SEQ ID NO: 149)

8H8E9 Light Chain Variable Region

MESQTQALISLLWVYGTCTGDIVMTQSPFSLAVSEGEMVTINCKSSQGLLSSGNQKNYLA
WYQQRPGQSPKLLIYASTRQSGVPDRFIGGGSGTDFTLTISDVQAEDLADYYCLQHYS
YPPTFGSGTKLEIK (SEQ ID NO: 150)

6E5C11 Heavy Chain Variable Region

MAVLVLLLCLVTFPSCALSQVQLRESGPGLVQPSQTLSTCTVSGFSLTSNSVTWVRQPPG
KGLEWMGAIWSDGSTDYNSLTKSRLSISRDTSKSQVFLKMSSLQTEDTAIYFCTRSHW
EPFDYWGQGVMTVSS (SEQ ID NO: 151)

6E5C11 Light Chain Variable Region

MESQTQALISLLLWVYGTCTGDIVMTQSPLSLAVSEGETVTMNC**KSSQSLFSSGNQKNYLA**
 WYQQKPGQSPKLLIYY**ASTRQSGVPDRFIGSGSGTDFTLTISDVQTEDLADYYCLQHYN**
 YPPTFGSGTKLEIK (SEQ ID NO: 152)

7D8B10 Heavy Chain Variable Region

MDLRLTYVFIVAILKGVLC**EVKLEESGGGLVQPGMSVKLSCATSGFIFSDYWM**EWVRQAP
 GKGLEWVAEIRNKANNYATYY**GKSMKGRFTISRDDSKSIVYLQVNSIRSEDTAIYYCA**
 PNFDYWGGQGMVTVSS (SEQ ID NO: 153)

7D8B10 Light Chain Variable Region

MSPVQSLFLLLLWILGTHG**DVVL**TQTPPTLSATIGQSVSIS**CRSSQSLLHSTGNTYLNWLL**
 QRPQPPQLLIY**LSRLES**GVPNRFSASGSGTDFTLKISGIEADLG**VYYCVQSSHTPYT**
 FGTGTKLELK (SEQ ID NO: 154)

18E10F10 Heavy Chain Variable Region

MDIRLSLVFLVLFMKGV**QCEVQLVESGGGLVQPGRSLKLS**CAASRFTFSD**YNMAWVRQA**
 PKKGLEWVA**TIYHDDSGSYRDSVKGRFTISRNN**AKSTLYLQ**MDSL**RSEDMATYYCA
 RHNGFDYWGGQGMVTVAS (SEQ ID NO: 155)

18E10F10 Light Chain Variable Region

MKWPVRLVLFFWIPASG**GDV**MTQTPVSLPVRLGGQASIS**CRSSQSLVHSNGNTYLHW**
 YLQKPGQSPQLLINRV**SNRFS**GV**PDRFSGSGSGTDFTLKINR**VEPEDLG**DYYCLQSTHFP**
 LTFGSGTKLETK (SEQ ID NO: 156)

40G10H11 Heavy Chain Variable Region

MDIRLSLGFLVLFIKGD**QCAVQLVESGGGLVQPGRSLKLS**CAASRITFTD**YYMAWVRQA**
 PTKGLEWVA**TISSDGGDTFYRDSVKGRFTISR**DNAKSTLYLQ**MVSL**RSEDTATYYCST
 DRGAQFGYWGGTLVTVSS (SEQ ID NO: 157)

40G10H11 Light Chain Variable Region

MAPVQLLGLLLIWLPAMRCDIQMTQSPSFLSASVGDRVSIN**CKASQNVHENLNWYQQKL**
 GEAPKRLIYNTNN**LQTGIPSRFSGSGSGADYTLTIS**LQPEDFATYF**CLQHNAFPYTFGP**
 GTKLELK (SEQ ID NO: 158)

Mouse mAb sequences

FR1-**CDR1**-FR2-**CDR2**-FR3-**CDR3**-FR4

9-G05 Heavy Chain Variable Region

EVQLQQSGPELVKPGASVKIPCKASGYTF**PDYNMDWVKQSHGKSLEWIGYINPDNGGT**
 IYNQKFKGKATLTVDKSSSTAYMELRSLTSEDTAVYYCAR**LDSSGYGYAMDYWGQG**
 TSVTVSS (SEQ ID NO: 103)

9-G05 Light Chain Variable Region

DIVLTQSPASLAVSLGQRATISCRASESVDNYGISFMHWYQKPGQPPKLLIYRASNLD
SEIPARFSGSGSRTDFTLTIDPVETDDVATYYCQQSYKDPRTFGGGTKLEIK (SEQ ID
NO: 104)

8-P20 Heavy Chain Variable Region

KVMLVESGGALVKPGGSLKLSVASGFTFSNYAMSWVRQTPEKRLEWVATISSGGYY
TYYPDSVKGRFTISRDNARNTLFLQMSSLRSEDAMFYCAREDDYGRYSYTM DYWGQ
GTSVTVSS (SEQ ID NO: 105)

8-P20 Light Chain Variable Region

DVVMTQTPLSLPVSLGDQVSI SCRCQS L VHSNGNTYLHWYLQKPGQSPQLLIYKISNR
FSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPYTFGGGTELEIK (SEQ ID
NO: 106)

8-G15 Heavy Chain Variable Region

EVQLQQSGPELVKPGASVRISCKASGYTFTDYYIHWVKQKPGQGLECIGEIYPGTDNTY
YSKKFRGKATLTADKSSDAYMQLSSLTSEDSAVYFCARGDYRGRYFDVWGAGTTVT
VSS (SEQ ID NO: 107)

8-G15 Light Chain Variable Region

DVVMTQTSLTSLVTIGQPASISCKSSQSLLHSNGKTYLNWLLQRPQGSPKFLIYLVSKL
ESGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCLQSTHFPWTFGGGTELEIK (SEQ ID
NO: 108)

8-I14 Heavy Chain Variable Region

EVQLQQSGPELVKPGASVKISCKASGYTFTDYYMHWVKQKPGQGLEWIGKIYPGSGN
THYNEKFKGKATLTADKSSDAYMQLSSLTSEDSAVYFCATNYYGYRAMNYWGQSS
VTVSS (SEQ ID NO: 109)

8-I14 Light Chain Variable Region

DIHLTQSPSSLSASLGERISLTCRASQDIYISLNWFQKPDGTIKLLIYGTSSLDSGVPKRF
SGSRSGDYSLTISSEDFADYYCLQYASSPYTFGGGTELEIK (SEQ ID NO: 110)

9-E16 Heavy Chain Variable Region

EVQLQQSGPELVKPGASVKISCKASGYTFTDYYMHWVKQKPGQGLEWIGEIYPGSGNP
YYNEKFKGKATLTADKSSSAYMQLSSLTSEDSAVYFCARTSYGRVGTGFAYWGQGT
LTVSA (SEQ ID NO: 111)

9-E16 Light Chain Variable Region

NFVMTQTPLSLPVSLGDQASISCRSSQSLLHSNGNTYLHWYLQKPGQSPKLLIYKVSNR
FSGVPDRFSGSGSGTDFTLKINRVETEDLGIYFCSQSSHVPTFGAGTKLELK (SEQ ID
NO: 112)

8-J17 Heavy Chain Variable Region

QVQLQQSGAELAKPGASVKMSCKASGYTFTNYWMHWVKQRPQGQGLEWIGYINPNNG
YTEYNQRFKDKATLTADRSSTTAYMQLSSLTSEDSAVYYCARSDIITTDYWGQGTTLT
VSS (SEQ ID NO: 113)

8-J17 Light Chain Variable Region

DVVMTQTPLSLPVSLGDAQISCRSSQSLVYSNGNTYLHWYLQKPGQSPKLLIYKVSNR
FSGVPDRFSGSGGTDFTLKISRVEAEDLGVYFCSQSTHVPWTFGGGTKLEIK (SEQ ID
NO: 114)

9-B11 Heavy Chain Variable Region

QVQLQQPGAELVRPGTSVKLSCKASGYTFTSYWMHWVQRPQGQGLEWIGVIDPSDSY
TNYNQKFKGKATLTVDTSSSSAYMQLSSLTSEDSAVYYCARDDVAMDYWGQGTSTV
SS (SEQ ID NO: 115)

9-B11 Light Chain Variable Region

DIVVTQSPASLAVSLGQRATISCRASESVDSYGNSFIHWYQQKPGQPPKLLIYRASNLKS
GIPARFSGSGSRTDFTLTINPVEADDVATYYCQSQSNEDPYTFGGGTKLEIK (SEQ ID NO:
116)

For SEQ ID NO: 117-144, CDR3 is represented by bold and underlined text.

6-O12 Heavy Chain Variable Region

EVKLEESGGGLVQPGGSMKLSAASGFTFSDAWMDWVRQSPEAGLEWVAEIRNKAHN
PATYYAESVKGRFTISRDDSKSSVYLQMNSLRAEDTGIYYCTLVAPDAMDYWGQGT
STVSS (SEQ ID NO: 117)

6-O12 Light Chain Variable Region

DIVMSLSPSSLAVSVGEKVTMSCKSSQSLLYSRNQKNYLAWYQQKPGQSPKLLIYWAST
RASGVPDRFTGSGSGTDFTLTISSVKAEDLAVYYCQYYSYPTYTFGGGTKLEIK (SEQ
ID NO: 118)

10-L15 Heavy Chain Variable Region

QVQLQQSGPELVRPGASVKMSCKASGYTFTSYWMHWVKQRPQGQGLEWIGMIDPSNSE
TWNQKFKDKATLNVDKSSNTAYMQLSSLTSEDSAVYYCARYDGYDDYWGQGT
TLTVSS (SEQ ID NO: 119)

10-L15 Light Chain Variable Region

NIVLTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQQKPGQPPKLLIYLASNVES
GVPARFSGSGSRTDFTLTIDPVEADDAATYYCQONNEDPWTFGGGTKLEIK (SEQ ID
NO: 120)

7-H14 Heavy Chain Variable Region

QVQLQQPGAELVRPGASVKLSCKPSGYTFTSYWMNWVKQRPQGQGLEWIGMIDPSDSET
HYNQMFKDKATLTVDKSSNTAYMQLSSLTSEDSAVYYCAQIYYAYDKAYWGQGT
LTVSA (SEQ ID NO: 121)

7-H14 Light Chain Variable Region

DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSSHQKNYLAWYQQKPGQSPKLLIYWAST
RESGVPDRFTGSGSGTDFSLTISSVKAEDLAVYYCQEYYSWTFGGGKLEIK (SEQ ID
NO: 122)

6-B21 Heavy Chain Variable Region

EVQLQQSGPELVKPGASVKISCKASGYTFTDYMNWVKQSHGKSLEWIGDINPHNGGT
SFIQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCAPLGRKEGFAYWGQGTLLTV
SA (SEQ ID NO: 123)

6-B21 Light Chain Variable Region

DTVLTQSPASLVVSLGQRATISCRASKSVSTSGYSYMHWYQQKPGQPPKLLIYLASNLES
GVPARFSGSGSGTAFTLNHPVEEEDAATYYCQHSRELPYTFGGGKLEIK (SEQ ID
NO: 124)

10-F23 Heavy Chain Variable Region

QVTLKESGPGILQPSQTLSTCSFSGFSLSTFAMGVGWIRQPSGKGLEWLAHIWWDDDK
YYNPALKSRLTISKDTSKNHVFLKIANVDTADTATYYCARMPLTFYFDYWGQGTLLTV
SS (SEQ ID NO: 125)

10-F23 Light Chain Variable Region

DVLLTQTPLSLPVSLGDQASISCRSSQSIVHSNGHTYLEWYLQKPGQSPKLLIYKVSNRFS
GVPDRFSGSGSGTDFTLKISRVEAEDLGYYCFQGSHPVPTFGGGKLEIK (SEQ ID
NO: 126)

6-A12 Heavy Chain Variable Region

QVTLKESGPGILQPSQTLSTCSFSGFSLRTFAMGVGWIRQPSGKGLEWLAHIWWDDDK
YYNPALKSRLTISKDTSKNQVFLKIANVDTADTATYYCARMPLTFYFDYWGQGTLLTV
SS (SEQ ID NO: 127)

6-A12 Light Chain Variable Region

DVLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSTRF
SGVPDRFSGSGSGTDFTLKISRVEAEDLGYYCFQGSHPVPTFGGGKLEIK (SEQ ID
NO: 128)

6-M8 Heavy Chain Variable Region

QVQLQQPGAELVMPGASVKLSCKASGYTFTNYWMHWVKQRPQGLEWIGEIDPSDSY
TNYNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTROGSTYAWGQGTSTVVS
S (SEQ ID NO: 129)

6-M8 Light Chain Variable Region

DIVMTQAAFSNPVTLGTSASISCRSSKSLHSNGITYLYWYLQKPGQSPQLLIYQMSNLA
SGVPDRFSSSGSGTDFTLRISRVEAEDVGYYCAQNLELPPTFGGGKLEIK (SEQ ID
NO: 130)

2-A3 Heavy Chain Variable Region

EVQLQQSGPELVKPGASVKMSCKASGYTFTDYMMWVKQSHGKSLEWIGDINPYNGG
SSYNPKFKGRATLTVDKSSSTAYMQLNSLTSEDSAVYYCARGTYWGQGTTLTVSA
(SEQ ID NO: 131)

2-A3 Light Chain Variable Region

DVVMQTPTLTSLVTIGQPASISCKSSQSLLDSAGKTYLNWLLQRPQGSPKRLMYLVSKL
DSGVPDRFTGSGSGTDFTLKISRVEAEDLGVIYCWQGTTFPYTFGGGKLEIK (SEQ
ID NO: 132)

6-O17 Heavy Chain Variable Region

QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWIKQRPQGQGLEWIGEINPSNGGS
NYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYHCKSRGYWGQGTTLTVSS (SEQ
ID NO: 133)

6-O17 Light Chain Variable Region

DVVMQTPTLTSLVTIGQPASISCKSSQSLLDSYGKTYLNWLLQRPQGSPKRLIYLVSKLD
SGVPDRFTGSGSGTDFTLKISRVEAEDLGIYCWQGTTFPHTFGSGKLEIK (SEQ ID
NO: 134)

3-G5 Heavy Chain Variable Region

QVQLQQSGAELARPGASVKLSCKASGYTFTSYGISWVKQRTGQGLEWIGEIFPRSSNTY
YNEKFKGKATLTADKSSSTVYMEFRSLTSEDSAVYFCAREGGLAWFAYWGQGTTLTV
SA (SEQ ID NO: 135)

3-G5 Light Chain Variable Region

DVVMQTPTLTSLVTIGQPASISCKSSQSLLYTNGNTYLNWLLQRPQGSPKRLIYLVSKLD
SGIPDRFTGSGSGTDFTLRISRVEAEDLGVIYCLQSTHFPFTFGSGKLEIK (SEQ ID
NO: 136)

6-A15 Heavy Chain Variable Region

EVQLQQSGPELVKPGASVKMSCKASGYTITDYMMWLKQSHGKSLEWIGDINPYTGGT
SYNQKFKGKATLTVDKSSSTAYLQLHSLTSEDSAVYYCARGAYWGQGTTLTVSS (SEQ
ID NO: 137)

6-A15 Light Chain Variable Region

DVVMQTPTLTSLVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLD
SGVPDRFTGSGSGTDFTLKISRVEAEDLGVIYCWQGTTFPYTFGGGKLEIK (SEQ ID
NO: 138)

10-K10 Heavy Chain Variable Region

EVQLQQSGPELVKPGASVKMSCKASGYTITDYMMWLKQSHGKSLEWIGDINPYTGGT
SYNQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARGAYWGQGTTLTVSS
(SEQ ID NO: 139)

10-K10 Light Chain Variable Region

DVVMTQTPLTSLVTIGQPASISCKSSQSLLSDSGKTYLNLWLLQRPQGSPKRLLIYLVSKLD
SGVPDRFTGSGSGTDFTLQISRVEAEDLGVIYYCWQGTHTFPYTFGGGKLEIK (SEQ ID NO: 140)

6-P20 Heavy Chain Variable Region

EVQLQQSGPELVKPGASVKISCKASGYTFTDYIMNWVKQSHGRSLEIGDINPNNGGSN
FNQKFRGKATLTVDKSSSTAYMELRSLTSEDSAIYYCARMGYWGQGTLLTVSA (SEQ ID NO: 141)

6-P20 Light Chain Variable Region

DVVMTQTPLTSLVTIGQPASISCKSSQSLLHSDGKTYLNLWMFQRPQGSPKRLLIYLVSKLD
SGVPYRFTGGGSGTDFTLQISRVEDLGVIYYCWQGTHTFPRTFGGGKLEIK (SEQ ID NO: 142)

7-08 Heavy Chain Variable Region

EVQLQQSGPELVKPGASVKMSCKASGYTFTDYIHWVKQKPGQGLEYIGEIPGSGNT
YYNGKFRGKATLTADKSSSTAYMQLSSLTSEDSAVYFCGSGYFDYWGQGTLLTVSS
(SEQ ID NO: 143)

7-08 Light Chain Variable Region

DVVMTQTPLTSLVTIGQPASISCKSSQSLLYSNGKTYLNLWLLQSPGQSPKLLIYLVSKLES
GVPDRFSGSGSGTDFTLKLRSRVEAEDLGVIYYCVQGTHTFPFTFGSGKLEIK (SEQ ID NO: 144)

Rabbit mAb sequences

A11B1_16G7 Heavy Chain

METGLRWLLLVAVFKGVQCQEQLVESGGDLVKPGASLTCTASGFSFNKNYWMCWV
RQAPGKGLEWIGCIYNGDGNTYYASWVNGRFTISKTSSTTVTLQMTSLTVADTAIFYCA
RLLNMWGPGLTVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLPEPVTVTWNS
GTLTNGVRTFSPVRQSSGLYSLSSVSVTSSSQPVTCTNVAHPATNTKVDKTVAPSTCSKP
MCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRTA
RPPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEPK
VYTMGPPREELSSRSVSLTCMINGFYPSDISVEWENKGAEDNYKTTPTVLSDGSYFL
YSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO: 159)

A11B1_16G7 Light Chain

MDTRAPTQLLGLLLWLPGARCAIVMTQTPASVEAAVGGTVTIKCQASESIGNALAW
YQKPGQPPKLLIYTAATLASGVPSRFSGSGSGTEFTLTISGVQCDDAATYYCQSYFTS
VSSYGNAFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWE
VDGTTQTGTIENSKTPQNSADCTYNLSSLTTLTSTQYNHKEYTCKVTQGTTSVVQSFNR
GDC* (SEQ ID NO: 160)

A11B1_16E10 Heavy Chain

METGLRWLLLVAVLKGVCQCSLEESGGDLVKPGASLTLCRVSGFSFSSSYMCWVRQ
APGKGLEWIIACIGTTRGSTYYATWAKGRFTISKISSTTVTLQMTSLTDADTATYFCARDA
TGYRINTIGLYFNLWGPGTLVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLPE
PVTVTWNSGTLTNGVRTFSPVRQSSGLYSLSSVSVTSSSQPVTCNVAHPATNTKVDKT
VAPSTCSKPMCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYI
NNEQVRTARPPLEQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKA
RGQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPVL
DSDGSYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO:
161)

A11B1_16E10 Light Chain

MDTRAPTQLLGLLLLWLPGARCAFELTQTPSSVEAAVGGTPTIKCQASQTIYSYLSWYQ
QKPGQPPKLLIYEASKLASGVPSRFSGSGSDTYTLTISDLECAADATYYCQSYHGTAST
EYNTFGGGTEVVVRGDPVAPTFLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVDG
TTQTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNSHKEYTCKVTQGTTSVVQSFNRGDC
* (SEQ ID NO: 162)

A11B1_15G10 Heavy Chain

METGLRWLLLVAVLKGVCQCCQLVESGGGLVKPGAALTFTCTASGFSFSGNYWICWV
RQAPGKGLEWIIACIGTITSRTYYASWAKGRFTISKTSSTTVTLQMTSLTAADTATYFCAR
GAVVSSGNAPYYYFTLWGPGTLVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYL
PEPVTVTWNSGTLTNGVRTFSPVRQSSGLYSLSSVSVTSSSQPVTCNVAHPATNTKVD
KTVPSTCSKPMCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFT
WYINNEQVRTARPPLEQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTI
SKARGQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTP
TVLDSDGSYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID
NO: 163)

A11B1_15G10 Light Chain

MDTRAPTQLLGLLLLWLPGARCAFELTQTPSSVEAAVGGTVTIKCQASQSISSYLSWYQ
QKPGQPPKLLIYRASTLESVPSRFKSGSGTEFTLTISDLECAADATYFCQSYYGVTFSG
FAFGGGTEVVVKGDPVAPTFLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVDGTT
QTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNSHKEYTCKVTQGTTSVVQSFNRGDC*
(SEQ ID NO: 164)

A11B1_14H1 Heavy Chain

METGLRWLLLVAVLKGVCQCSLEESGGDLVKPGASLTLTCKASGIDFNHYWITWVRQA
PGKGLEWIIACIYVGITGRWYANWAKGRFTISKASSTVDLKMTSLTAADTATYFCARN
GDGGIYALNLWGPGTLVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLPEPVT
VTWNSGTLTNGVRTFSPVRQSSGLYSLSSVSVTSSSQPVTCNVAHPATNTKVDKTVAP
STCSKPMCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNE
QVRTARPPLEQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQ
PLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPVLDSG
SYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO: 165)

A11B1_14H1 Light Chain

MDTRAPTQLLGLLLLWLPGATFAQVLTQTASSVSAAVGGTVTISCQSSQSVYNNNWLA
WYQQKPGQPPKLLIYRASTLTSGVPSRFKSGSGTQFTLTISDLECDDAATYYCAGGYS
GNIYVNDFFGGGTEVVVKGDPVAPTFLIFPPAADQVATGTVTIVCVANKYFPDVTVTWE
VDGTTQTGTIENSKTPQNSADCTYNLSSTLTLTSTQYNHKEYTCKVTQGTTSVVQSFNR
GDC* (SEQ ID NO: 166)

A11B1_13G4 Heavy Chain

METGLRWLLLVAVLKGVQCQEQLLEESGGDLVKPGGSLTLTCKASGFSFSNTYWACWV
RQAPGKGLEWIACMNPASSGSSYYASWAKGRFTISKTSSTTVTLHMPSLTAADTATYFC
AKWDTAFDVWGPGLTVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLPEPVTV
TWNSTLTNGVRTFPSVRQSSGLYSLSSVSVTSSSQPVTVCNVAHPATNTKVDKTVAPS
TCSKPMCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNE
QVRTARPPLEQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQ
PLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSDG
SYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO: 167)

A11B1_13G4 Light Chain

MDTRAPTQLLGLLLLWLPGARCAADVMTQTPSSVEAAVGGTVTIKQASQSISSYLAW
YQQKPGQPPKLLIYGASNLESGVPSRFKSGSGTEYTLTISGVQCDDAATYYCQNYAI
DTYGHAFGGGTEVVVKGDPVAPTFLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEV
DGTQTGTIENSKTPQNSADCTYNLSSTLTLTSTQYNHKEYTCKVTQGTTSVVQSFNRG
DC* (SEQ ID NO: 168)

A11B1_13C3 Heavy Chain

METGLRWLLLVAVLKGVQCQEQLLEESGGDLVKPGASLTLTCTASGFSFSSNYHICWVR
QAPGKGLELIACIYVGDGSTYYASWAKGRFTISKSSSTTVLQMTSLTAADTATYFCGR
MFNLWGPGLTVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLPEPVTVTWNSG
TLTNGVRTFPSVRQSSGLYSLSSVSVTSSSQPVTVCNVAHPATNTKVDKTVAPSTCSKPM
CPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRTAR
PLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEPKVY
TMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSDGSYFLYSK
LSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO: 169)

A11B1_13C3 Light Chain

MDTRAPTQLLGLLLLWLPGAICDPVLTQTPSSVSAAVGVTVTINCQSSPSVYSNYLSWY
QQKPGQPPKLLIYLASTLASGVPSRFKSGSGTQFTLTISDVQCDDAATYYCAGTYSGNI
WSFGGGTEVVVKGDPVAPTFLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVDGTT
QTGTIENSKTPQNSADCTYNLSSTLTLTSTQYNHKEYTCKVTQGTTSVVQSFNRGDC*
(SEQ ID NO: 170)

A11B1_12F2 Heavy Chain

METGLRWLLLVAVLKGVQCQQQLVESGGGLVKPGASLTLTCTASGFSFSSGYHMCWV
RQAPGKGLEWIAFCGVYTGTTYASWAKGRFTISKTSSTTVTLQMTSLTVADTATYFCA
RISAENGDDLWGPGLTVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLPEPVTV

TWNSGTLTNGVRTFPSVRQSSGLYSLSSVSVTSSSQPVTCNVAHPATNTKVDKTVAPS
TCSKPMCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNE
QVRTARPPLEQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQ
PLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSDG
SYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO: 171)

A11B1_12F2 Light Chain

MDTRAPTQLLGLLLLWLPGARCDVVMQTTPASVEAAVGGTVTIKCQASQSSISNYFSWY
QQKPGQPPKLLIYRASTLASGVPSRFGSGSGTEFTLTISDLECADSATYYCQCTYGSSST
GFGFGGGTEVVVKGDVPAPTVPFPPAADQVATGTVTIVCVANKYFPDVTVTWEVDGT
TQTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNHKEYTCKVTQGTTSVVQSFNRGDC*
(SEQ ID NO: 172)

A11B1_11D10 Heavy Chain

METGLRWLLLVAVLKGVQCQSLEESGGDLVKPGASLTLTCMASGIDFSSGYGMWWVR
QAPGKGLEIYIGYIDTGDDNTYYANWAKGRFTISKTSSTTVTLQMTSLTVADTATYFCAK
GGAILDWPGTGLTVVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLPEPVTVTWN
SGTLTNGVRTFPSVRQSSGLYSLSSVSVTSSSQPVTCNVAHPATNTKVDKTVAPSTCSK
PMCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRT
ARPPLEQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEP
KVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSDGSYF
LYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO: 173)

A11B1_11D10 Light Chain

MDTRAPTQLLGLLLLWLPGARCADIVMTQTPASVEAAVGGTVTIKCQASQSSISYLAWY
QQKPGQRPKLLIYRASTLKSVPFRFGSGSGTEYTLTISDLECADAAATYYCQAYYSSS
ISYGNTFGGGTEVVVKGDVPAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVD
GTTQTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNHKEYTCKVTQGTTSVVQSFNRGD
C* (SEQ ID NO: 174)

A11B1_10F9 Heavy Chain

METGLRWLLLVAVLKGVQCQSLEESGGDLVKPGASLTLTCTASGFSLSGYGMCWVR
QAPGKGLEWIGYTDATGTIHYASWAKGRFTISKTSSTTVTLQMTSLTAADTATYFCAK
GGAMDLWPGTGLTVVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLPEPVTVTW
NSGTLTNGVRTFPSVRQSSGLYSLSSVSVTSSSQPVTCNVAHPATNTKVDKTVAPSTCS
KPMCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVR
TARPPLEQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEP
KVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSDGSYF
LYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO: 175)

A11B1_10F9 Light Chain

MDTRAPTQLLGLLLLWLPGARCADIVMTQTPASVEAAVGGTVTIKCQASQSSISYLAWY
QQKPGQPPKLLIYRTSTLASGVPSRFGSGSGTEYTLTISDLECADAAATYYCQSYAYSSSS
SYGNAFGGGTEVVVKGDVPAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVD
GTTQTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNHKEYTCKVTQGTTSVVQSFNRGD
C* (SEQ ID NO: 176)

A11B1_7H12 Heavy Chain

METGLRWLLLVAVLKGVQCQSLEESGGDLVKPGASLTCTCTGSGIDFSSSYWICWVRQ
APGKGLEWIIACIDGSDGNTYYASWARGRFTISKTSSTTVTLQMASLTAADTATYFCTR
LRLWGPGLTVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLPEPVTVTWNSGT
LTNGVRTFSPVRQSSGLYSLSSVSVTSSSQPVTCNV AHPATNTKV DKT VAPSTCSKPM
CPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRTAR
PLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEPKVY
TMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSDGSYFLYSK
LSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO: 177)

A11B1_7H12 Light Chain

MDTRAPTQLLGLLLWLPGARCA DIVLTQTPASVSAAVGGT VTINCQASQNVYSNNAL
AWHQKPGQRPNLLIYKASTLASGVPSRFKGS GSGTQFTLTISDVQCDDAATYYCLGEF
SCSSGDCVFVGGGTEVVVKGDPVAPT VLI FPPAADQVATGTVTIVCVANKYFPDVTVTW
EVDGTTQT TGIENSKTPQNSADCTYNLSSTLTLTSTQYN SHKEYTCKVTQGTTSVVQSFN
RGDC* (SEQ ID NO: 178)

A11B1_7G12 Heavy Chain

METGLRWLLLVAVLKGVQCQSLEESGGDLVKPGASLTCTCMASGIDFSSGYGMWWVR
QAPGKGLEIYIGYIDTGDDNTYYANWAKGRFTISKTSSTTVTLQMTSLTVADTATYFCAK
GGAILDWGPGLTVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLPEPVTVTWN
SGTLTNGVRTFSPVRQSSGLYSLSSVSVTSSSQPVTCNV AHPATNTKV DKT VAPSTCSK
PMCPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRT
ARPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEP
KVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSDGSYF
LYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO: 179)

A11B1_7G12 Light Chain

MDTRAPTQLLGLLLWLPGARCA DIVMTQTPASVEAAVGGT VTIKCQASQSISSYLAWY
QQKPGQRPKLLIYRASTLKSGVPSRFKGS GSGTEYTLTISDLECADAATYYCQAYYLS
ISYGNFTFGGTEVVVKGDPVAPT VLI FPPAADQVATGTVTIVCVANKYFPDVTVTWEVD
GTTQT TGIENSKTPQNSADCTYNLSSTLTLTSTQYN SHKEYTCKVTQGTTSVVQSFNRGD
C* (SEQ ID NO: 180)

A11B1_6G4 Heavy Chain

METGLRWLLLVAVLKGVQCQQQLEESGGGLVKPGGTLTLTCKASGVALNPYYMCW
VRQAPGKGLEWIIACVDADSSGSTYYASWAKGRFTISKTSSTTVTLKMTSLTAADTATYF
CARESDYSSVGIGYVHGTDLWGPGLTVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLG
CLVKGYLPEPVTVTWNSGTLTNGVRTFSPVRQSSGLYSLSSVSVTSSSQPVTCNV AHP
ATNTKV DKT VAPSTCSKPMCPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQD
DPEVQFTWYINNEQVRTARPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKAL
PAPIEKTISKARGQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAED
NYKTTPTVLDSDGSYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK*
(SEQ ID NO: 181)

A11B1_6G4 Light Chain

MDTRAPTQLLGLLLLWLPGARCA DIVVTQTPSSVSAAVGGTVTIKCQASQSSISNYFSWY
QQKPGQPPKLLIYRASTLASGVPSRFKSGSGTEFTLTISDLECAATAATYYCQCTYGRSN
SNFFYGFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEV
DGTTQTGTGIENSKTPQNSADCTYNLSSLTLTSTQYNHKEYTCKVTQGTTSVVQSFNRG
DC* (SEQ ID NO: 182)

A11B1_6F9 Heavy Chain

METGLRWLLLVAVLKGVQCQSLEESGGDLVKPGASLTCTASGSSFSSTYWNCWVRQ
APGKGLEWIIACINAGSGTTYASWAKGRFTVSKTSSTTVTLQMTSLTAADTATYFCTR
SDGRFSSGYFNLWGPGLTVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLPEP
VTVTWNSGTLTNGVRTFPSVRQSSGLYSLSSVSVTSSSQPVTCNVAHPATNTKVDKTV
APSTCSKPMCPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYIN
NEQVRTARPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKAR
GQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDS
DGSYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO:
183)

A11B1_6F9 Light Chain

MDTRAPTQLLGLLLLWLPGATFAQVLTQTASPVSAAVGGTVTINCQSSQSVYDNNWLA
WYQQKPGQPPKLLIDASKLTSGVSSRFKSGSGTQFTLTISGVQCDDAATYYCQGAYY
SSGWYWAFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWE
VDGTTQTGTGIENSKTPQNSADCTYNLSSLTLTSTQYNHKEYTCKVTQGTTSVVQSFNR
GDC* (SEQ ID NO: 184)

A11B1_6C7 Heavy Chain

METGLRWLLLVAVLKGVQCQQQLEESGGGLVKPGGTLTCTKASGIDFSSYYYMCWV
RQAPGKGLELIVCIYTSSGGTWYASWVNGRLTISRSTSLNTVDLKMTSLTAADTATYFC
ARGVYSGSSDYPTRLDLWGQGLTVTVSLGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKG
YLPEPVTVTWNSGTLTNGVRTFPSVRQSSGLYSLSSVSVTSSSQPVTCNVAHPATNTK
VDKTVAPSTCSKPMCPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQF
TWYINNEQVRTARPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKT
ISKARGQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTT
TVLDS DGSYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID
NO: 185)

A11B1_6C7 Light Chain

MDTSTSTALLGLLLLWLTGARCAIEMTQSPPSLSASVGETVRIRCLASEDIYSGISWYQQ
KPEKPPTLLISGASNLESGVPPRFSGGGSGTDYTLTIGGVQAEDVATYYCLGGYSFSSTG
LTFGAGTKVEIKRDPVAPSVLLFPFSKEELTTGTATIVCVANKYFPDVTVTWEVDGTTQT
GTGIENSKTPQNSADCTYNLSSLTLTSTQYNHKEYTCKVTQGTTSVVQSFNRGDC*
(SEQ ID NO: 186)

A11B1_6B6 Heavy Chain

METGLRWLLLVAVLKGVQCQQHLVESGGGLVKPGASLTCTASGFSFTTGYHMCWV
RQAPGKGLEWIIACFGVYTSTTTYASWAKGRFTISKTSSTTVTLQMTSLTVADTATYFCA

RISAEDGGDLWGPGLTLTVSSGQPKAPSVFPLAPCCGDTSPSSTVTLGCLVKGYLPEPVT
TWNSGTLTNGVRTFPSVRQSSGLYSLSSVSVTSSSQPVTCNVAHPATNTKVDKTVAP
TCSKPMCPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNE
QVRTARPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQ
PLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWENKGAEDNYKTTPTVLDSDG
SYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO: 187)

A11B1_6B6 Light Chain

MDTRAPTQLLGLLLLWLPGARCDVVMQTTPASVEAAVGGTVTITCQASQSNYFSWY
QQKPGQPPKLLIYRASTLASGVPSRFGSGSGTQFTLTISDLECADSATYACQCTYGSST
GFGFGGGTEVVVKGDPVAPTFLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVDGT
TQTTGIENSKTPQNSADCTYNLSSLTLTSTQYNHKEYTCKVTQGTTSVVQSFNRGDC*
(SEQ ID NO: 188)

A11B1_5F7 Heavy Chain

METGLRWLLLVAVLKGVQCQSLEESGGDLVKPGASLTLTCKASGFSFSSYFWICWVRQ
APGKGLEWSACIYGDSSGSSYYASWAKGRFTISKTSSTTVTLQMTSLTAADTATYFCAS
YGSSSYYYSNLWGPGLTLTVSSGQPKAPSVFPLAPCCGDTSPSSTVTLGCLVKGYLPEPVT
VTWNSGTLTNGVRTFPSVRQSSGLYSLSSVSVTSSSQPVTCNVAHPATNTKVDKTVAP
STCSKPMCPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNE
QVRTARPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQ
PLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWENKGAEDNYKTTPTVLDSDG
SYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO: 189)

A11B1_5F7 Light Chain

MDTRAPTQLLGLLLLWLPGAICDPVMTQTPSSTSAAVGGTVTISCQSSQSVYNNNYLAW
YQQKPGQPPKRLIYESSKLASGVPSRFRGSGGAQFTLTISDLECDAAATYCYCLGAYYTT
LDFGGGTEVVVRGDPVAPTFLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVDGTT
QTTGIENSKTPQNSADCTYNLSSLTLTSTQYNHKEYTCKVTQGTTSVVQSFNRGDC*
(SEQ ID NO: 190)

A11B1_5D7 Heavy Chain

METGLRWLLLVAVLKGVQCQEQLVESGGGLVQPEGSLTLTCKASGFDFFSSNAMCWVR
QAPGKLEWIACIYNGDGSTYYASWVNGRFTISKTSSTTVTLQMTSLTAADTATYFCAR
GLSNWNRDNLWGPGLTLTVSSGQPKAPSVFPLAPCCGDTSPSSTVTLGCLVKGYLPEPVT
VTWNSGTLTNGVRTFPSVRQSSGLYSLSSVSVTSSSQPVTCNVAHPATNTKVDKTVAP
STCSKPMCPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNE
QVRTARPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQ
PLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWENKGAEDNYKTTPTVLDSDG
SYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO: 191)

A11B1_5D7 Light Chain

MDTRAPTQLLGLLLLWLPGATFAQVLTQTPSSVSAAVGGTATINCQASQSLYSPKNLAW
YQQTPGQPPKLLIYSASKLASGVPSRFKSGSGTQFTLTISGVQCDDAAIYYCQGEFSCTT
AACFAFGGGTEVVVKGDPVAPTFLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVD

GTTQTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNHKEYTCKVTQGTTSVVQSFNRGDC* (SEQ ID NO: 192)

A11B1_5A7 Heavy Chain

METGLRWLLLVAVLKGVQCQSLEESGGGLVQPEGSLTLACTASGFSFSSYYYICWVRQ
APGTGLEWIGCINTGSDDTHYASWLKGRFTFSKASSTTLTLQMTSLTAADTATYFCARS
SGSSDDAYDLWGPGTLVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLPEPVT
VTWNSGTLTNGVRTFPSVRQSSGLYSLSSVSVTSSSQPVTCNVAHPATNTKVDKTVAP
STCSKPMCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNE
QVRTARPPLEQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQ
PLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSDG
SYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO: 193)

A11B1_5A7 Light Chain

MDTRAPTQLLGLLLWLPGARCDVVMTPASVSEPVGGAVTIKCQASQSIGSNLAWY
QHKPGQPPKLLIYFASSLASGVSSRFKGGSGTQFTLTISDLECADAAATYYCHCTYYPLS
YVTFGGGTEVVVKGDPVAPTFLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVDGT
TQTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNHKEYTCKVTQGTTSVVQSFNRGDC*
(SEQ ID NO: 194)

A11B1_4E1 Heavy Chain

METGLRWLLLVAVLKGVQCQSLEESGGDLVKPGTSLTLSTASGFSFGSYYYMCWVRQ
APGKGLEWIACIDVGSSGDTYYASWVNGRFTISKTSSTTVTLQMTSLTAADTATYFCAR
DDTAAGGFGNLELWGPGTLVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLPE
PVTVTWNSGTLTNGVRTFPSVRQSSGLYSLSSVSVTSSSQPVTCNVAHPATNTKVDKT
VAPSTCSKPMCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYI
NNEQVRTARPPLEQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKA
RGQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVL
DSDGSYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO:
195)

A11B1_4E1 Light Chain

MDTRAPTQLLGLLLWLPGARCAFELTQTPSSVSEPVGGTVTIKCQASQSIYSYFSWYQ
QKPGQPPKRLIYQASTLASGVPSRFKGSSTGDTFTLTISDLECADAAATYYCQNNYGRGS
GSYFFGFGGGTEVVVKGDPVAPTFLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEV
DGTTQTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNHKEYTCKVTQGTTSVVQSFNRG
DC* (SEQ ID NO: 196)

A11B1_3H9 Heavy Chain

METGLRWLLLVAVLKGVQCQSLEESGGDLVKPGASLTLTCKASGIDFSSGYGMWWVR
QAPGKLEYIGYIDTGSSTYYANWAKGRFTISKTSSTMVTLQMTSLTVADTATYFCAK
GGAIDLWGPGTLVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLPEPVTVTWN
SGTLTNGVRTFPSVRQSSGLYSLSSVSVTSSSQPVTCNVAHPATNTKVDKTVAPSTCSK
PMCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRT
ARPPLEQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEP

KVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSGDSYF
LYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO: 197)

A11B1_3H9 Light Chain

MDTRAPTQLLGLLLLWLPGARCAIVMTQTPASVEAAVGGTVTIKCQASQSISSYLAWY
QQKPGQRPKLLIYRASTLASGVPSRFKGSMSGTDYTLTISDLECADAATYYCHTYLSSS
ISYGNTFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVD
GTTQTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNHKEYTCKVTQGTTSVVQSFNRGD
C* (SEQ ID NO: 198)

A11B1_3G2 Heavy Chain

METGLRWLLLVAVLKGVQCQEQLSESGGDLVKPEGSLTLTCKASGFSFSSIWICWVRQ
APGKGLEWIACTTVVKSGRTYYANWAKGRFTISKTSSTTVTLQMTSLTAADTATYFCA
REFVDGGGSSGRDLWPGTLTVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLP
EPVTVTWNSGTLTNGVRTFPSVRQSSGLYSLSSVSVTSSSQPVTCNVAHPATNTKVDK
TVAPSTCSKPMCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTW
YINNEQVRTARPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTIS
KARGQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPT
VLDSGDSYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID
NO: 199)

A11B1_3G2 Light Chain

MDTRAPTQLLGLLLLWLPGARCAIDMTQTPASVEAAVGGTVTIKCQASQSISRDLRWY
QQKPGQPPKRLIYKASTLASGVPSRFKGSMSGTDFTLTISDLECADAATYYCQQGYSSID
VDNDFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVDG
TTQTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNHKEYTCKVTQGTTSVVQSFNRGDC
* (SEQ ID NO: 200)

A11B1_3B1 Heavy Chain

METGLRWLLLVAVLKGVQCQEQLSESGGLVKPEGSLTLTCKASGFDLSSGYDMCWV
RQAPGKGLEWIAICYADYSGSTYYASWVNGRFTISSSTSLNTVDLKMSTLTAADTATYF
CARGATGNGGYGYFNLWPGTLTVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVK
GYLPEPVTVTWNSGTLTNGVRTFPSVRQSSGLYSLSSVSVTSSSQPVTCNVAHPATNT
KVDKTVAPSTCSKPMCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEV
QFTWYINNEQVRTARPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIE
KTISKARGQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKT
TPTVLDSGDSYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ
ID NO: 201)

A11B1_3B1 Light Chain

MDTRAPTQLLGLLLLWLPGARCAIVMTQTPASVSEPVGGTVTIKCQASQNINSGLAWY
QQKPGQPPKLLIYKASTLASGVSSRFKGSMSGTEFTLTISDLECADAATYYCQTYYYSSS
SSDNAFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVD
GTTQTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNHKEYTCKVTQGTTSVVQSFNRGD
C* (SEQ ID NO: 202)

A11B1_2D3 Heavy Chain

METGLRWLLLVAVLKGVQCQSLEESGGDLVKPGASLTLTCTASGFSFSSSYWICWVRQ
 APGKGLEWYIACIYGGSSGNIAYASWAKGRFTISKTSSTTVTLQMTSLTAADTATYFCAR
 DIPSDAFTLDLWPGTGLVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLPEPVT
 VTWNSGTLTNGVRTFSPVRQSSGLYSLSSVSVTSSSQPVTCNVAHPATNTKVDKTVAP
 STCSKPMCPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNE
 QVRTARPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQ
 PLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSDG
 SYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO: 203)

A11B1_2D3 Light Chain

MDTRAPTQLLGLLLWLPGATFAQVLTQTPSSVSAAVGSTVTINCQASQSVYKDNLA
 WYQQKPGQPPKLLIYKASTLASGVPSRFKSGSGTQFTLTISGVQCEDAATYYCQGEFS
 CGSADCFAGGGTEVVVKGDPVAPTFLIFPPAADQVATGTVTIVCVANKYFPDVTVTWE
 VDGTQTGTGIENSKTPQNSADCTYNLSSTLTLTSTQYNHKEYTCKVTQGTTSVVQSFNR
 GDC* (SEQ ID NO: 204)

A11B1_2A7 Heavy Chain

METGLRWLLLVAVLKGVQCQSLEESGGDLVKPGASLTLTCKGSGIDFSSGYGMWWVR
 QAPGKGLEIYIGYIDTGYGSTYYASWAKGRFTISKTSSTTVTLQMTSLTVADTATYFCAK
 GGAILDLWPGTGLVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLPEPVTVTWN
 SGTLTNGVRTFSPVRQSSGLYSLSSVSVTSSSQPVTCNVAHPATNTKVDKTVAPSTCSK
 PMCPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRT
 ARPPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEP
 KVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSDGSYF
 LYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO: 205)

A11B1_2A7 Light Chain

MDTRAPTQLLGLLLWLPGATFAAVLTQTPASTSAAVGGTGTINCQSSQSVYRSNWL
 WYQQKPGQPPKLLIYDVFNLASGVPSRFKSGSGTQFTLTISGVQCADAATYYCQGSYY
 SGNWYSAFGGGTEVVVKGDPVAPTFLIFPPAADQVATGTVTIVCVANKYFPDVTVTWE
 VDGTQTGTGIENSKTPQNSADCTYNLSSTLTLTSTQYNHKEYTCKVTQGTTSVVQSFNR
 GDC* (SEQ ID NO: 206)

*Human mAb sequences**Heavy Chain and Light Chain Variable Region Sequences***2004_04_B03**

Heavy Chain FR1	QVQLVESGGGVVQPGRSLRLSCAAS (SEQ ID NO: 208)
Heavy Chain CDR1	GFTFSNYG (SEQ ID NO: 209)
Heavy Chain FR2	MNWVRQAPGKLEWVSY (SEQ ID NO: 210)
Heavy Chain CDR2	ISSSGSTV (SEQ ID NO: 211)
Heavy Chain FR3	YYADSVKGRFTISRDNKNSLYLQMNSLRDEDTA VYYCAS (SEQ ID NO: 212)
Heavy Chain CDR3	GQLDTSDAFDI (SEQ ID NO: 213)

Heavy Chain FR4	WGQGTLLVTVSS (SEQ ID NO: 214)
Heavy Chain V Gene Segment	IGHV3-48
Light Chain FR1	DIEMTQSPSSPSASVGDRVTITCRAS (SEQ ID NO: 215)
Light Chain CDR1	QSISSY (SEQ ID NO: 216)
Light Chain FR2	LNWYQQKPGKAPKLLIY (SEQ ID NO: 217)
Light Chain CDR2	AAS (SEQ ID NO: 218)
Light Chain FR3	SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC (SEQ ID NO: 219)
Light Chain CDR3	QQSYSTPLT (SEQ ID NO: 220)
Light Chain FR4	FGGGTKVEIK (SEQ ID NO: 221)
Light Chain V Gene Segment	IGKV1-39;IGKV1D-39
Light Chain Locus	kappa

2004_05_A06

Heavy Chain FR1	EVQLLESGGGVVQSGRSLRVSCAAS (SEQ ID NO: 222)
Heavy Chain CDR1	GFSFSSYG (SEQ ID NO: 223)
Heavy Chain FR2	MHWVRQAPGKGLEWVSY (SEQ ID NO: 224)
Heavy Chain CDR2	ISSSGSTI (SEQ ID NO: 225)
Heavy Chain FR3	YYADSVKGRFTISRDNALNSLYLQMNSLRRAEDTAVYYCAR (SEQ ID NO: 226)
Heavy Chain CDR3	DLGHFDGSSYFDY (SEQ ID NO: 213)
Heavy Chain FR4	WGQGTLLVTVSS (SEQ ID NO: 214)
Heavy Chain V Gene Segment	IGHV3-48
Light Chain FR1	DIQMTQSPSSLSASVGDRVTITCRAS (SEQ ID NO: 227)
Light Chain CDR1	QGISNY (SEQ ID NO: 228)
Light Chain FR2	LAWYQQKPGKVPKLLIY (SEQ ID NO: 229)
Light Chain CDR2	AAS (SEQ ID NO: 218)
Light Chain FR3	TLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC (SEQ ID NO: 230)
Light Chain CDR3	QQSYSTPLT (SEQ ID NO: 220)
Light Chain FR4	FGGGTKVEVK (SEQ ID NO: 231)
Light Chain V Gene Segment	IGKV1-27
Light Chain Locus	kappa

2004_04_C12

Heavy Chain FR1	EVQLLESGGGVVQPGRSLRLSCAAS (SEQ ID NO: 232)
Heavy Chain CDR1	GFTFSNYG (SEQ ID NO: 209)
Heavy Chain FR2	MNWVRQAPGKGLEWVSY (SEQ ID NO: 210)
Heavy Chain CDR2	ISSSSSTI (SEQ ID NO: 233)
Heavy Chain FR3	YYADSVKGRFTISRDNALNSLYLQMNSLRDEDTAVYYCAS (SEQ ID NO: 212)

Heavy Chain CDR3	GQXDXSDAFDI (SEQ ID NO: 234)
Heavy Chain FR4	WGQGTLLVTVSS (SEQ ID NO: 214)
Heavy Chain V Gene Segment	IGHV3OR16-8
Light Chain FR1	DIEMTQSPSSPSASVGDRVTITCRAS (SEQ ID NO: 215)
Light Chain CDR1	QSISSY (SEQ ID NO: 216)
Light Chain FR2	LNXYQQKPGKAPKLLXY (SEQ ID NO: 235)
Light Chain CDR2	XAS (SEQ ID NO: 236)
Light Chain FR3	SLQSGVPSRFSGSGSGTDFTLTISSLQPEDXATYYC (SEQ ID NO: 237)
Light Chain CDR3	QQSYSTPLT (SEQ ID NO: 220)
Light Chain FR4	FGGGXKXEIK (SEQ ID NO: 238)
Light Chain V Gene Segment	IGKV1-39; IGKV1D-39
Light Chain Locus	kappa

2002_02_B07

Heavy Chain FR1	EVQLLESGGGVVQPGRSLRLSCAAS (SEQ ID NO: 232)
Heavy Chain CDR1	GFTFSTYG (SEQ ID NO: 209)
Heavy Chain FR2	MHWVRQAPGKGLEWVSY (SEQ ID NO: 224)
Heavy Chain CDR2	ISSSGSTI (SEQ ID NO: 225)
Heavy Chain FR3	YYADSVKGRFAISRDNKNTLYLQMNSLRAEDTALYYCAK (SEQ ID NO: 239)
Heavy Chain CDR3	ATRYDILTGYSDGVDYFDY (SEQ ID NO: 240)
Heavy Chain FR4	WGQGTLLVTVSS (SEQ ID NO: 214)
Heavy Chain V Gene Segment	IGHV3-48
Light Chain FR1	DIQMTQSPSSLSASVGDRVTITCRAS (SEQ ID NO: 227)
Light Chain CDR1	QSISSY (SEQ ID NO: 216)
Light Chain FR2	LNWYQQKPGKAPKLLIY (SEQ ID NO: 217)
Light Chain CDR2	AAS (SEQ ID NO: 218)
Light Chain FR3	SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC (SEQ ID NO: 219)
Light Chain CDR3	HQSYSTPYT (SEQ ID NO: 241)
Light Chain FR4	FGQGTKLEIK (SEQ ID NO: 242)
Light Chain V Gene Segment	IGKV1-39; IGKV1D-39
Light Chain Locus	kappa

2004_05_B04

Heavy Chain FR1	QVQLVESGGGLVQPGGSLRLSCAAS (SEQ ID NO: 243)
Heavy Chain CDR1	GFTFSSYW (SEQ ID NO: 209)
Heavy Chain FR2	MSWVRQAPGKGLEWVAN (SEQ ID NO: 244)
Heavy Chain CDR2	IKQDGSEK (SEQ ID NO: 245)

Heavy Chain FR3	YYVDSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCAR (SEQ ID NO: 246)
Heavy Chain CDR3	VTSPHAFDI (SEQ ID NO: 247)
Heavy Chain FR4	WGRGTLVTVSS (SEQ ID NO: 248)
Heavy Chain V Gene Segment	IGHV3-7
Light Chain FR1	DIQMTQSPSAMSASVGDRVTITCRAS (SEQ ID NO: 249)
Light Chain CDR1	QGISNY (SEQ ID NO: 228)
Light Chain FR2	LAWFQQKPGKVPKRLIY (SEQ ID NO: 250)
Light Chain CDR2	AAS (SEQ ID NO: 218)
Light Chain FR3	SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC (SEQ ID NO: 219)
Light Chain CDR3	QQSYSTPLT (SEQ ID NO: 220)
Light Chain FR4	FGGGTKVEVK (SEQ ID NO: 231)
Light Chain V Gene Segment	IGKV1-39; IGKV1D-17; IGKV1D-39
Light Chain Locus	kappa

2003_03_E12

Heavy Chain FR1	QVQLVESGGGVVRPGGSLRLSCAAS (SEQ ID NO: 251)
Heavy Chain CDR1	GFTFDDYG (SEQ ID NO: 209)
Heavy Chain FR2	MSWVRQAPGKGLEWVSG (SEQ ID NO: 252)
Heavy Chain CDR2	INWNGGST (SEQ ID NO: 253)
Heavy Chain FR3	GYADSVKGRFTISRDNKNTLYLQMNSLRGEDTAVYYCVT (SEQ ID NO: 254)
Heavy Chain CDR3	QGSAFDI (SEQ ID NO: 255)
Heavy Chain FR4	WGRGTLVTVSS (SEQ ID NO: 248)
Heavy Chain V Gene Segment	IGHV3-20
Light Chain FR1	SYELTQPPSLSVSPGQTARITCSGD (SEQ ID NO: 256)
Light Chain CDR1	ALAKQY (SEQ ID NO: 257)
Light Chain FR2	AYWYQQTPGQAPVLVIY (SEQ ID NO: 258)
Light Chain CDR2	KDT (SEQ ID NO: 259)
Light Chain FR3	ERPSGIPERFSGSSSGTTVTLTISGVQAEDEVYYC (SEQ ID NO: 260)
Light Chain CDR3	QSTDSSGTQV (SEQ ID NO: 261)
Light Chain FR4	FGGGTKLTVL (SEQ ID NO: 262)
Light Chain V Gene Segment	IGLV3-25
Light Chain Locus	lambda

1994_01_C07

Heavy Chain FR1	QVQLVQSGAEVKKPGASVKVCKAS (SEQ ID NO: 263)
Heavy Chain CDR1	GYTFTSYG (SEQ ID NO: 209)
Heavy Chain FR2	ISWVRQAPGQGLEWMGW (SEQ ID NO: 264)

Heavy Chain CDR2	ISAYNGNT (SEQ ID NO: 265)
Heavy Chain FR3	NYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAAYYCAR (SEQ ID NO: 266)
Heavy Chain CDR3	VTGITGTTIDP (SEQ ID NO: 267)
Heavy Chain FR4	WGQGTMTVTSS (SEQ ID NO: 268)
Heavy Chain V Gene Segment	IGHV1-18
Light Chain FR1	DIQMTQSPSSLSASVGDRVTITCRAS (SEQ ID NO: 227)
Light Chain CDR1	QSISSY (SEQ ID NO: 216)
Light Chain FR2	LNWYQQKPGKAPKLLIY (SEQ ID NO: 217)
Light Chain CDR2	DAS (SEQ ID NO: 269)
Light Chain FR3	SLESGVPSRFSGSGSGTEFTLTISLQPDFAVYYC (SEQ ID NO: 270)
Light Chain CDR3	QQYNNWPQT (SEQ ID NO: 271)
Light Chain FR4	FGQGTKVEIK (SEQ ID NO: 272)
Light Chain V Gene Segment	IGKV1-13; IGKV1D-13
Light Chain Locus	kappa

1995_01_G07

Heavy Chain FR1	QVQLVESGGGLVKPGGSLRLSCAAS (SEQ ID NO: 273)
Heavy Chain CDR1	GFTFSSYA (SEQ ID NO: 209)
Heavy Chain FR2	MSWVRQAPGKGLEWVSA (SEQ ID NO: 274)
Heavy Chain CDR2	ISGSGGST (SEQ ID NO: 275)
Heavy Chain FR3	YYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAR (SEQ ID NO: 276)
Heavy Chain CDR3	DYGGYDGVYFDY (SEQ ID NO: 277)
Heavy Chain FR4	WGRGTLTVSS (SEQ ID NO: 248)
Heavy Chain V Gene Segment	IGHV3-23
Light Chain FR1	SYELTQDPAVSVALGQTVRITCQGD (SEQ ID NO: 278)
Light Chain CDR1	SLRSYY (SEQ ID NO: 279)
Light Chain FR2	ASWYQQKPGQAPVLVIY (SEQ ID NO: 280)
Light Chain CDR2	GKN (SEQ ID NO: 281)
Light Chain FR3	NRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYC (SEQ ID NO: 282)
Light Chain CDR3	NSRDSSGNHVV (SEQ ID NO: 283)
Light Chain FR4	FGGGTKVTVL (SEQ ID NO: 284)
Light Chain V Gene Segment	IGLV3-19
Light Chain Locus	lamdba

1995_01_G05

Heavy Chain FR1	EVQLLES GGGLVKPGGSLRLSCAAS (SEQ ID NO: 285)
Heavy Chain CDR1	GFTFSSYA (SEQ ID NO: 209)

Heavy Chain FR2	MHWVRQAPGKGLEWVAV (SEQ ID NO: 286)
Heavy Chain CDR2	ISYDGSNK (SEQ ID NO: 287)
Heavy Chain FR3	YYADSVKGRFAISRDNKNTLYLQMNSLRAEDTAVYYCAR (SEQ ID NO: 288)
Heavy Chain CDR3	DRDVGPTYYYYGMDV (SEQ ID NO: 289)
Heavy Chain FR4	WGQGTMTVTSS (SEQ ID NO: 268)
Heavy Chain V Gene Segment	IGHV3-30
Light Chain FR1	SYELTQPPSLSVSPGQTARITCSGH (SEQ ID NO: 290)
Light Chain CDR1	ALPKQY (SEQ ID NO: 291)
Light Chain FR2	AYWYQQTPGQAPVLVIY (SEQ ID NO: 258)
Light Chain CDR2	KDT (SEQ ID NO: 259)
Light Chain FR3	ERPSGIPERFSGSSSGTTVTLTISGVQAEDEADYYC (SEQ ID NO: 292)
Light Chain CDR3	QSADSSGPYQV (SEQ ID NO: 293)
Light Chain FR4	FGGGTQLTVL (SEQ ID NO: 294)
Light Chain V Gene Segment	IGLV3-25
Light Chain Locus	Iambda

2004_03_G10

Heavy Chain FR1	EVQLLESGGGVVQPGRSLRLSCAAS (SEQ ID NO: 232)
Heavy Chain CDR1	GFTFSSYA (SEQ ID NO: 209)
Heavy Chain FR2	MSWVRQAPGKGLEWVSA (SEQ ID NO: 274)
Heavy Chain CDR2	ISGSGGST (SEQ ID NO: 275)
Heavy Chain FR3	YYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAK (SEQ ID NO: 295)
Heavy Chain CDR3	DREYIAVAADY (SEQ ID NO: 296)
Heavy Chain FR4	WGQGTMTVTSS (SEQ ID NO: 297)
Heavy Chain V Gene Segment	IGHV3-23
Light Chain FR1	DIQMTQSPSSLSASVGDITISITCRAS (SEQ ID NO: 298)
Light Chain CDR1	QSISSY (SEQ ID NO: 216)
Light Chain FR2	LNWYQQKPGKAPKLLIY (SEQ ID NO: 217)
Light Chain CDR2	AAS (SEQ ID NO: 218)
Light Chain FR3	SLQSGVPSRFSGSGSRTDFTLTISVQPEDFATYYC (SEQ ID NO: 299)
Light Chain CDR3	QQSYSTPFT (SEQ ID NO: 300)
Light Chain FR4	FGPGTKVEIK (SEQ ID NO: 301)
Light Chain V Gene Segment	IGKV1-39; IGKV1D-39
Light Chain Locus	kappa

2002_02_B05

Heavy Chain FR1	EVQLLESGGGVVQPGRSLRLSCAAS (SEQ ID NO: 232)
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Heavy Chain CDR1	GFTFSTYG (SEQ ID NO: 209)
Heavy Chain FR2	MHWVRQAPGKGLEWVSY (SEQ ID NO: 224)
Heavy Chain CDR2	ISSSGSTI (SEQ ID NO: 225)
Heavy Chain FR3	YYADSVKGRFAISRDNANTLYLQMNSLRAEDTALYYCAK (SEQ ID NO: 239)
Heavy Chain CDR3	ATRYDILTGYSDDGVDYFDY (SEQ ID NO: 240)
Heavy Chain FR4	WGQGTLLTVSS (SEQ ID NO: 214)
Heavy Chain V Gene Segment	IGHV3-48
Light Chain FR1	DIQMTQSPSSLSASVGDRVTITCRAS (SEQ ID NO: 227)
Light Chain CDR1	QSISSY (SEQ ID NO: 216)
Light Chain FR2	LNWYQQKPGKAPKLLIY (SEQ ID NO: 217)
Light Chain CDR2	AAS (SEQ ID NO: 218)
Light Chain FR3	SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC (SEQ ID NO: 219)
Light Chain CDR3	QSYSTPFT (SEQ ID NO: 300)
Light Chain FR4	FGPGTKVEIK (SEQ ID NO: 301)
Light Chain V Gene Segment	IGKV1-39; IGKV1D-39
Light Chain Locus	kappa

2003_03_F05

Heavy Chain FR1	EVQLVESGAIEVKKPGASVKVSCAS (SEQ ID NO: 302)
Heavy Chain CDR1	GYTFTRY (SEQ ID NO: 209)
Heavy Chain FR2	MHWVRQAPGQGLEWMGI (SEQ ID NO: 303)
Heavy Chain CDR2	INPSGGST (SEQ ID NO: 304)
Heavy Chain FR3	IYAQKFQGRVTMTTRDTSTSTVYMELSSLRSED TAVYYCAR (SEQ ID NO: 305)
Heavy Chain CDR3	SLRDGYNIGSLGY (SEQ ID NO: 306)
Heavy Chain FR4	WGQGTLLTVSS (SEQ ID NO: 214)
Heavy Chain V Gene Segment	IGHV1-46
Light Chain FR1	QSELTQPPSASGTPGQRTISCSGS (SEQ ID NO: 307)
Light Chain CDR1	SSNIGSNY (SEQ ID NO: 308)
Light Chain FR2	VYWYQQLPGTAPKLLIY (SEQ ID NO: 309)
Light Chain CDR2	RNN (SEQ ID NO: 310)
Light Chain FR3	QRPSGVPDRFSGSKSGTSASLAIRGLQSEDEAGYYC (SEQ ID NO: 311)
Light Chain CDR3	AAWDDSLNGLNWV (SEQ ID NO: 207)
Light Chain FR4	FGGGTQLTVL (SEQ ID NO: 294)
Light Chain V Gene Segment	IGLV1-44; IGLV1-47
Light Chain Locus	lambda

1994_01_A07

Heavy Chain FR1	QVQLVESGGGLVQPGGSLRLSCAAS (SEQ ID NO: 243)
Heavy Chain CDR1	GFTFDDYA (SEQ ID NO: 312)
Heavy Chain FR2	MHWVRQAPGKGLEWVSG (SEQ ID NO: 313)
Heavy Chain CDR2	ISWNSGST (SEQ ID NO: 314)
Heavy Chain FR3	YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAG (SEQ ID NO: 315)
Heavy Chain CDR3	GSRRYDSSGYYYESFDY (SEQ ID NO: 316)
Heavy Chain FR4	WGQGTTVTVSS (SEQ ID NO: 297)
Light Chain FR1	DIQMTQSPSSLSASVGDRTITCRAS (SEQ ID NO: 227)
Light Chain CDR1	QSISSY (SEQ ID NO: 216)
Light Chain FR2	LNWYQQKPGKAPKLLIY (SEQ ID NO: 217)
Light Chain CDR2	DAS (SEQ ID NO: 269)
Light Chain FR3	NLETGVPSRFSGSGSGTDFLTITSLQPEDFATYYC (SEQ ID NO: 317)
Light Chain CDR3	QQSYHTPYT (SEQ ID NO: 318)
Light Chain FR4	FGQGTKVEIK (SEQ ID NO: 272)
Light Chain Locus	kappa

1994_01_A09

Heavy Chain FR1	QMQLVQSGAEVKKPGSSVKV SCKAS (SEQ ID NO: 319)
Heavy Chain CDR1	GGTFSSYA (SEQ ID NO: 320)
Heavy Chain FR2	ISWVRQAPGQGLEWMGR (SEQ ID NO: 321)
Heavy Chain CDR2	IIPILGIA (SEQ ID NO: 322)
Heavy Chain FR3	NYAQKFQGRVTITADKSTSTAYMELSSLRSED TAVYYCAR (SEQ ID NO: 323)
Heavy Chain CDR3	DINRYNWNFRAFDI (SEQ ID NO: 324)
Heavy Chain FR4	WGQGTLLVTVSS (SEQ ID NO: 214)
Light Chain FR1	DIVMTQSPDSLAVSLGERATINCKSS (SEQ ID NO: 435)
Light Chain CDR1	QSVLYSSNNKNY (SEQ ID NO: 325)
Light Chain FR2	LAWYQQKPRQPPKLLIY (SEQ ID NO: 326)
Light Chain CDR2	WAS (SEQ ID NO: 327)
Light Chain FR3	TRESGVPDRFSGNGSGTDFLTITSLQAEDVAAYYC (SEQ ID NO: 328)
Light Chain CDR3	QQHYSTPLT (SEQ ID NO: 329)
Light Chain FR4	FGPGTKVEIK (SEQ ID NO: 301)
Light Chain Locus	kappa

1994_01_D12

Heavy Chain FR1	QVQLVQSGAEVKKPGSSVKV SCKAS (SEQ ID NO: 330)
Heavy Chain CDR1	GYTFTSYG (SEQ ID NO: 209)
Heavy Chain FR2	ISWVRQAPGQGLEWMGW (SEQ ID NO: 264)
Heavy Chain CDR2	ISAYNGNT (SEQ ID NO: 265)
Heavy Chain FR3	NYAQKLQGRVTMTTNTSTSTAYMELRSLRSDDTAVYYCAR (SEQ ID NO: 331)
Heavy Chain CDR3	VTGITGTTIDP (SEQ ID NO: 267)

Heavy Chain FR4	WGQGTLLTVSS (SEQ ID NO: 214)
Light Chain FR1	DIQMTQSPSSLSASVGDRVTITCRAS (SEQ ID NO: 227)
Light Chain CDR1	QSISSY (SEQ ID NO: 216)
Light Chain FR2	LNWYRQKPGKAPKLLIY (SEQ ID NO: 332)
Light Chain CDR2	AAS (SEQ ID NO: 218)
Light Chain FR3	SLQSGVPSRFSGSGSGTDFLTISLQPEDAATYYC (SEQ ID NO: 333)
Light Chain CDR3	QQYDSQSGT (SEQ ID NO: 334)
Light Chain FR4	FGQGTKLEIK (SEQ ID NO: 242)
Light Chain Locus	kappa

1995_01_F05

Heavy Chain FR1	EVQLVESGGGVVQPGSRRLSCAAS (SEQ ID NO: 335)
Heavy Chain CDR1	GFTFSSYA (SEQ ID NO: 209)
Heavy Chain FR2	MHWVRQAPGKGLEWVAV (SEQ ID NO: 286)
Heavy Chain CDR2	ISYDGVKK (SEQ ID NO: 336)
Heavy Chain FR3	YYADSVKGRFTISRDNKSTLYLQMNSLRVDDTAVYYCAK (SEQ ID NO: 337)
Heavy Chain CDR3	DLGWQNDY (SEQ ID NO: 338)
Heavy Chain FR4	WGQGTLLTVSS (SEQ ID NO: 214)
Light Chain FR1	QSVLTQPASVSGSPGQSITISCTGT DLGWQNDY (SEQ ID NO: 339)
Light Chain CDR1	SSDVGGHNY (SEQ ID NO: 340)
Light Chain FR2	VSWYQQHPGKAPKLLMIY (SEQ ID NO: 341)
Light Chain CDR2	DVS (SEQ ID NO: 342)
Light Chain FR3	NRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYC (SEQ ID NO: 343)
Light Chain CDR3	SSYTSSSPWV (SEQ ID NO: 344)
Light Chain FR4	FGGGTKLTVLG (SEQ ID NO: 345)
Light Chain Locus	lambda

1995_01_F09

Heavy Chain FR1	EVQLVESGGGLVQPGGSLRLSCAAS (SEQ ID NO: 346)
Heavy Chain CDR1	GFTFSSYA (SEQ ID NO: 209)
Heavy Chain FR2	MSWVRQAPGKGLEWVSA (SEQ ID NO: 274)
Heavy Chain CDR2	ISGSGGST (SEQ ID NO: 275)
Heavy Chain FR3	YYADSVKGRFTISRDNKSNALYLQMNSLRAEDTAVYYCRG (SEQ ID NO: 347)
Heavy Chain CDR3	YCSSTSCYGRRGAFDI (SEQ ID NO: 348)
Heavy Chain FR4	SGQGTLLTVSS (SEQ ID NO: 349)
Light Chain FR1	QAVLTQPPSASGTPGQRTISCSGR (SEQ ID NO: 350)
Light Chain CDR1	NSNIGSNN (SEQ ID NO: 351)
Light Chain FR2	VNWWYQHLPGTAPKLLIY (SEQ ID NO: 352)
Light Chain CDR2	SNN (SEQ ID NO: 353)

Light Chain FR3	QRPSGVPDRFSASKSGTSASLAISGLQSEDEADYYC (SEQ ID NO: 354)
Light Chain CDR3	AAWDDRMNGPV (SEQ ID NO: 355)
Light Chain FR4	IGGGTKVTVLG (SEQ ID NO: 356)
Light Chain Locus	lambda

1996_01_H07

Heavy Chain FR1	QVQLVESGGGLVQPGGSLRLSCAAS (SEQ ID NO: 243)
Heavy Chain CDR1	GFTFSSYW (SEQ ID NO: 209)
Heavy Chain FR2	MHWVRQAPAKGLVWVSR (SEQ ID NO: 357)
Heavy Chain CDR2	INSDGSST (SEQ ID NO: 358)
Heavy Chain FR3	SYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR (SEQ ID NO: 359)
Heavy Chain CDR3	DFWSGRPYYYMDV (SEQ ID NO: 360)
Heavy Chain FR4	WGQGTTVTVSS (SEQ ID NO: 297)
Light Chain FR1	DIQMTQSPSSLSASVGDRTITCRAS (SEQ ID NO: 227)
Light Chain CDR1	QDIGDD (SEQ ID NO: 361)
Light Chain FR2	LAWFQQKPGKAPKRLIY (SEQ ID NO: 362)
Light Chain CDR2	AAS (SEQ ID NO: 218)
Light Chain FR3	TLQGGVPSRFSGSGSGTDFTLTISLQPEDFATYYC (SEQ ID NO: 363)
Light Chain CDR3	QQSYSTPRT (SEQ ID NO: 364)
Light Chain FR4	FGPGTKVEIK (SEQ ID NO: 301)
Light Chain Locus	kappa

1997_02_B01

Heavy Chain FR1	EVQLVESGGGVVQPGSLRLSCAAS (SEQ ID NO: 335)
Heavy Chain CDR1	GFTFSSYA (SEQ ID NO: 209)
Heavy Chain FR2	MHWVRQAPGKGLEWVAV (SEQ ID NO: 286)
Heavy Chain CDR2	ISYDGSNK (SEQ ID NO: 287)
Heavy Chain FR3	YYADSVKGRFTISRDN SKNTLYLQMNSRRAEDTAVYYCAR (SEQ ID NO: 365)
Heavy Chain CDR3	WGIVAARPNYYYGMDV (SEQ ID NO: 366)
Heavy Chain FR4	WGQGTTLVTVSS (SEQ ID NO: 214)
Light Chain FR1	QSALTQPRSVSGSPGQSVTISCTGT (SEQ ID NO: 367)
Light Chain CDR1	SSDVGGYNY (SEQ ID NO: 368)
Light Chain FR2	VSWYQQHPGKAPKLMYI (SEQ ID NO: 341)
Light Chain CDR2	DVS (SEQ ID NO: 342)
Light Chain FR3	KRPSGVPDRFSGSKSGNTASLTISGLQAEDEADYHC (SEQ ID NO: 368)
Light Chain CDR3	SSYANNSPWV (SEQ ID NO: 369)
Light Chain FR4	FGGGTKVTVLG (SEQ ID NO: 370)
Light Chain Locus	lambda

2002_02_E01

Heavy Chain FR1	QVQLVQSGAEVRKPGASVKVSCAS (SEQ ID NO: 371)
Heavy Chain CDR1	GYTFTSYG (SEQ ID NO: 209)
Heavy Chain FR2	ISWVRQAPGQGLEWMGW (SEQ ID NO: 264)
Heavy Chain CDR2	ISAYNGNT (SEQ ID NO: 265)
Heavy Chain FR3	NYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR (SEQ ID NO: 372)
Heavy Chain CDR3	VTGITGTTIDP (SEQ ID NO: 267)
Heavy Chain FR4	WGQGTLLTVSS (SEQ ID NO: 214)
Light Chain FR1	DIQMTQSPSSLSASVGDRVTITCQAS (SEQ ID NO: 373)
Light Chain CDR1	QDISNY (SEQ ID NO: 374)
Light Chain FR2	LNWYQQKPGKAPKLLIY (SEQ ID NO: 217)
Light Chain CDR2	DAS (SEQ ID NO: 269)
Light Chain FR3	NLETGVPSRFSGSGSGTDFTFITISLQPEDATYYC (SEQ ID NO: 375)
Light Chain CDR3	QQYANLPLT (SEQ ID NO: 376)
Light Chain FR4	FGGGTKVEIK (SEQ ID NO: 221)
Light Chain Locus	kappa

2002_02_G11

Heavy Chain FR1	EVQLVESGGGLVQPGGSLRLSCAAS (SEQ ID NO: 346)
Heavy Chain CDR1	GFTVSSNY (SEQ ID NO: 377)
Heavy Chain FR2	MSWVRQAPGKGLEWVSV (SEQ ID NO: 378)
Heavy Chain CDR2	IYSGGST (SEQ ID NO: 379)
Heavy Chain FR3	YYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAR (SEQ ID NO: 276)
Heavy Chain CDR3	GGLTGDDAFDI (SEQ ID NO: 380)
Heavy Chain FR4	WGQGTLLTVSS (SEQ ID NO: 214)
Light Chain FR1	DIQMTQSPSSLSASVGDRVTITCRAS (SEQ ID NO: 227)
Light Chain CDR1	QSISF (SEQ ID NO: 381)
Light Chain FR2	LNWYQQKPGTAPKLLIY (SEQ ID NO: 382)
Light Chain CDR2	TTS (SEQ ID NO: 383)
Light Chain FR3	SLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYC (SEQ ID NO: 219)
Light Chain CDR3	QQGNSLPLT (SEQ ID NO: 384)
Light Chain FR4	FGGGTKVEIK (SEQ ID NO: 221)
Light Chain Locus	kappa

2003_03_A09

Heavy Chain FR1	QVQLVESGGGVVQPGRSLRLSCAAS (SEQ ID NO: 208)
Heavy Chain CDR1	GFTFSSYA (SEQ ID NO: 209)
Heavy Chain FR2	MHWVRQAPGKGLEWVAV (SEQ ID NO: 286)
Heavy Chain CDR2	ISYDGSNK (SEQ ID NO: 287)
Heavy Chain FR3	YYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAR (SEQ ID NO: 276)
Heavy Chain CDR3	DKELSY (SEQ ID NO: 385)

Heavy Chain FR4	WGQGTLVTVSS (SEQ ID NO: 214)
Light Chain FR1	QSGLTQPASVSGSPGQSITISCTGT (SEQ ID NO: 386)
Light Chain CDR1	SSDVGGYNY (SEQ ID NO: 368)
Light Chain FR2	VSWYQQHPGKAPKLMYI (SEQ ID NO: 341)
Light Chain CDR2	EVS (SEQ ID NO: 387)
Light Chain FR3	NRPSGVPDRFSGSKSGNTASLTISGLQAED EADYYC (SEQ ID NO: 388)
Light Chain CDR3	SSYTSSSPWV (SEQ ID NO: 344)
Light Chain FR4	FGGGTKLTVLG (SEQ ID NO: 345)
Light Chain Locus	lambda

2004_04_D03

Heavy Chain FR1	QVQLVESGGGVVQPGRSLRLSCAAS (SEQ ID NO: 208)
Heavy Chain CDR1	GFTFSNYG (SEQ ID NO: 209)
Heavy Chain FR2	MNWVRQAPGKGLEWVSY (SEQ ID NO: 210)
Heavy Chain CDR2	ISSSSSTI (SEQ ID NO: 233)
Heavy Chain FR3	YYADSVKGRFTISRDNKNSLYLQMNSLRDEDTAVYYCAS (SEQ ID NO: 212)
Heavy Chain CDR3	GQLDTSDAFDI (SEQ ID NO: 213)
Heavy Chain FR4	WGQGTTVTVSS (SEQ ID NO: 297)
Light Chain FR1	DIQMTQSPSSLSASVGDRVTITCRAS (SEQ ID NO: 227)
Light Chain CDR1	QSISSY (SEQ ID NO: 216)
Light Chain FR2	LNWYQQKPGKAPKLLIY (SEQ ID NO: 217)
Light Chain CDR2	KTS (SEQ ID NO: 389)
Light Chain FR3	NLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYC (SEQ ID NO: 390)
Light Chain CDR3	QQSYSTPLT (SEQ ID NO: 220)
Light Chain FR4	FGGGTKVEIK (SEQ ID NO: 221)
Light Chain Locus	kappa

2004_04_F01

Heavy Chain FR1	EVQLVESGGGLVQPGGSLRLSCAAS (SEQ ID NO: 346)
Heavy Chain CDR1	GFTFSSYA (SEQ ID NO: 209)
Heavy Chain FR2	MSWVRQAPAKGLEWVSA (SEQ ID NO: 391)
Heavy Chain CDR2	ISGSGGST (SEQ ID NO: 275)
Heavy Chain FR3	YYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAK (SEQ ID NO: 295)
Heavy Chain CDR3	DRPYSGKNDAFDI (SEQ ID NO: 392)
Heavy Chain FR4	WGQGTTVTVSS (SEQ ID NO: 297)
Light Chain FR1	DIQMTQSPSSLSASVGDRVTITCQAS (SEQ ID NO: 373)
Light Chain CDR1	QDVSNY (SEQ ID NO: 393)
Light Chain FR2	LNWYRQKPGKAPKLLIY (SEQ ID NO: 332)
Light Chain CDR2	AAS (SEQ ID NO: 218)
Light Chain FR3	SLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYC (SEQ ID NO: 219)

Light Chain CDR3	QQSYSTPLT (SEQ ID NO: 220)
Light Chain FR4	FGGGTKLEIK (SEQ ID NO: 394)
Light Chain Locus	kappa

2005_05_E05

Heavy Chain FR1	EVQLVQSGAEVKKPGASVKVSCAS (SEQ ID NO: 395)
Heavy Chain CDR1	GYTFTSYY (SEQ ID NO: 396)
Heavy Chain FR2	MHWVRQAPGQGLEWMGI (SEQ ID NO: 303)
Heavy Chain CDR2	INPSGGST (SEQ ID NO: 304)
Heavy Chain FR3	SYAQKFQGRVTMTTRDTSTSTVYMELSSLRSED TAVYYCAR (SEQ ID NO: 397)
Heavy Chain CDR3	SPWLITFGGVIAMGY (SEQ ID NO: 402)
Heavy Chain FR4	WGQGTLLTVSS (SEQ ID NO: 214)
Light Chain FR1	QSVLTQPPSASGTPGQRTISCSGS (SEQ ID NO: 403)
Light Chain CDR1	SSNIGSNY (SEQ ID NO: 308)
Light Chain FR2	VYWYQQLPGTAPKLLIY (SEQ ID NO: 309)
Light Chain CDR2	RNN (SEQ ID NO: 310)
Light Chain FR3	QRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC (SEQ ID NO: 404)
Light Chain CDR3	AAWDDSLSGVV (SEQ ID NO: 405)
Light Chain FR4	FGGGTQLTVLG (SEQ ID NO: 406)
Light Chain Locus	lambda

1994_01_D04

Heavy Chain FR1	QVQLVQSGAEVRKPGASVKVSCAS (SEQ ID NO: 371)
Heavy Chain CDR1	GYTFTSYG (SEQ ID NO: 209)
Heavy Chain FR2	ISWVRQAPGQGLEWMGW (SEQ ID NO: 264)
Heavy Chain CDR2	ISAYNGNT (SEQ ID NO: 265)
Heavy Chain FR3	NYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR (SEQ ID NO: 372)
Heavy Chain CDR3	VTGITGTTIDP (SEQ ID NO: 267)
Heavy Chain FR4	WGQGTLLTVSS (SEQ ID NO: 214)
Light Chain FR1	DIVMTQSPSSLSASVGDRTITCRAS (SEQ ID NO: 407)
Light Chain CDR1	QSISSY (SEQ ID NO: 216)
Light Chain FR2	LNWYQQKPGKAPKLLIY (SEQ ID NO: 217)
Light Chain CDR2	DAS (SEQ ID NO: 269)
Light Chain FR3	NLETGVPSRFSGSGSGTDFTLTISLQPEDFATYYC (SEQ ID NO: 317)
Light Chain CDR3	QQFNNYPLT (SEQ ID NO: 408)
Light Chain FR4	FGGGTKLEIK (SEQ ID NO: 394)
Light Chain Locus	kappa

1997_02_B03

Heavy Chain FR1	QVQLVESGAIEVKKPGASVKVSCAS (SEQ ID NO: 409)
Heavy Chain CDR1	GYTFTSYY (SEQ ID NO: 396)

Heavy Chain FR2	MHWVRQAPGQGLEWMGI (SEQ ID NO: 303)
Heavy Chain CDR2	INPSGGST (SEQ ID NO: 304)
Heavy Chain FR3	SYAQKFQGRVTMTRDTSTSTVYMELSSLRSED TAVYYCAR (SEQ ID NO: 397)
Heavy Chain CDR3	AGGYYYYYMDV (SEQ ID NO: 398)
Heavy Chain FR4	WGQGLTVTVSS (SEQ ID NO: 214)
Light Chain FR1	QSGLTQPPSASGTPGQRTISCSGS (SEQ ID NO: 399)
Light Chain CDR1	GPNIGNNY (SEQ ID NO: 400)
Light Chain FR2	VYWYQQLPGTAPKLLMY (SEQ ID NO: 401)
Light Chain CDR2	RNN (SEQ ID NO: 310)
Light Chain FR3	QRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYC (SEQ ID NO: 410)
Light Chain CDR3	AAWDDSLNGYV (SEQ ID NO: 411)
Light Chain FR4	FGTGTKLTVLG (SEQ ID NO: 412)
Light Chain Locus	lambda

Humanized mAb sequences

Humanized 79E3E3 Heavy Chain Variable Region

QIQLVQSGAEVKKPGESLKISCKASGYTFTDYAIGWVRQMPGKGLEWMGIINTQTGKPK
YSPSFQGGFIFSLDTSINTTYLQWSSLKASDTAIYFCTRLGTGNTKGFAYWGQGTITVS
S (SEQ ID NO: 413)

Humanized 79E3E3 Light Chain Variable Region

DIQITQSPSSLSASLGDKVTITCRSSQSLLYSENNQDYLAWYQQKPGKAPKLLIYGASNL
QSGVPSRFSGRGSGTDFTLTISSLQPEDFATYYCEQTYRYPFTFGPGTKVDIKR (SEQ ID
NO: 414)

Humanized 9-G05 Heavy Chain VH_1

*Leader sequence-VH-hIgG1CH-Stop codon**

MGWSCILFLVATATGVHSQVLVQSGAEVKKPGASVKVSKASGYTFPDYNMDWVR
QAPGQRLEWMGYINPDNNGGTIYNQKFKGRVTLTVDTASTAYMELSSLRSED TAVYYC
ARLDSSGYGYYAMDYWGQGTSTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHK
PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV
VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNG
KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
HEALHNHYTQKSLSLSPGK* (SEQ ID NO: 415)

Humanized 9-G05 Heavy Chain VH_2

*Leader sequence-VH-hIgG1CH-Stop codon**

MGWSCILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFPDYNMDWVR
QAPGQRLEWIGYINPDNGGTIYNQKFKGRVTLTVDTASTAYMELSSLRSEDTAVYYCA
RLDSSGYGYAMDYWGQGTSTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS
NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGK
EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHE
ALHNHYTQKSLSLSPGK* (SEQ ID NO: 416)

Humanized 9-G05 Heavy Chain VH_3

*Leader sequence-VH-hIgG1CH-Stop codon**

MGWSCILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFPDYNMDWVR
QAPGQRLEWMGYINPDNGGTIYNQKFKGRATLTVDTASTAYMELSSLRSEDTAVYYC
ARLDSSGYGYAMDYWGQGTSTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHK
PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV
VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNG
KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVM
HEALHNHYTQKSLSLSPGK* (SEQ ID NO: 417)

Humanized 9-G05 Heavy Chain VH_4

*Leader sequence-VH-hIgG1CH-Stop codon**

MGWSCILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFPDYNMDWVR
QAPGQSLEWIGYINPDNGGTIYNQKFKGRATLTVDTASTAYMELSSLRSEDTAVYYCA
RLDSSGYGYAMDYWGQGTSTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS
NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGK
EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHE
ALHNHYTQKSLSLSPGK* (SEQ ID NO: 418)

Humanized 9-G05 Light Chain VL_1

*Leader sequence-VL-hIgKCL-Stop codon**

MGWSCILFLVATATGVHSDIVMTQSPDSLAVSLGERATINCRASESDNYGISFMHWY
QQKPGQPPKLLIYRASNLDSGVPDRFSGSGSGTDFTLTISSLQAEDVATYYCQQSYKDPR
TFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFN
RGEC* (SEQ ID NO: 419)

Humanized 9-G05 Light Chain VL_2

*Leader sequence-VL-hIgKCL-Stop codon**

**MGWSCILFLVATATGVHSDIVLTQSPASLAVSPGQRATITCRASESVDNYGISFMHWYQ
QKPGQPPKLLIYRASNLDSVPPARFSGSGSRTDFTLTINPVEANDTATYYCQQSYKDPRT
FGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR
GEC* (SEQ ID NO: 420)**

16E10 Heavy Chain Variable Region

QSLEESGGDLVKPGASLTLTCRVSGFSFSSSYMCWVRQAPGKGLEWVSCIGTTRGSTY
YATWAKGRFTISKISSTTVTLQMTSLTDADTATYFCARDATGYRINTIGLYFNLWGPGTL
VTVSS (SEQ ID NO: 421)

Humanized 16E10 Heavy Chain Variable Region VH_1

QSLLES GGGLVKPGGSLRLSCAVSGFSFSSSYMCWVRQAPGKGLEWVSCIGTTRGSTY
YADSAKGRFTISKISKNTVYTLQMTSLRAEDTAVYFCARDATGYRINTIGLYFNLWGPGT
LTVSS (SEQ ID NO: 422)

Humanized 16E10 Heavy Chain Variable Region VH_2

EVQLLES GGGLVKPGGSLRLSCAVSGFSFSSSYMCWVRQAPGKGLEWVSCIGTTRGST
YYADSAKGRFTISKDNSKNTVYTLQMTSLRAEDTAVYFCARDATGYRINTIGLYFNLWG
QGT LTVSS (SEQ ID NO: 423)

Humanized 16E10 Heavy Chain Variable Region VH_3

QSLLES GGGLVKPGGSLRLSCAVSGFSFSSSYMCWVRQAPGKGLEWVSCIGTTRGSTY
YADSAKGRFTISKESKNTVYTLQMSSLRAEDTAVYFCARDATGYRINTIGLYFNLWGPGT
LTVSS (SEQ ID NO: 424)

Humanized 16E10 Heavy Chain Variable Region VH_4

EVQLLES GGGLVKPGGSLRLSCAVSGFSFSSSYMCWVRQAPGKGLEWVSCIGTTRGST
YYADSAKGRFTISKDNSKNTVYTLQMSSLRAEDTAVYFCARDATGYRINTIGLYFNLWG
QGT LTVSS (SEQ ID NO: 425)

Humanized 16E10 Heavy Chain Variable Region VH_5

QSLLES GGGLVKPGGSLRLSCAVSGFSFSSSYMCWVRQAPGKGLEWVSCIGTTRGSTY
YADSAKGRFTISKESKNTVYTLQMSSLRAEDTAVYFCARDATGYRIQTIGLYFNLWGPGT
LTVSS (SEQ ID NO: 426)

Humanized 16E10 Heavy Chain Variable Region VH_6

EVQLLES GGGLVKPGGSLRLSCAVSGFSFSSSYMCWVRQAPGKGLEWVSCIGTTRGST
YYADSAKGRFTISKDNSKNTVYTLQMSSLRAEDTAVYFCARDATGYRIQTIGLYFNLWG
QGT LTVSS (SEQ ID NO: 427)

16E10 Light Chain Variable Region

ELTQTPSSVEAAVGGTPTIKCQASQTIYSYLSWYQQKPGQPPKLLIYEASKLASGVPSRFS
GSGSGTDYTLTISDLECAATYYCQSYHGTASTEYNTFGGGTEVVK (SEQ ID NO:
428)

Humanized 16E10 Light Chain Variable Region VL_1

QLTQSPSSLSASVGDRVTITCQASQTIYSYLSWYQQKPGKPPKLLIYEASKLASGVPSRFS
GSGSGTDYTLTISSLQPEDFATYYCQSYHGTASTEYNTFGGGTKVEIK (SEQ ID NO:
429)

Humanized 16E10 Light Chain Variable Region VL_2

DIQLTQSPSSLSASVGDRVTITCQASQTIYSYLSWYQQKPGKPPKLLIYEASKLASGVPSR
FSGSGSGTDYTLTISSLQPEDFATYYCQSYHGTASTEYNTFGGGTKVEIK (SEQ ID NO:
430)

Humanized 16E10 Light Chain Variable Region VL_3

QLTQSPSSLSASVGDRVTITCQASQTIYSYLSWYQQKPGKPPKLLIYEASKLASGVPSRFS
GSGSGTDYTLTISSLQPEDTATYYCQSYHGTASTEYNTFGGGTKVEIK (SEQ ID NO:
431)

Humanized 16E10 Light Chain Variable Region VL_4

DIQLTQSPSSLSASVGDRVTITCQASQTIYSYLSWYQQKPGKPPKLLIYEASKLASGVPSR
FSGSGSGTDYTLTISSLQPEDTATYYCQSYHGTASTEYNTFGGGTKVEIK (SEQ ID NO:
432)

Humanized 16E10 Light Chain Variable Region VL_5

QLTQSPSSLSASVGDRVTITCQASQTIYSYLSWYQQKPGKPPKLLIYEASKLASGVPSRFS
GSGSGTDYTLTISSLQPEDTATYYCQSYHGTASTEYQTFGGGTKVEIK (SEQ ID NO:
433)

Humanized 16E10 Light Chain Variable Region VL_6

DIQLTQSPSSLSASVGDRVTITCQASQTIYSYLSWYQQKPGKPPKLLIYEASKLASGVPSR
FSGSGSGTDYTLTISSLQPEDTATYYCQSYHGTASTEYQTFGGGTKVEIK (SEQ ID NO:
434)

EQUIVALENTS

[0138] It is to be understood that while the invention has been described in conjunction with the detailed description thereof, the foregoing description is intended to illustrate and not limit the scope of the invention, which is defined by the scope of the appended claims. Other aspects, advantages, and modifications are within the scope of the following claims.

CLAIMS

1. An anti-integrin alpha 11 beta 1 ($\alpha 11\beta 1$) antibody, or antigen-binding fragment thereof, comprising an amino acid sequence selected from a group consisting of SEQ ID NO: 103-435.
2. An anti- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, comprising a CDR sequence encompassed within any one of SEQ ID NO: 103-207, 209, 211, 213, 216, 218, 220, 223, 225, 228, 233, 234, 236, 240, 241, 245, 247, 253, 255, 257, 259, 261, 265, 267, 269, 271, 275, 277, 279, 281, 283, 287, 289, 291, 293, 296, 300, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 325, 327, 329, 334, 336, 338, 340, 342, 344, 348, 351, 353, 355, 358, 360, 361, 364, 366, 368, 369, 374, 376, 377, 379, 380, 381, 383, 384, 385, 387, 389, 392, 393, 396, 398, 400, 402, 405, 408, 411, or 413-435.
3. An anti- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, comprising CDR1, CDR2, and CDR3 encompassed within any one of SEQ ID NO: 103-206, or 413-435.
4. The anti- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, of claim 1, comprising an amino acid sequence selected from a group consisting of SEQ ID NO: 103-114, 207-311, and 312-435.
5. The anti- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, of claim 2, comprising a CDR sequence encompassed within any one of SEQ ID NO: 103-114, 207, 209, 211, 213, 216, 218, 220, 223, 225, 228, 233, 234, 236, 240, 241, 245, 247, 253, 255, 257, 259, 261, 265, 267, 269, 271, 275, 277, 279, 281, 283, 287, 289, 291, 293, 296, 300, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 325, 327, 329, 334, 336, 338, 340, 342, 344, 348, 351, 353, 355, 358, 360, 361, 364, 366, 368, 369, 374, 376, 377, 379, 380, 381, 383, 384, 385, 387, 389, 392, 393, 396, 398, 400, 402, 405, 408, 411, or 413-435.
6. The anti- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, of claim 2, comprising one or more CDR sequences encompassed within any one of SEQ ID NO: 103-114, or 413-434.

7. The anti- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, of claim 3, comprising CDR1, CDR2, and CDR3 encompassed within any one of SEQ ID NO: 103-114 or 413-434.
8. The anti- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, of any one of claims 1-7, wherein the antibody, or antigen-binding fragment thereof, is a monoclonal antibody, or antigen-binding fragment thereof.
9. The anti- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, of any one of claims 1-8, wherein the antibody, or antigen-binding fragment thereof, is a humanized antibody, or antigen-binding fragment thereof.
10. The anti- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, of any one of claims 1-9, wherein the antibody, or antigen-binding fragment thereof, reduces interaction of $\alpha 11\beta 1$ with collagen in human $\alpha 11\beta 1$ -expressing cells.
11. An anti- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, that competes with the antibody, or antigen-binding fragment thereof, of any one of claims 1-10.
12. A nucleic acid, comprising a nucleic acid sequence encoding an antibody, or antigen-binding fragment thereof, of any one of claims 1-11.
13. The nucleic acid of claim 11, wherein the nucleic acid sequence comprises a sequence selected from a group consisting of SEQ ID NO: 1-102.
14. A vector comprising the nucleic acid of claim 12 or 13.
15. A host cell comprising the nucleic acid of claim 12 or 13 or the vector of claim 14.
16. A method of producing an antibody, or antigen-binding fragment thereof, comprising culturing the host cell of claim 14 under conditions suitable for expression of the antibody or antigen-binding fragment thereof.

17. A method of treating a subject having or at risk of a fibrotic disorder, the method comprising administering to the subject a therapeutically effective amount of the antibody, or antigen-binding fragment thereof, of any one of claims 1-11.

18. The method of claim 17, wherein the fibrotic disorder is idiopathic pulmonary fibrosis (IPF), chronic kidney disease, diabetic cardiomyopathy, primary sclerosing cholangitis (PSC), primary biliary cirrhosis (PBC), non-alcoholic fatty liver disease (NAFLD/NASH), Crohn's disease, ulcerative colitis, or systemic sclerosis.

19. A method of treating a subject having or at risk of cancer, the method comprising administering to the subject a therapeutically effective amount of the antibody, or antigen-binding fragment thereof, of any one of claims 1-11.

20. The method of claim 19, wherein the cancer is a head and neck squamous cell carcinoma, pancreatic ductal adenocarcinoma, non-small cell lung cancer, adrenocortical carcinoma, acute myeloid leukemia, bladder urothelial carcinoma, invasive breast carcinoma, cervical squamous cell carcinoma, cholangiocarcinoma, colorectal adenocarcinoma, diffuse large B-cell lymphoma, esophageal adenocarcinoma, glioblastoma multiforme, liver hepatocellular carcinoma, lung adenocarcinoma, lung squamous cell carcinoma, skin cutaneous melanoma, mesothelioma, ovarian serous cystadenocarcinoma, pheochromocytoma and paraganglioma, prostate adenocarcinoma, sarcoma, stomach adenocarcinoma, testicular germ cell tumors, thymoma, thyroid carcinoma, uterine corpus endometrial carcinoma, uterine carcinosarcoma, uveal melanoma, kidney renal clear cell carcinoma, kidney chromophobe, kidney renal papillary cell carcinoma, or a combination thereof.

21. The method of claim 19 or 20, further comprising administering to the subject an effective amount of a chemotherapeutic agent or an oncolytic therapeutic agent.