

ANTIBODIES AGAINST INTEGRIN ALPHA 11 BETA 1**CROSS-REFERENCE TO RELATED APPLICATIONS**

[0001] This application claims the benefit of priority of U.S. Provisional Application No. 63/127,849, filed December 18, 2020, and U.S. Provisional Application No. 63/213,973, filed June 23, 2021, which are incorporated by reference herein, in their entireties and for all purposes.

SEQUENCE LISTING

[0002] The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on November 19, 2021, is named 2010403_0592_SL.txt and is 440,570 bytes in size.

BACKGROUND

[0003] 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

[0004] 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.

[0005] 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: 103-443. 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 413-443. In another aspect, the present disclosure provides 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. 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 312-443. 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 413-443. 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.

[0006] 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, an anti- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, competes with an antibody, or antigen-binding fragment thereof, described herein.

[0007] 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.

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

[0009] In another aspect, the present disclosure provides a host cell comprising a nucleic acid described herein or a vector described herein.

[0010] 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.

[0011] In another aspect, the present disclosure provides a method of treating a subject having or at risk of chronic kidney disease, the method comprising administering to the subject a therapeutically effective amount of the antibody, or antigen-binding fragment thereof, described herein. In some embodiments, a chronic kidney disease is or comprises Primary Glomerular Disease (including, but not limited to, IgA Nephropathy and focal segmental glomerular sclerosis), Secondary Glomerular Disease (including, but not limited to, lupus nephritis), Thrombotic Microangiopathy, Tubulointerstitial Diseases (including, but not limited to, Obstructive Uropathy), Diabetic Nephropathy, Hypertensive Nephropathy, Ischemic Nephropathy, Cardiorenal Syndromes in CKD, Inherited Disorders of the Glomerulus (including, but not limited to, Alport syndrome), Cystic Diseases of the Kidney (including, but not limited to, Polycystic Kidney Disease), or Inherited Disorders of the Renal Tubule. In some embodiments, administering a therapeutically effective amount of an antibody, or antigen-binding fragment thereof results in a reduction in a measured marker, sign and/or symptom by at least about 10%, 15%, 20%, 25%, 30%, 35%, 40%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85% or 90% relative to a control. In some embodiments, a control comprises a level of measured marker, sign and/or symptom in a subject prior to administration of an antibody. In some embodiments, a control comprises a level of measured marker, sign and/or symptom in a subject suffering from a kidney-related disorder. In some embodiments, a control comprises an average level of measured marker, sign and/or symptom in a population of subjects suffering

from a kidney-related disorder. In some embodiments, a measured marker, sign and/or symptom is or comprises: COL1A1, Fibronectin, PAI-1, IL-11, CXCL1, MCP-1, IL-6, TIMP-1, Hyaluronic acid, TGF β , CTGF, PDGF, MMP9, or a combination thereof.

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 $\alpha 11\beta 1$.

[0015] **Figure 2B** shows a chart illustrating an exemplary ELISA analysis of binding of mouse monoclonal antibodies to mouse $\alpha 11\beta 1$.

[0016] **Figure 3A** shows a graph illustrating an ELISA analysis of binding of exemplary rat monoclonal antibodies to a human $\alpha 11\beta 1$ I domain.

[0017] **Figure 3B** shows a graph illustrating an ELISA analysis of binding of exemplary mouse monoclonal antibodies to a human $\alpha 11\beta 1$ 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 $\alpha 11\beta 1$.

[0019] **Figure 4B** shows a graph illustrating an FACS analysis of binding of exemplary mouse monoclonal antibodies to CHO-K1 cells expressing human $\alpha 11\beta$.

[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 $\alpha 11$ 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 $\alpha 11$ 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 $\alpha 11$ 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 $\alpha 11$ -mediated rat tail type I collagen gel contraction.

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

[0029] **Figure 10A** and **Figure 10B** show graphs illustrating the affinity of exemplary monoclonal antibodies for human $\alpha 11\beta 1$ 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 $\alpha 11\beta 1$ 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 $\alpha 11\beta 1$ 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 $\alpha 11$ 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).

[0037] **Figure 18A**, **Figure 18B** and **Figure 18 C** illustrate the effect of exemplary monoclonal antibodies on the soluble pro-fibrogenic marker Colla1 from Precision-Cut Kidney Slices (PCKS).

DETAILED DESCRIPTION

[0038] 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

[0039] 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.

[0040] 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.

[0041] 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.

[0042] 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. $\alpha 11 \beta 1$ 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 $\alpha 11 \beta 1$ 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

[0043] 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.

[0044] 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 a 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.

[0045] 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.

[0046] 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

[0047] 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.

[0048] 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.

[0049] 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.

[0050] 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.

[0051] 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.

[0052] 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.

[0053] 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.

[0054] 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.

[0055] 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.

[0056] 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”.

[0057] 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

[0058] 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.

[0059] 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.

[0060] 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: 103-443. 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 413-443. 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 312-443. 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 413-443. 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: 103-443. 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: 103-443.

[0061] 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

[0062] In some embodiments, the present disclosure provides an anti- $\alpha 11\beta 1$ 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- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, wherein the anti- $\alpha 11\beta 1$ 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 $\alpha 11\beta 1$. In some embodiments, the present disclosure provides an anti- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, comprising between 1 and 30 additions, deletions, or substitutions relative to an anti- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, wherein the anti- $\alpha 11\beta 1$ 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 $\alpha 11\beta 1$. 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% 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 $\alpha 11\beta 1$. 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 a group consisting of SEQ ID NO: 103-114, 413, 414 and 421-434 and, e.g., the antibody or fragment selectively binds $\alpha 11\beta 1$.

[0063] In some embodiments, the present disclosure provides an anti- $\alpha 11\beta 1$ 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- $\alpha 11\beta 1$ antibody, or antigen-binding fragment thereof, wherein the 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: 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 $\alpha 11\beta 1$.

[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: 103-114. 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.

[0065] 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 413-443. 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 413-443. 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 413-443, 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 413-443. 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.

[0066] The present disclosure provides, among other things, methods of making an anti- $\alpha 11\beta 1$ 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

[0067] 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.

[0068] 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.

[0069] 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 $\alpha 11\beta 1$

[0070] 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 Sapidyn Instruments (Boise, Id.) can also be used.

[0071] 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.

[0072] 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

[0073] In some embodiments, one or more anti- $\alpha 11\beta 1$ 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.

[0074] 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.

[0075] In some embodiments, one or more anti- $\alpha 11\beta 1$ 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.

[0076] In some embodiments, one or more anti- $\alpha 11\beta 1$ antibodies described herein are used to treat a subject having or at risk of a chronic kidney disease (CKD), e.g., CKD associated with fibrosis. CKDs are known in the art (see, e.g., Brenner, Barry M. (ed) Brenner & Rector's The Kidney, 11th edition 2019). CKDs include, e.g., Primary Glomerular Disease (including, but not limited to, IgA Nephropathy and focal segmental glomerular sclerosis), Secondary Glomerular Disease (including, but not limited to, lupus nephritis), Thrombotic Microangiopathy, Tubulointerstitial Diseases (including, but not limited to, Obstructive Uropathy), Diabetic Nephropathy, Hypertensive Nephropathy, Ischemic Nephropathy, Cardiorenal Syndromes in CKD, Inherited Disorders of the Glomerulus (including, but not limited to, Alport syndrome), Cystic Diseases of the Kidney (including, but not limited to, Polycystic Kidney Disease), and Inherited Disorders of the Renal Tubule (Brenner, Barry M. (ed) Brenner & Rector's The Kidney, 11th edition 2019).

[0077] In some embodiments, an anti- $\alpha 11\beta 1$ antibody described herein, upon administration to a subject, reduces one or more markers, signs and/or symptoms of a kidney-related disorder described herein. Markers, signs and/or symptoms of kidney-related disorders include, e.g., COL1A1, IL-6, TIMP-1, Hyaluronic acid, TGF β , CTGF, PDGF, and MMP9. In some embodiments, upon administration to a subject, an anti- $\alpha 11\beta 1$ antibody can reduce a measured marker, sign and/or symptom by at least about 10%, 15%, 20%, 25%, 30%, 35%, 40%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85% or 90%, relative to a control (e.g., a level of measured marker, sign and/or symptom in the subject prior to administration of the antibody, a level of measured marker, sign and/or symptom in a subject suffering from the kidney-related disorder, and/or an average level of measured marker, sign and/or symptom in a population of subjects suffering from the kidney-related disorder).

[0078] In some embodiments, an anti- $\alpha 11\beta 1$ antibody described herein reduces levels of COL1A1, IL-6, TIMP-1, Hyaluronic acid, TGF β , CTGF, PDGF, MMP9, or a combination thereof by at least about 10%, 15%, 20%, 25%, 30%, 35%, 40%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85% or 90%, relative to a control, as measured in a model of kidney-related disorder (e.g., human Precision-Cut Kidney Slices (PCKS), a ReninAAV Unx db/db mouse model, or a

5/6 Nephrectomy model). In some embodiments, markers, signs and/or symptoms of kidney-related disorders can be determined by measuring protein levels, RNA levels, DNA levels, or a combination thereof. In some embodiments, markers, signs and/or symptoms of kidney-related disorders can be determined using ELISA, PCR, RNAseq, a biochemical assay (e.g., an analytical procedure to detect and quantify cellular processes (e.g. apoptosis, cell signaling) or metabolic reactions), cytology, immunohistochemistry, or a combination thereof.

[0079] In some embodiments, markers, signs and/or symptoms of kidney-related disorders can be determined by testing a biological sample from a subject. Examples of suitable biological samples include, but are not limited to, serum, plasma, cerebrospinal fluid, urine, circulating blood cells (e.g., peripheral blood mononuclear cells), and biopsy specimens. In some embodiments, a sample comprises cells or tissues. In some embodiments, provided methods further comprises a step of lysing cells or performing a tissue biopsy and one or more markers include one or more intracellular markers. Biological samples suitable for the present disclosure may be fresh or frozen samples collected from a subject, or archival samples with known diagnosis, treatment and/or outcome history. Biological samples may be collected by any invasive or non-invasive means, such as, for example, by drawing CSF or blood from a subject, or using fine needle aspiration or needle biopsy, or by surgical biopsy. In some embodiments, biological samples may be used without or with limited processing of the sample.

Combination Therapy

[0080] In some embodiments, an anti- $\alpha 11\beta 1$ 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.

[0081] 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, thiotepa, melphalan, busulfan, procarbazine, streptozocin, temozolomide, dacarbazine, and bendamustine), antitumor antibiotics (e.g., daunorubicin, doxorubicin, idarubicin, epirubicin, mitoxantrone, bleomycin, mytomyacin 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, goserelin, 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.

[0082] 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).

[0083] 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.

[0084] In some embodiments, combined administration of an anti- α 11 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 11 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- α 11 β 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.

[0085] 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- α 11 β 1 antibody described herein, or composition thereof.

Formulations and Administration

[0086] 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)).

[0087] 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.

[0088] 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.

[0089] 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.

[0090] 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. In some embodiments, compositions can be targeted to the kidneys. In some embodiments, compositions can be targeted to renal cells.

[0091] 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. In some embodiments, the route of administration is or comprises dialysis. In some embodiments, the route of administration is or comprises hemodialysis. In some embodiments, the route of administration is or comprises peritoneal dialysis.

[0092] 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.

[0093] 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.

[0094] 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.

[0095] 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.

[0096] 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.

[0097] 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, 11/2 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).

[0098] 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).

[0099] 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.

[0100] 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.

[0101] 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.

[0102] 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.

[0103] 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.

[0104] 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).

[0105] 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.

[0106] 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.

[0107] 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.

[0108] 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.

[0109] 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.

[0110] 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

[0111] 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

[0112] 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

[0113] 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

[0114] 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

[0115] 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

[0116] 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

[0117] 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)

[0118] 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 $\alpha 11\beta 1$ and bound antibody were removed with an injection of 10mM glycine at pH 1.5.

Cell Adhesion Inhibition

[0119] 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)

[0120] 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- $\alpha 11$ antibodies. A polyclonal rabbit anti-human $\alpha 11$ 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 (Becton Dickinson) 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

[0121] 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

[0122] 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)

[0123] 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 µg/mL control antibodies (Groups 2 and 3 – either mouse IgG2a or rabbit IgG), or with a combination of TGF-β1 (3 ng/mL) and PDGF-ββ (50 ng/mL) (Groups 2-10). PCLS were cultured in the presence or absence of 10 µM Alk5i (Group 4) as a positive control or novel inhibitors (16E10, 79E3E3, and 9G05) at 2 escalating doses (10 and 100 µg/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.

[0124] 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.

[0125] 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, αSMA, TIMP-1, TGF-β1, IL-6 and β-actin/GAPDH.

Precision-Cut Kidney Slices (PCKS)

[0126] PCKS were prepared from explanted fibrotic human kidney tissue and rested for 24 hours to allow the post-slicing stress period to elapse before experiments began. PCKS were cultured with TGF-β1 (3 ng/mL) and PDGFββ (50 ng/mL) in the presence or absence of Alk5i (10 µM, positive control), test anti-α11β1 antibodies over three doses (1, 10 and 50 µg/mL) or in the presence of IgG control antibodies at a single high dose. PCKS culture media was harvested every 24 hours for a total of 3 time points. Levels of Collagen type I α1 (col1a1) in the tissue culture supernatants were quantified using R&D DuoSet ELISA kits. Statistics were performed using Two-way ANOVA followed by Dunnett's multiple comparisons test.

Example 1. Generation of Novel Monoclonal Antibodies Against $\alpha 11\beta 1$ and Determination of Binding Affinity

[0127] Antibody discovery was performed by immunizing rats and rabbits with recombinant human $\alpha 11\beta 1$, and by immunizing mice with both human and mouse $\alpha 11\beta 1$. 51 novel anti-human $\alpha 11\beta 1$ 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.

[0128] ELISA results illustrating exemplary binding of selected mouse monoclonal antibodies to recombinant human $\alpha 11\beta 1$ are shown in **Figure 2A**. Three of those mAbs also bound to mouse $\alpha 11\beta 1$, as shown in **Figure 2B**.

[0129] 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.

[0130] $\alpha 11\beta 1$ 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

[0131] 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 $\alpha 11$).

[0132] **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 $\alpha 11\beta 1$.

[0133] 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 EC_{50} 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 EC_{50} for mouse mAbs

mAb	Conc. ($\mu\text{g/mL}$)	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

[0134] 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.

[0135] 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 $\alpha 11\beta 1$

[0136] 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.

[0137] 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.

[0138] 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.

[0139] 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

[0140] Cell-mediated contraction of CD collagen I gels is a process previously shown to be α 11 β 1-mediated, and a more recent study showed that α 11 β 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.

[0141] 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 α 11-mediated collagen gel contraction. Of note, CHO-hu α 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

[0142] 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- $\alpha 11\beta 1$ antibodies on human Precision-Cut Liver Slices (PCLS)

[0143] 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*.

[0144] As shown in **Figures 17A-17C**, all anti- $\alpha 11\beta 1$ 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).

Example 6. Effect of anti- α 11 β 1 antibodies on human Precision-Cut Kidney Slices (PCKS)

[0145] Human Precision-Cut Kidney Slices (PCKS) are prepared from human kidney tissue with moderate fibrosis. After resting for 24 hours, PCKS are cultured with novel anti- α 11 β 1 monoclonal antibodies, at different doses and over time. At each time point, PCKS culture media is collected. At the harvest time point, culture media is collected and subsequently, RNA is extracted from each tissue slices. A range of profibrotic mediators are measured in the culture media as secreted proteins (including, but not limited to, COL1A1, Fibronectin, PAI-1, IL-11, CXCL1, MCP-1, IL-6, TIMP-1, Hyaluronic acid, TGF β , CTGF, PDGF, and MMP9) and also at the transcriptional level (including, but not limited to, COL1A1, IL-6, TIMP-1, Hyaluronic acid, TGF β , CTGF, α SMA, and ITGA11).

[0146] As described in the methods above, PCKS were prepared from explanted fibrotic human kidney tissue and rested for 24 hours to allow the post-slicing stress period to elapse before experiments began. PCKS were cultured with TGF- β 1 (3 ng/mL) and PDGF $\beta\beta$ (50 ng/mL) in the presence or absence of Alk5i (10 μ M, positive control), test anti- α 11 β 1 antibodies over three doses (1, 10 and 50 μ g/mL) or in the presence of IgG control antibodies at a single high dose. PCKS culture media was harvested every 24 hours for a total of 3 time points. Levels of Collagen type I α 1 (col1a1) in the tissue culture supernatants were quantified using R&D Duoset ELISA kits. Statistics were performed using Two-way ANOVA followed by Dunnett's multiple comparisons test.

[0147] As shown in **Figures 18A-18C**, for each anti- α 11- β 1 antibody, at least one dose at at least one time point provided a significant inhibition of col1a1 secretion. There was a significant inhibition of col1a1 secretion by 1994_01_C07 novel mAb at 72- and 96-hour time points at each dose tested. This is an important finding as collagen type I deposition is the major culprit of fibrotic tissue.

Example 7. Effect of anti- α 11 β 1 antibodies on in vivo kidney fibrosis model

[0148] Two different kidney fibrosis models are employed, a 5/6 Nephrectomy model and a ReninAAV Unx db/db mouse model. These two models are characterized by significant renal fibrosis with measurable reduced renal function. Anti- α 11 β 1 mAbs are tested in those

models and the effect they have on renal morphology (fibrosis) as well as renal function (GFR and albuminuria) are measured.

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

ATGGATTGGTTGTGGAACCTTGCTATTCCCTGATGGTAGTTGCCCAAAGTGCTCAAGCACAG
ATCCAGTTGGTACAGTCTGGACCTGAAGTAAAGAAGCCTGGAGAGTCAGTGAAGAT
CTCCTGCAAGGCCTCTGGGTATACCTTCACAGACTATGCAATGAACTGGGTGAAAC
AGGCTCCAGGAAATGGCCTGAAGTGGATGGGCTGGATCAACACCCAAACTGGAAA
GCCAACATATGCGGATGATTTCAAACAACGGTTTGTCTTCTCTTTGGAACTTCTG
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
CTGTGTAGCCTCAGGATACACTTTTCAGTAACTACTGGATGGACTGGGTTCCGCAGT
CTCCTGGAAAGTCCCTGGAATGGATTGGAGAGATTAACACGGATGGCAGAAGGAC
CAACTATGCACCATCCATAAAGGATCGATTACAAATCTCCAGAGACAATGCCAAG
AGCACCCCTGTATCTGCAGATGAGCAATGTGAAATCAGATGACACAGCCATTTATTAC
TGTACCATACTACGGGTATACCCCCACTACTTTGATTACTGGGGCCAAGGAGTCA
TGGTCACAGTCTCCTCA (SEQ ID NO: 3)

24E4G6 Light Chain Variable Region

ATGATGAGTCCTGCCCAGTTCCTGTTTCTGCTAATGCTCTGGATCCAGGAAGCCCGC
GGAGATGTTGTGATGACCCAGACACCACCGTCTTTGTCTGGTTGCCATTGGACAATCA
GTCTCCATCTCTTGCAAGTCAAGTCAGAGCCTCGTATATAGTGATGGAGAGACAT
ATTTGCATTGGTTTTTACAGAGTCCTGGCAGGTCTCCGAAGCGCCTAATTTATCACG
TGTCTAATCTGGGCTCTGGAGTCCCTGACAGGTTCAAGTGGCACTGGATCACTGACA

GATTTTACACTTAGAATCAGCAGAGTGGAGGCTGAGGATTTGGGAGTTTATTACTGC
GCGCAAACCTACACATTTTCCTCCCACGTTTGGAGCTGGGACCAAGCTGGAAGTGA
AA (SEQ ID NO: 4)

8H8E9 Heavy Chain Variable Region

ATGGCTGTCCTGGTGCTGTTGCTCTGCCTGGTGACATTTCCAAGCTGTGCCCTGTCCCAG
GTGCAGTTGAAGGAGTCAGGACCTGGTCTGGTGCAGCCCTCACAGACCCTGTCCCTC
ACCTGCACTGTCTCTGGGTTCTCATTAAACCAGCAATAGTGTTAGCTGGGTTGCGCA
GGCTCCGGGAAAGGGTCTGGAGTGGATGGGAGCAATATGGAGTGGTGGAAGCAC
AGATTATAATTCAGCTCTCAAATCCCGACTGAGCATCAGCAGGGACACCTCCAAG
AGCCAAGTTTTCTTAAAAATGAACAGTCTGCAAACCTGAAGACACAGCCATTTACTTC
TGTACCAGATCTCACTGGGAGCCCTTTGATTACTGGGGCCAAGGAGTCATGGTCA
CAGTCTCCTCA (SEQ ID NO: 5)

8H8E9 Light Chain Variable Region

ATGGAATCACAACTCAGGCCCTCATATCCCTGCTGCTCTGGGTATATGGTACCTGTGGG
GACATTGTGATGACCCAGTCTCCATTCTCCCTGGCTGTGTCAGAAGGAGAGATGGTC
ACTATAAACTGCAAGTCCAGTCAGGGTCTTTTATCCAGTGGAAACCAAAAGAAC
TACTTGGCCTGGTACCAGCAGAGACCAGGGCAGTCTCCTAACTACTGATCTACTA
TGCATCCACTAGGCAATCAGGGGTCCCTGATCGCTTCATAGGCGGTGGATCTGGGA
CAGACTTCACTCTGACCATCAGCGATGTGCAGGCTGAAGACCTGGCAGATTATTACT
GCCTGCAGCATTACAGCTATCCTCCCACGTTCTGGTCTGGGACCAAGCTGGAGAT
CAAA (SEQ ID NO: 6)

6E5C11 Heavy Chain Variable Region

ATGGCTGTCCTGGTGCTGTTGCTCTGCCTGGTGACATTTCCAAGCTGTGCCCTGTCCCAG
GTGCAGCTGAGGGAGTCAGGACCTGGTCTGGTGCAGCCCTCACAGACCCTGTCCCTC
ACCTGCACTGTCTCTGGGTTCTCATTGACCAGCAATAGTGTTGACCTGGGTTGCGCA
GCCTCCGGGAAAGGGTCTGGAGTGGATGGGAGCGATATGGAGTGATGGAAGCAC
AGATTATAATTCAACTCTCAAATCCCGACTGAGCATCAGTAGGGACACCTCCAAG
AGCCAAGTTTTCTTAAAAATGAGCAGTCTGCAAACCTGAAGACACAGCCATTTACTTC
TGTACCAGATCCCACTGGGAGCCCTTTGATTACTGGGGCCAAGGAGTCATGGTCA
CAGTCTCCTCA (SEQ ID NO: 7)

6E5C11 Light Chain Variable Region

ATGGAATCACAACTCAGGCCCTCATATCCCTGCTGCTCTGGGTATATGGTACCTGTGGG
GACATTGTGATGACCCAGTCTCCACTCTCCCTGGCTGTGTCAGAAGGAGAGACGGTC
ACTATGAACTGCAAGTCCAGTCAGAGTCTTTTTTCCAGTGGAAATCAAAAGAAC
TACTTGGCCTGGTACCAGCAGAAACCAGGGCAGTCTCCTAACTACTGATCTACTA
TGCATCCACTAGGCAATCAGGGGTCCCTGATCGCTTCATAGGCAGTGGATCTGGGA
CAGACTTCACTCTGACCATCAGCGATGTGCAGACTGAAGACCTGGCAGATTATTACT
GCCTGCAGCATTACAACCTATCCTCCCACGTTCTGGTCTGGGACCAAGCTGGAGA
(SEQ ID NO: 8)

7D8B10 Heavy Chain Variable Region

*ATGGACTTGCGACTGACTTATGTCTTTATTGTTGCTATTTTAAAAGGTGTCTTGTGTGAGGT
GAAACTGGAGGAATCTGGGGGAGGTTTGGTGCAACCTGGAATGTCCGTGAAACTCT
CTTGTGCAACCTCTGGATTCATTTTCAGTGACTACTGGATGGAATGGGTCCGCCAG
GCTCCAGGGAAGGGGCTAGAATGGGTAGCCGAAATTAGAAACAAAGCTAATAATT
ATGCAACATACTATGGGAAGTCTATGAAAGGCAGATTCACCATCTCAAGAGATGA
TTCCAAAAGTATAGTCTACCTACAAGTGAACAGCATAAGATCTGAAGATACTGCTAT
TTATTACTGTGCACCGAATTTTGATTACTGGGGCCAAGGAGTCATGGTCACGGTCTC
CTCA (SEQ ID NO: 9)*

7D8B10 Light Chain Variable Region

*ATGAGTCCTGTCCAGTCCCTGTTTTGCTATTGCTTTGGATTCTGGGAACCCATGGTGATG
TTGTGCTGACCCAGACTCCACCCACTTTATCGGCTACCATTTGGACAATCAGTCTCTAT
CTCTTGCAAGGTCAAGTCAGAGTCTCTTACATAGTACTGGAAACACCTATTTAAAT
TGGTTGCTACAGAGGCCAGGCCAACCTCCGCAACTTCTAATTTATTTGGTTTCCAG
ACTGGAATCTGGGGTCCCCAACAGGTTTCAGTGCCAGTGGGTCAGGAACTGATTTCA
CACTCAAAATCAGTGGAATAGAGGGCTGAGGATTTGGGGGTTTATTACTGCGTGCAA
AGTTCCCATACTCCGTACACGTTTGGGACTGGGACCAAGCTGGAAGTGAAG (SEQ
ID NO: 10)*

18E10F10 Heavy Chain Variable Region

*ATGGACATCAGGCTCAGCTTGGTTTTCTTGTCTTTTATGAAAGGTGTCCAGTGTGAGG
TGCAGTTGGTGGAGTCTGGGGGAGGCTTAGTGACGCCTGGAAGGTCCCTGAAACTCT
CCTGTGCAGCCTCACGATTCACCTTTTAGTGACTATAACATGGCCTGGGTCCGCCAG
GCTCCAAAGAAGGGTCTGGAGTGGGTCGCAACCATTTATCATGATGATAGTGGTT
CTTACTATCGAGACTCCGTGAAGGGCCGATTACCATCTCCAGAAATAATGCAAA
AAGCACTCTGTACCTGCAGATGGACAGTCTGAGGTCTGAGGACATGGCCACTTATTA
CTGTGCAAGACATAACAATGGCTTTGATTACTGGGGCCAAGGAGTCATGGTCACA
GTCGCCTCA (SEQ ID NO: 11)*

18E10F10 Light Chain Variable Region

*ATGAAGTGGCCTGTTAGGCTGTTGGTGCTGTTCTTCTGGATTCTGCTTCCGGGGGTGAT
GTTGTGATGACACAACTCCAGTCTCCCTGCCTGTCCGCCTTGGAGGTCAAGCCTCT
ATCTCTTGCCGGTCAAGTCAGAGCCTGGTACACAGTAATGGAAACACCTACTTG
CATTGGTACCTACAGAAGCCAGGCCAGTCTCCACAGCTCCTCATCAATCGGGTTTC
CAACAGATTTTCTGGGGTGCCAGACAGGTTTCAGTGGCAGTGGGTCAGGGACAGATT
TCACCCTCAAGATCAACAGAGTAGAGCCTGAGGACTTGGGAGATTATTACTGCTTA
CAAAGTACACATTTTCCACTCACGTTTCGGTTCTGGGACCAAGCTGGAGACCAAA
(SEQ ID NO: 12)*

40G10H11 Heavy Chain Variable Region

*ATGGACATCAGGCTCAGCTTGGGTTTTCTTGTCTTTTCATAAAAGGTGACCAGTGTGCGG
TGCAACTGGTGGAGTCTGGGGGAGGCTTAGTGACGCCTGGAAGGTCCCTGAAACTC
TCCTGTGCAGCCTCAAGAATCACTTTCACTGACTATTACATGGCCTGGGTCCGCCA
GGCTCCAACGAAGGGTCTGGAGTGGGTCGCAACCATTAGTTCTGATGGTGGTGAC
ACTTTCTATCGAGACTCCGTGAAGGGCCGATTTACTATCTCCAGAGACAAATGCAA
AAAGCACCTATATTTGCAAATGGTCAGTCTGAGGTCTGAGGACACGGCCACTTATT*

ACTGTTCAACAGATCGGGGAGCTCAGTTTGGTTACTGGGGCCAAGGCACTCTGGT
CACTGTCTCTTCA (SEQ ID NO: 13)

40G10H11 Light Chain Variable Region

ATGGCTCCAGTCCAGCTCTTAGGGCTGCTGCTGATTTGGCTCCCAGCCATGAGATGTGAC
ATCCAGATGACCCAGTCTCCTTCATTCTGTCTGCATCTGTGGGAGACAGAGTCTCT
ATCAACTGCAAAGCAAGTCAGAATGTTTCACGAGAACCTAAACTGGTATCAGCAAA
AGCTTGGAGAAGCTCCCAAACGCCTGATATATAATACAAACAATTTGCAAAACAGG
CATCCCATCAAGGTTCAAGTGGCAGTGGATCTGGTGCAGATTACACACTCACCATCAG
CAGCCTGCAGCCTGAAGATTTTGCCACATATTTCTGTTTGCAGCATAATGCTTTTC
CGTACACGTTTGGACCTGGGACGAAGCTGGAAGTAAA (SEQ ID NO: 14)

Mouse mAb sequences

9-G05 Heavy Chain Variable Region

GAGGTCCAGCTGCAACAGTCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAA
GATACCTGCAAGGCTTCTGGATACACATTCCTGACTACAACATGGACTGGGTGAA
GCAGAGCCATGGAAAAGAGCCTTGAGTGGATTGGATATATTAATCCTGACAATGGTG
GTACTATCTACAACCAGAAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAGTCC
TCCAGCACAGCCTACATGGAGCTCCGCAGCCTGACATCTGAGGACACTGCAGTCTAT
TACTGTGCAAGATTAGACAGCTCAGGCTACGGTTACTATGCTATGGACTACTGGGGT
CAAGGAACCTCAGTCACCGTCTCTCA (SEQ ID NO: 15)

9-G05 Light Chain Variable Region

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

8-P20 Heavy Chain Variable Region

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

8-P20 Light Chain Variable Region

GATGTTGTGATGACCCAACTCCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGTC
TCCATCTCTTGCAGATGTAGTCAGAGCCTGTACACAGTAATGGAAACACCTATTTA
CATTGGTACCTGCAGAAGCCAGGCCAGTCTCCACAGCTCCTGATCTACAAAATTTCC

AACCGATTTTCTGGGGTCCCAGACAGGTTTCAGTGGCAGTGGATCAGGGACAGATTTCACTCAAGATCAGCAGAGTGGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAAGTACACATGTTCCGTACACGTTTCGGAGGGGGGACCGAGCTGGAAATAAAA (SEQ ID NO: 18)

8-G15 Heavy Chain Variable Region

GAGGTCCAGCTGCAGCAGTCTGGACCTGAGCTGGTAAAGCCTGGGGCTTCAGTGAGGATATCCTGCAAGGCTTCTGGATACACATTCAGTACTACTACATACACTGGGTGAA GCAGAAGCCTGGGCAGGGCCTTGAATGCATTGGAGAGATTTATCCTGGAAGTGTATACTTACTACAGTAAAAAATTCAGGGGCAAGGCCACACTGACTGCAGACAAATCC TCCGACACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCAGTCTAT TTCTGTGCAAGAGGAGACTACTATAGGGGGTACTTCGATGTCTGGGGCGCAGGGAC CACGGTCACCGTCTCCTCA (SEQ ID NO: 19)

8-G15 Light Chain Variable Region

GATGTTGTGATGACTCAGACCTCACTCACTTTGTTCGGTTACCATTGGACAACCAGCC TCCATCTCTTGCAAGTCAAGTCAGAGCCTCTTACATAGTAATGGAAAGACATATTTG AATTGGTTATTACAGAGGCCAGGCCAGTCTCCAAAGTTCCTAATCTATCTGGTGTCT AAAGTGAATCTGGAGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGGACAGATTT CACACTGAAAATCAGCAGAGTGGAGGCTGAGGATTTGGGGGTTTATTACTGCTTGCA ATCTACACATTTTCTTGGACGTTTCGGTGGAGGCACCAAGCTGGAAATCAAA (SEQ ID NO: 20)

8-I14 Heavy Chain Variable Region

GAGGTCCAGCTGCAGCAGTCTGGACCTGAGCTGGTAAAGCCTGGGGCTTCAGTGAA GAAATCCTGCAAGGCTTCTGGATACACATTCAGTACTACTACATGCAGTGGGTGAA GCAGAAGCCTGGGCAGGGCCTTGAGTGGATTGGAAAGATTTATCCTGGAAGTGGTA ATACTCACTACAATGAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGACAAATCC TCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCAGTCTAT TTCTGTGCAACCAATTACTACGGCTACAGGGCAATGAACTATTGGGGTCAAGGATCC TCAGTCACCGTCTCCTCA (SEQ ID NO: 21)

8-I14 Light Chain Variable Region

GACATCCATTTGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAATC AGTCTCACTTGCCGGGCAAGTCAGGACATTTATATTAGCTTAAACTGGTTTCAGCAG AAACCAGATGGAATATTAACTCCTGATCTACGGCACATCCAGTTTAGATTCTGGT GTCCCCAAAAGGTTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGC AGCCTTGAGTCTGAAGATTTTGCAGACTATTACTGTCTACAATATGCTAGTTCTCCGT ACACGTTTCGGAGGGGGGACCAAGCTGGAAATAAAA (SEQ ID NO: 22)

9-E16 Heavy Chain Variable Region

GAGGTCCAGCTGCAGCAGTCTGGACCTGAGCTGGTAAAGCCTGGGGCTTCAGTGAA GATATCCTGCAAGGCTTCTGGATACACATTCAGTACTACTACATGCAGTGGGTGAA GCAGAAGCCTGGGCAGGGCCTTGAATGGATTGGAGAGATTTATCCTGGAAGTGGTA ATCCTTACTACAATGAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGACAAATCA TCCAGCTCAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCAGTCTAT

TTCTGTGCAAGAACCTCCTACGGTAGAGTAGGGACAGGGTTTGCTTACTGGGGCCAA
GGGACTCTGGTCACTGTCTCTGCA (SEQ ID NO: 23)

9-E16 Light Chain Variable Region

AATTTTGTGATGACCCAAACTCCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCCT
CCATCTCTTGCAGATCTAGTCAGAGCCTTCTACACAGTAACGGAAACACCTATTTAC
ATTGGTACCTGCAGAAGCCAGGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCA
ACCGATTTTCTGGGGTCCCAGACAGGTTTCAGTGGCAGTGGATCAGGGACAGATTTCA
CACTCAAGATCAACAGAGTGGAGACTGAGGATCTGGGAATTTATTTCTGCTCTCAAA
GTTCACATGTTCCACGTTCCGGTGCTGGGACCAAGCTGGAGCTGAAA (SEQ ID NO:
24)

8-J17 Heavy Chain Variable Region

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

8-J17 Light Chain Variable Region

GATGTTGTGATGACCCAAACTCCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCC
TCCATCTCTTGCAGATCTAGTCAGAGCCTTGTATATAGTAATGGAAATACCTATTTAC
ATTGGTACCTGCAGAAGCCAGGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCA
ACCGATTTTCTGGGGTCCCAGACAGGTTTCAGTGGCAGTGGATCAGGGACAGATTTCA
CACTCAAGATAAGCAGAGTGGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAA
GTACACATGTTCCGTGGACGTTCCGGTGGAGGCACCAAGCTGGAAATCAAA (SEQ ID
NO: 26)

6-O12 Heavy Chain Variable Region

GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAA
ACTCTCTTGTGCTGCCTCTGGATTCACTTTTGTAGTGACGCCTGGATGGACTGGGTCCGC
CAGTCTCCAGAGGCGGGGCTTGAGTGGGTTGCTGAAATTAGAAACAAAGCTCATAA
TCCTGCAACATACTATGCTGAGTCTGTGAAAGGGAGATTCACCATCTCAAGAGATGA
TTCCAAAAGTAGTGTCTACCTGCAAATGAACAGCTTAAGAGCTGAAGACACTGGCA
TTTATTACTGTACCTTAGTAGCCCCTGATGCTATGGACTACTGGGGTCAAGGAACCT
CAGTCACCGTCTCCTCA (SEQ ID NO: 27)

6-O12 Light Chain Variable Region

GACATTGTGATGTCAGTGTCTCCATCCTCCCTAGCTGTGTCAGTTGGAGAGAAGGTT
ACTATGAGCTGCAAGTCCAGTCAGAGCCTTTTATATAGTCGCAATCAAAAGAACTAC
TTGGCCTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATTTACTGGGCA
TCCACTAGGGCATCTGGAGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGAT
TTCATCTCACCATCAGCAGTGTGAAGGCTGAAGACCTGGCAGTTTATTACTGTCAG

CAATATTATAGCTATCCGTACACGTTCTGGAGGGGGGACCAAGCTGGAAATAAAA
(SEQ ID NO: 28)

10-L15 Heavy Chain Variable Region

CAGGTCCAACCTGCAGCAGTCTGGGCCTGAGCTGGTGAGGCCTGGGGCTTCAGTGAA
GATGTCTCTGCAAGGCTTCAGGCTATACCTTCACCAGCTACTGGATGCACTGGGTGAA
ACAGAGGCCTGGACAAGGCCTTGAGTGGATTGGCATGATTGATCCTTCCAATAGTGA
AACTTGGTTAAATCAGAAGTTCAAGGACAAGGCCACATTGAATGTAGACAAATCCT
CCAACACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCAGTCTATT
ACTGTGCAAGATATGATGGTTACTACGACTACTGGGGCCAAGGCACCACTCTCACAG
TCTCCTCA (SEQ ID NO: 29)

10-L15 Light Chain Variable Region

AACATTGTGCTGACCCAATCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCC
ACCATATCCTGCAGAGCCAGTGAAAGTGTTGATAGTTATGGCAATAGTTTTATGCAC
TGGTACCAGCAGAAACCAGGACAGCCACCCAACTCCTCATCTATCTTGCATCCAAC
GTAGAATCTGGGGTCCCTGCCAGGTTCAAGTGGCAGTGGGTCTAGGACAGACTTCACC
CTCACCATTGATCCTGTGGAGGCTGATGATGCTGCAACCTATTACTGTCAGCAAAAT
AATGAGGATCCGTGGACGTTCTGGTGGAGGCACCAAGCTGGAAATCAAA (SEQ ID
NO: 30)

7-H14 Heavy Chain Variable Region

CAGGTCCAACCTGCAGCAGCCTGGGGCTGAGCTGGTGAGGCCTGGGGCTTCAGTGAA
GCTGTCTCTGCAAGCCTTCTGGCTACACCTTCACCAGCTACTGGATGAACTGGGTGAA
GCAGAGGCCTGGACAAGGCCTTGAATGGATTGGTATGATTGATCCTTCAGACAGTG
AAACTCACTACAATCAAATGTTCAAGGACAAGGCCACATTGACTGTTGACAAATCCT
CCAACACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATT
ACTGTGCGCAGATCTACTATGCTTACGACAAGGCTTACTGGGGCCAAGGGACTCTGG
TCACTGTCTCTGCA (SEQ ID NO: 31)

7-H14 Light Chain Variable Region

GACATTGTGATGTCACAGTCTCCATCCTCCCTAGCTGTGTGTCAGTTGGAGAGAAGGTT
ACTATGAGCTGCAAGTCCAGTCAGAGCCTTTTATATAGTAGCCATCAAAAGAACTAC
TTGGCCTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATTTACTGGGCA
TCCACTAGGGAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGAT
TTCAGTCTCACCATCAGCAGTGTGAAGGCTGAAGACCTGGCAGTTTATTACTGTCAG
GAATATTATAGCTGGACGTTCTGGTGGAGGCACCAAGCTGGAAATCAAA (SEQ ID
NO: 32)

6-B21 Heavy Chain Variable Region

GAGGTCCAGCTGCAACAATCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAA
GATATCCTGTAAAGCTTCTGGATACACGTTCACTGACTACTACATGAACTGGGTGAA
GCAGAGCCATGGAAAGAGCCTTGAGTGGATTGGAGATATTAATCCTCACAATGGTG
GTACTAGCTTCATCCAGAAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAGTCTT
CCAGCACAGCCTACATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCAGTCTATT

ATTGTGCCCCCTCTGGGACGAAAGGAGGGGTTTGCTTACTGGGGCCAAGGGACTCTG
GTCAGTGTCTCTGCA (SEQ ID NO: 33)

6-B21 Light Chain Variable Region

GACACTGTGCTGACACAGTCTCCTGCTTCCTTAGTTGTATCTCTGGGGCAGAGGGCC
ACCATCTCATGCAGGGCCAGCAAAAGTGTACGTACATCTGGCTATAGTTATATGCAC
TGGTACCAACAGAAACCAGGACAGCCACCCAACTCCTCATCTATCTTGCATCCAAC
CTAGAATCTGGGGTCCCTGCCAGGTTTCAGTGGCAGTGGGTCTGGGACAGCCTTCACC
CTCAACATCCATCCTGTGGAGGAGGAGGATGCTGCAACCTATTACTGTCAGCACAGT
AGGGAGCTTCCGTACACGTTCCGAGGGGGGACCAAGCTGGAAATAAAA (SEQ ID
NO: 34)

10-F23 Heavy Chain Variable Region

CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCCAGACCCCTCAGT
CTGACTTGTTCTTTCTCTGGGTTTTCAGTGAAGCTTTTGCTATGGGTGTAGGCTGGA
TTCGTCAGCCTTCAGGGAAGGGTCTGGAGTGGCTGGCACACATTTGGTGGGATGATG
ATAAGTACTATAACCCAGCCCTGAAGAGCCGGCTCACAATCTCCAAGGATACCTCC
AAAAACCATGTATTCCTCAAGATCGCCAATGTGGACACTGCAGATACTGCCACATAC
TACTGTGCTCGAATGCCGCTAACTTTCTACTTTGACTACTGGGGCCAAGGCACCACT
CTCACAGTCTCCTCA (SEQ ID NO: 35)

10-F23 Light Chain Variable Region

GATGTTTTGCTGACCCAACTCCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCCT
CCATCTCTTGAGATCTAGTCAGAGCATTGTACATAGTAATGGACACACCTATTTAG
AATGGTACCTGCAGAAACCAGGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCA
ACCGATTTTCTGGGGTCCCAGACAGGTTTCAGTGGCAGTGGATCAGGGACAGATTTCA
CACTCAAGATCAGCAGAGTGGAGGCTGAGGATCTGGGAGTTTATTACTGCTTTCAAG
GTTACATGTTCCGTTACGTTCCGAGGGGGGACCAAGCTGGAAATAAAA (SEQ ID
NO: 36)

6-A12 Heavy Chain Variable Region

CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCCAGACCCCTCAGT
CTGACTTGTTCTTTCTCTGGGTTTTCAGTGAAGCTTTTGCTATGGGTGTAGGCTGGA
TTCGTCAGCCTTCAGGGAAGGGTCTGGAGTGGCTGGCACACATTTGGTGGGATGATG
ATAAGTACTATAACCCAGCCCTGAAGAGCCGGCTCACAATCTCCAAGGATACCTCC
AAAAACCAAGTATTCCTCAAGATCGCCAATGTGGACACTGCAGATACTGCCACATA
CTACTGTGCTCGAATGCCGCTAACTTTCTACTTTGACTACTGGGGCCAAGGCACCAC
TCTCACAGTCTCCTCA (SEQ ID NO: 37)

6-A12 Light Chain Variable Region

GATGTTTTGATGACCCAACTCCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCCT
CCATCTCTTGATAGATCTAGTCAGAGCATTGTACATAGTAATGGAAACACCTATTTAG
AATGGTACCTGCAGAAACCAGGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCA
CCCGATTTTCTGGGGTCCCAGACAGGTTTCAGTGGCAGTGGATCAGGGACAGATTTCA
CACTCAAGATCAGCAGAGTGGAGGCTGAGGATCTGGGAGTTTATTACTGCTTTCAAG

GTTCACATGTTCCGTTACGTTTCGGAGGGGGGACCAAGCTGGAAATAAAA (SEQ ID NO: 38)

6-M8 Heavy Chain Variable Region

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

6-M8 Light Chain Variable Region

GATATTGTGATGACGCAGGCTGCATTCTCCAATCCAGTCACTCTTGGAACATCAGCT
TCCATCTCTGCAAGTCTAGTAAGAGTCTCCTACATAGTAATGGCATCACTTATTTGT
ATTGGTATCTGCAGAAGCCAGGCCAGTCTCCTCAGCTCCTGATTTATCAGATGTCCA
ACCTTGCTCAGGAGTCCCAGACAGGTTCAAGTAGCAGTGGGTGAGGAATGATTTCA
CACTGAGAATCAGCAGAGTGGAGGCTGAGGATGTGGGTGTTTATTACTGTGCTCAA
AATCTAGAACTTCTCCGACGTTTCGGTGGAGGCACCAAGCTGGAAATCAAA (SEQ ID NO: 40)

2-A3 Heavy Chain Variable Region

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

2-A3 Light Chain Variable Region

GATGTTGTGATGACCCAGACTCCACTCACTTTGTTCGGTTACCATGGACAACCAGCC
TCCATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGCTGGAAAGACATATTTG
AATTGGTTGTTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATGTATCTGGTGTCT
AACTGGACTCTGGAGTCCCTGACAGGTTCACTGGCAGCGGATCAGGGACAGATTT
CACACTGAAAATCAGCAGAGTGGAGGCTGAGGATTTGGGAGTTTATTATTGCTGGC
AAGGTACACATTTTCCGTACACGTTTCGGAGGGGGGACCAAGCTGGAAATAAAA
(SEQ ID NO: 42)

6-O17 Heavy Chain Variable Region

CAGGTCCAACTGCAGCAGCCTGGGGCTGAGCTTGTGAAGCCTGGGGCTTCAGTGAA
GTTGTCTCTGCAAGGCTTCTGGCTACACCTTCACCAGCTACTGGATGCACTGGATAAA
GCAGAGACCTGGACAAGGCCTTGAGTGGATTGGAGAGATTAACCCTAGCAATGGTG
GTTCTAACTACAATGAGAAGTTCAAGAGCAAGGCCACACTGACTGTAGACAAATCC
TCCAGCACAGCCTACATGCAACTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTAT

CACTGTAAAAGCAGAGGCTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA
(SEQ ID NO: 43)

6-O17 Light Chain Variable Region

GATGTTGTGATGACCCAGACTCCACTCACTTTGTCGGTTACCATTGGACAACCAGCC
TCCATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTTATGGAAAGACATATTG
AATTGGTTGTTACAGCGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGGTGTCT
AAATTGGACTCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTT
ACACTGAAAATCAGCAGAGTGGAGGCTGAGGATTTGGGAATTTATTATTGCTGGCA
AGGTACACATTTTCTCACACGTTCTGGCTCGGGGACAAAGTTGGAAATAAAA (SEQ
ID NO: 44)

3-G5 Heavy Chain Variable Region

CAGGTTTCAGCTGCAGCAGTCTGGAGCTGAGCTGGCGAGGCCTGGGGCTTCAGTGAA
ACTGTCTCTGCAAGGCTTCTGGCTACACCTTCACAAGCTATGGTATAAGCTGGGTGAA
ACAGAGAACTGGACAGGGCCTTGAGTGGATTGGAGAGATTTTTCTAGAAAGTAGTA
ATACTTACTATAATGAGAAAGTTCAAGGGCAAGGCCACACTGACTGCAGACAAGTCC
TCCAGCACAGTGTACATGGAGTTCGCGAGCCTGACATCTGAGGACTCTGCGGTCTAT
TTCTGTGCAAGAGAGGGGGGCTGGCCTGGTTTGCTTACTGGGGCCAAGGGACTCTG
GTCACTGTCTCTGCA (SEQ ID NO: 45)

3-G5 Light Chain Variable Region

GATGTTGTGATGACCCAGACTCCACTCACTTTGTCGGTTACCATTGGACAACCAGCT
TCCATCTCTTGCAAGTCAAGTCAGAGCCTCTTATATACTAATGGAAACACCTATTG
AATTGGTTATTACAGAGGCCAGGCCAGTCTCCAAAACGCCTAATCTATCTGGTGTCT
AAATTGGACTCTGGAATCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTT
ACACTGAGAATCAGCAGAGTGGAGGCTGAGGATTTGGGAGTTTATTACTGCTTGCA
GAGTACACATTTTCCATTACGTTCTGGCTCGGGGACAAAGTTGGAAATAAAA (SEQ
ID NO: 46)

6-A15 Heavy Chain Variable Region

GAGGTCCAGCTGCAACAATCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAA
GATGTCTCTGTAAGGCTTCTGGATACACAATCACTGACTACTACATGATGTGGTTGAA
GCAGAGTCATGGAAAGAGCCTTGAATGGATTGGAGATATTAATCCTTACACTGGTG
GTACTAGCTACAACCAGAAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAATCC
TCCAGCACAGCCTACCTGCAGCTCCACAGCCTGACATCTGAGGACTCTGCAGTCTAT
TACTGTGCAAGAGGGGCCTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA
(SEQ ID NO: 47)

6-A15 Light Chain Variable Region

GATGTTGTGATGACCCAGACTCCACTCACTTTGTCGGTTACCATTGGACAACCAGCC
TCCATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGATGGAAAGACATATTG
AATTGGTTGTTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGGTGTCT
AAACTGGACTCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTT
ACACTGAAAATCAGCAGAGTGGAGGCTGAGGATTTGGGAGTTTATTATTGCTGGCA

AGGTACACATTTTCCGTACACGTTCTGGAGGGGGGACCAAGCTGGAAATAAAA (SEQ ID NO: 48)

10-K10 Heavy Chain Variable Region

GAGGTCCAGCTGCAACAATCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAA
GATGTCTCTGTAAGGCTTCTGGATACACAATCACTGACTACTACATGATGTGGTTGAA
GCAGAGTCATGGAAAAGAGCCTTGAATGGATTGGAGATATTAATCCTTACACTGGTG
GTACTAGCTACAACCAGAAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAATCC
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
GATATCCTGTAAGGCTTCTGGATACACGTTCACTGACTACTACATGAACTGGGTGAA
GCAGAGCCATGGCAGGAGCCTTGAGTTGATTGGAGATATTAATCCTAACAAATGGTG
GTTCTAACTTCAACCAGAAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAGTCC
CCAGCACAGCCTATATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCAATCTATT
ACTGTGCAAGAATGGGTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCA (SEQ
ID NO: 51)

6-P20 Light Chain Variable Region

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

7-O8 Heavy Chain Variable Region

GAGGTCCAGCTGCAGCAGTCTGGACCTGAACTGGTCAAGCCTGGGGCTTCAGTGAA
GATGTCTCTGCAAGGCTTCTGGATACACATTCAGTACTACTACATCACTGGGTGAA
GCAGAAGCCTGGGCAGGGCCTTGAGTACATTGGAGAGATTTATCCTGGAAGTGGTA
ATACTTACTACAATGGGAAGTTCAAGGGCAAGGCCACACTGACTGCAGACAAGTCC
TCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCAGTCTAT

TTCTGTGGTAGTGGCTACTTTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCC
TCA (SEQ ID NO: 53)

7-08 Light Chain Variable Region

GATGTTGTGATGACCCAGACTCCACTCACTTTGTCTGTTACCATTGGACAGCCAGCTT
CCATTTCTTGCAAGTCAAGTCAGAGCCTCTTATATAGTAATGGAAAAACCTATTTGA
ATTGGTTATTACAGAGTCCAGGCCAGTCTCCAAAGCTCCTAATCTATCTGGTGTCTA
AACTGGAATCTGGAGTCCCTGACAGATTCAAGTGGCAGTGGATCAGGGACAGATTTT
ACACTGAAACTCAGCAGAGTGGAGGCTGAGGATTTGGGAGTATATTACTGCGTGCA
AGGTACACATTTCCCATTCACGTTCCGGCTCGGGGACAAAGTTGGAAATAAAA (SEQ
ID NO: 54)

Rabbit mAb sequences

A11B1_16G7 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGTTCAAAGGTGTCCAGTGT
CAGGAGCAACTGGTGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGAC
ACTCACCTGCACAGCCTCTGGATTCTCCTTCAATAAGAATTATTGGATGTGCTGGGT
CCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGATGCATTTATAATGGTGATG
GCAACACATACTACGCGAGCTGGGTGAATGGCCGATTCACCATCTCCAAAACCTCGT
CGACCACGGTGAAGTCTGCAAATGACCAGTCTGACAGTCGCGGACACGGCCATCTATT
TCTGTGCGAGACTACTTAATATGTGGGGCCCAGGCACCCTGGTCACCGTCTCCTCAG
GGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCTGCTGCGGGGACACACCCA
GCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCTCCCGGAGCCAGTGACC
GTGACCTGGAAGTCCGGGACCCCTACCAATGGGGTACGCACCTTCCCGTCCGTCCGG
CAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCAGCCA
GCCCCGTCACCTGCAACGTGGCCACCCAGCCACCAACACCAAAGTGGACAAGACCG
TTGCGCCCTCGACATGCAGCAAGCCCATGTGCCCACCCCTGAACTCCCGGGGGGAC
CGTCTGTCTTCATCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCACGCACCC
CCGAGGTACATGCGTGGTGGTGGACGTGAGCCAGGATGACCCCGAGGTGCAGTTC
ACATGGTACATAAACAACGAGCAGGTGCGCACCGCCCCGGCCGCGCTACGGGAGCA
GCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCCTCCCCATCGCGCACCAAGGACT
GGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAGGCACTCCCGGCCCCC
ATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCCTGGAGCCGAAGGTCTACAC
CATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTGCGTCAGCCTGACCTGCATGA
TCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAGAAGAACGGGAAGGCA
GAGGACAACTACAAGACCACGCCGACCGTGCTGGACAGCGACGGCTCCTACTTCCT
CTACAGCAAGCTCTCAGTGCCACGAGTGAGTGAGTGGCAGCGGGGCGACGTCTTCACCT
GCTCCGTGATGCACGAGGCCTTGCACAACCACTACACGCAGAAGTCCATCTCCCGCT
CTCCGG GTAAATAG (SEQ ID NO: 55)

A11B1_16G7 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTACTGCTCTGGCTCCCAGGT
GCCAGATGTGCTGACATTGTGATGACCCAGACTCCAGCCTCCGTGGAGGCAGCTGTG
GGAGGCACAGTCAACATCAAGTGCCAGGCCAGTGAGAGCATTGGCAATGCATTAGC

CTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTATACTGCAGCCAC
TCTGGCATCTGGGGTCCCATCGCGGTTTCAGCGGCAGTGGATCTGGGACAGAGTTTCAC
TCTCACCATCAGTGGCGTGCAGTGTGACGATGCTGCCACTTACTACTGTCAAAGCTA
TTATTTTACTAGTGTAGTAGTTATGGCAATGCTTTCGGCGGAGGGACCGAGGTGGT
GGTCAAAGGTGATCCAGTTGCACCTACTGTCCTCATCTTCCCACCAGCTGCTGATCA
GGTGGCAACTGGAACAGTCAACATCGTGTGTGTGGCGAATAAAATACTTTCCCGATGT
CACCGTCACCTGGGAGGTGGATGGCACCACCCAAACAACCTGGCATCGAGAACAGTA
AAACACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGA
CCAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACG
ACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTAG (SEQ ID NO: 56)

A11B1_16E10 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACT
CACCTGCAGAGTCTCTGGATTCTCCTTCAGTAGCAGTTATTATATGTGTTGGGTCCGC
CAGGCTCCAGGGAAGGGGCTGGAATGGATCGCATGTATTGGTACTACTCGTGGTAG
CACTTACTACGCGACCTGGGCGAAAGGCCGATTACCATTTCTAAAATCTCGTCGAC
CACGGTGACTCTACAAATGACCAGTCTGACAGACGCGGACACGGCCACCTATTTCTG
TGCGAGAGATGCTACTGGTTATAGGATTAACACGATTGGCCTCTATTTTAATTTGTG
GGGCCCAGGCACCCTGGTCACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTT
CCCCTGGCCCCCTGCTGCGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCT
GGTCAAAGGCTACCTCCCGGAGCCAGTGACCGTGACCTGGAACCTCGGGCACCCCTCA
CCAATGGGGTACGCACCTTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGA
GCAGCGTGGTGAGCGTGACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGCCCAC
CCAGCCACCAACACCAAAGTGGACAAGACCGTTGCGCCCTCGACATGCAGCAAGCC
CATGTGCCCACCCCCTGAACTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCCAA
ACCCAAGGACACCCTCATGATCTCACGCACCCCCGAGGTCACATGCGTGGTGGTGG
ACGTGAGCCAGGATGACCCCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAG
GTGCGCACCGCCCGGCCGCCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGT
GGTCAGCACCCCTCCCCATCGCGCACCAAGGACTGGCTGAGGGGCAAGGAGTTCAAGT
GCAAAGTCCACAACAAGGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCC
AGAGGGCAGCCCCTGGAGCCGAAGGTCTACACCATGGGCCCTCCCCGGGAGGAGCT
GAGCAGCAGGTGCGTCAGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACAT
CTCGGTGGAGTGGGAGAAGAACGGGAAGGCAGAGGACAACCTACAAGACCACGCCG
ACCGTGCTGGACAGCGACGGCTCCTACTTCCTCTACAGCAAGCTCTCAGTGCCACG
AGTGAGTGGCAGCGGGGCGACGTCTTACCTGCTCCGTGATGCACGAGGCCTTGCA
CAACCACTACACGCAGAAGTCCATCTCCCGCTCTCCGGGTAAATAG (SEQ ID NO:
57)

A11B1_16E10 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCAGATGTGCGTTCGAATTGACCCAGACTCCATCCTCCGTGGAGGCTGCTGTGGGA
GGCAGCCCCACCATCAAGTGCCAGGCCAGTCAGACCATTACAGTTACTTATCCTGG
TATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTATGAAGCGTCCAACT
GGCCTCTGGGGTCCCATCGCGGTTTCAGCGGCAGTGGATCTGGGACAGACTACACTCT
CACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTACTACTGTCAAAGCTATCA

TGGTACTGCTAGTACTGAATATAATACTTTTCGGCGGGGGGACCGAGGTGGTGGTCAG
AGGTGATCCAGTTGCACCTACTGTCCCTCATCTTCCCACCAGCTGCTGATCAGGTGGC
AACTGGAACAGTCAACATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCACCGT
CACCTGGGAGGTGGATGGCACCACCCAAACAACCTGGCATCGAGAACAGTAAAACAC
CGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAGCA
CACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACCTCA
GTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 58)

A11B1_15G10 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGCAGCAGCTGGTGGAGTCCGGGGGAGGCCTGGTCAAGCCTGGGGCAGCCCTGAC
ATTCACCTGCACAGCCTCTGGATTCTCCTTCAGTGGCAATTATTGGATATGCTGGGTC
CGCCAGGCTCCAGGGAAGGGGTTGGAGTGGATCGCGTGCATTGGTACTATTACTAGT
AGGACATACTACGCGAGCTGGGCGAAAGGCCGATTACCATTTCCAAAACCTCGTC
GACCACGGTGACTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACGTATT
TCTGTGCGAGAGGTGCGGTTGTTAGTAGTGGTAATGCTCCCTACTACTTTACCTTGTG
GGGCCCAGGCACCCTGGTCACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTT
CCCACTGGCCCCCTGCTGCGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCT
GGTCAAAGGCTACCTCCCGGAGCCAGTGACCGTGACCTGGAACCTCGGGCACCCTCA
CCAATGGGGTACGCACCTTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGA
GCAGCGTGGTGAGCGTGACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGCCAC
CCAGCCACCAACACCAAAGTGGAACAAGACCGTTGCGCCCTCGACATGCAGCAAGCC
CATGTGCCCACCCCCTGAACTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCCAA
ACCCAAGGACACCCTCATGATCTCACGCACCCCGAGGTCACATGCGTGGTGGTGG
ACGTGAGCCAGGATGACCCCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAG
GTGCGCACCGCCCGGCCGCCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGT
GGTCAGCACCCCTCCCCATCGCGCACCAAGGACTGGCTGAGGGGCAAGGAGTTCAAGT
GCAAAGTCCACAACAAGGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCC
AGAGGGCAGCCCCTGGAGCCGAAGGTCTACACCATGGGCCCTCCCCGGGAGGAGCT
GAGCAGCAGGTGCGTCAGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACAT
CTCGGTGGAGTGGGAGAAGAACGGGAAGGCAGAGGACAACCTACAAGACCACGCCG
ACCGTGCTGGACAGCGACGGCTCCTACTTCCTCTACAGCAAGCTCTCAGTGCCACG
AGTGAGTGGCAGCGGGGCGACGTCTTCACCTGCTCCGTGATGCACGAGGCCTTGCA
CAACCACTACACGCAGAAGTCCATCTCCCGCTCTCCGGGTAAATAG (SEQ ID NO:
59)

A11B1_15G10 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCAGATGTGCATTTCGAATTGACGCAGACTCCATCCTCCGTGGAGGCAGCTGTGGGA
GGCAGAGTCACCATCAAGTGCCAGGCCAGTCAGAGCATTAGTAGTTACTTATCCTGG
TATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTACAGGGCATCCACTCTG
GAATCTGGGGTCCCATCGCGGTTTAAAGGCAGTGGATCTGGGACAGAGTTCACTCTC
ACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTACTTCTGTCAAAGCTATTAT
GGTGTTACTTTTATGTGGTTTTGCTTTTCGGCGGAGGGACCGAGGTGGTGGTCAAAGGT
GATCCAGTTGCACCTACTGTCCCTCATCTTCCCACCAGCTGCTGATCAGGTGGCAACT
GGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCACCGTCACC

TGGGAGGTGGATGGCACCACCCAAACAACCTGGCATCGAGAACAGTAAACACCCGCA
GAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAGCACACA
GTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACCTCAGTCG
TCCAGAGCTTCAATAGGGGTGACTGTAG (SEQ ID NO: 60)

A11B1_14H1 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACT
CACCTGCAAAGCCTCTGGAATCGACTTCAATAACTATTGGATAACCTGGGTCCGCCA
GGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATTTATGTTGGAATTACCGGCC
GCACATGGTACGCGAACTGGGCGAAAGGCCGATTACCATCTCCAAGGCCTCGAGC
ACGGTGGATCTGAAAATGACCACTCTGACAGCCGCGGACACGGCCACCTATTTCTGT
GCGAGGAATGGTGATGGTGGTATTTATGCTCTTAACTTGTGGGGCCCAGGCACCCTG
GTCACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCTGC
TGCGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCT
CCCGGAGCCAGTGACCGTGACCTGGAACCTCGGGCACCCCTACCAATGGGGTACGCA
CCTTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCG
TGACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGCCCACCCAGCCACCAACACC
AAAGTGGAACAAGACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCACCCCC
TGAACCTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCC AAAACCCAAGGACACCCT
CATGATCTCACGCACCCCCGAGGTCACATGCGTGGTGGTGGACGTGAGCCAGGATG
ACCCCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAGGTGCGCACCGCCCCG
CCGCCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCCTCC
CATCGCGCACCAAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACA
AGGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAGCCAGAGGGCAGCCCTG
GAGCCGAAGGTCTACACCATGGGCCCTCCCGGGAGGAGCTGAGCAGCAGGTCCGT
CAGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGA
GAAGAACGGGAAGGCAGAGGACAACCTACAAGACCACGCCGACCGTGCTGGACAGC
GACGGCTCCTACTTCCTCTACAGCAAGCTCTCAGTGCCACGAGTGAGTGGCAGCGG
GGCGACGTCTTACCTGCTCCGTGATGCACGAGGCCTTGCACAACCACTACACGCAG
AAGTCCATCTCCCGCTCTCCGGGTAAATAG (SEQ ID NO: 61)

A11B1_14H1 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCACATTTGCACAAGTGCTGACCCAGACTGCATCGTCCGTGTCTGCAGCTGTGGGA
GGCACAGTCACCATCAGTTGCCAGTCCAGTCAGAGTGTTTATAATAATAATTGGTTA
GCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTACAGGGCATC
CACTCTGACATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACACAGTT
CACTCTCACCATCAGCGACCTGGAGTGTGACGATGCTGCCACTTACTACTGTGCAGG
CGGTTATAGTGGTAATATTTACGTAAATGATTTTCGGCGGAGGGACCGAGGTGGTGGT
CAAAGGTGATCCAGTTGCACCTACTGTCTCATCTTCCCACAGCTGCTGATCAGGT
GGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTCCCGATGTCAC
CGTCACCTGGGAGGTGGATGGCACCACCCAAACAACCTGGCATCGAGAACAGTAAAA
CACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCA
GCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACC
TCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTAG (SEQ ID NO: 62)

A11B1_13G4 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGGAGCAGCTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGGATCCCTGAC
ACTCACCTGCAAAGCCTCTGGATTCTCCTTCAGTAATACCTACTGGGCATGCTGGGT
CCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATGAATCCTGCTAGTA
GTGGTAGCTCTTACTACGCGAGCTGGGCGAAAGGCCGATTACCATCTCCAAAACCT
CGTCGACCACGGTGACTCTGCACATGCCCAGTCTGACAGCCGCGGACACGGCCACC
TATTTCTGTGCGAAATGGGATACTGCTTTCGATGTGTGGGGGCCAGGCACCCTGGTC
ACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCCTGGCCCCCTGCTGC
GGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCTCCC
GGAGCCAGTGACCGTGACCTGGAACCTCGGGCACCCCTACCAATGGGGTACGCACCT
TCCCGTCCGTCCGGCAGTCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTGA
CCTCAAGCAGCCAGCCCGTCACTGCAACGTGGCCCCACCCAGCCACCAACACCAAA
GTGGACAAGACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCCCACCCCTGA
ACTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCCAAAAACCCAAGGACACCCTCAT
GATCTCACGCACCCCCGAGGTACATGCGTGGTGGTGGACGTGAGCCAGGATGACC
CCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAGGTGCGCACCCGCCCGGCCG
CCGTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTGGTACGACCCCTCCCAT
CGCGCACCAAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAG
GCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCTGGA
GCCGAAGGTCTACACCATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTCCGTCA
GCCTGACCTGCATGATCAACGGCTTCTACCTTCCGACATCTCGGTGGAGTGGGAGA
AGAACGGGAAGGCAGAGGACAACCTACAAGACCACGCCGACCGTGTGGACAGCGA
CGGCTCTACTTCTCTACAGCAAGCTCTCAGTGCCACGAGTGAGTGGCAGCGGGG
CGACGTCTTACCTGCTCCGTGATGCACGAGGCCTTGCAACAACCTACACGCAGAA
GTCCATCTCCCGCTCTCCGGGTAAATAG (SEQ ID NO: 63)

A11B1_13G4 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCAGATGTGCCGATGTTGTGATGACCCAGACTCCATCCTCCGTGGAGGCAGCTGTG
GGAGGCACAGTCACCATCAAGTGCCAGGCCAGTCAGAGCATTAGTAGCTACTTAGC
CTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTATGGTGCATCCAA
TCTGGAGTCTGGGGTCCCATCGCGTTCAAAGGCAGTGGATCTGGGACAGAGTACA
CTCTACCATCAGCGGCGTGCAGTGTGACGATGCTGCCACTTACTACTGTCAAACT
ATTATGCTATTGATACTTATGGTCATGCTTTCGGCGGAGGGACCGAGGTGGTGGTCA
AAGGTGATCCAGTTGCACCTACTGTCCTCATCTTCCCACCAGCTGCTGATCAGGTGG
CAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCACCG
TCACCTGGGAGGTGGATGGCACCAACCAAACTGGCATCGAGAACAGTAAACA
CCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAGC
ACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACCTC
AGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 64)

A11B1_13C3 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGGAGCAGCTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGAC

ACTCACCTGCACAGCCTCTGGATTCTCCTTTAGTAGCAACTATCACATCTGCTGGGTC
CGCCAGGCTCCAGGAAAGGGGCTGGAGTTGATCGCATGCATTTATGTTGGTGATGGC
AGCACATACTACGCGAGCTGGGCGAAAGGCCGATTACCATCTCCAAATCCTCGTC
GACCACGGTAGCTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATT
TCTGTGGGAGAATGTTTAACTTGTGGGGCCCAGGCACCCTGGTCAACCGTCTCCTCAG
GGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCTGCTGCGGGGACACACCCA
GCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCTCCCGGAGCCAGTGACC
GTGACCTGGAATCGGGCACCTCACCAATGGGGTACGCACCTTCCCGTCCGTCCGG
CAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCAGCCA
GCCCCGTACCTGCAACGTGGCCACCCAGCCACCAACACCAAAGTGGACAAGACCG
TTGCGCCCTCGACATGCAGCAAGCCCATGTGCCACCCCTGAACTCCCGGGGGGAC
CGTCTGTCTTCATCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCACGCACCC
CCGAGGTACATGCGTGGTGGTGGACGTGAGCCAGGATGACCCCGAGGTGCAGTTC
ACATGGTACATAAACAACGAGCAGGTGCGCACCCGCGCCGCGCTACGGGAGCA
GCAGTTCAACAGCACGATCCGCGTGGTCAGCACCTCCCCATCGCGCACCAAGGACT
GGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAGGCACTCCCGGCCCCC
ATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCTGGAGCCGAAGGTCTACAC
CATGGGCCCTCCCGGGAGGAGCTGAGCAGCAGGTGCGTCAGCCTGACCTGCATGA
TCAACGGCTTCTACCTTCCGACATCTCGGTGGAGTGGGAGAAGAACGGGAAGGCA
GAGGACAACATAAAGACCACGCCGACCGTGCTGGACAGCGACGGCTCCTACTTCT
CTACAGCAAGCTCTCAGTGCCCACGAGTGAGTGGCAGCGGGGCGACGTCTTACCT
GCTCCGTGATGCACGAGGCCTTGACAACCACTACACGCAGAAGTCCATCTCCCGCT
CTCCGGGTAAATAG (SEQ ID NO: 65)

A11B1_13C3 Light Chain

ATGGACACGAGGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCATATGTGACCCTGTGCTGACCCAGACTCCATCCTCCGTGTCTGCGGCTGTGGGA
GTCACAGTCACCATCAACTGCCAGTCCAGTCCGAGTGTTTATAGTAACTACTTATCC
TGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTCATCTATCTGGCATCTACT
CTGGCATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACACAGTTCCT
CTCACCATCAGCGACGTGCAGTGTGACGATGCTGCCACTTACTACTGTGCAAGGCACT
TATAGTGGTAATATTTGGTCTTTCGGCGGAGGGACCGAGGTGGTGGTCAAAGGTGAT
CCAGTTGCACCTACTGTCTCATCTTCCCACCAGCTGCTGATCAGGTGGCAACTGGA
ACAGTCACCATCGTGTGTGTGGCGAATAAATACTTCCCGATGTCACCGTCACCTGG
GAGGTGGATGGCACCAACCAAACTGGCATCGAGAACAGTAAAACACCGCAGA
ATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAGCACACAGT
ACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACCTCAGTCGTC
CAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 66)

A11B1_12F2 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGCAGCAGCTGGTGGAGTCCGGGGGAGGCCTGGTCAAGCCTGGGGCATCCCTGAC
ACTCACCTGCACAGCCTCTGGATTCTCCTTCACTAGCGGCTATCACATGTGCTGGGT
CCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCTTTGGTGTTTATACTGG
TACCACTACCTACGCGAGCTGGGCGAAAGGTCGATTACCATCTCCAAAACCTCGTC
GACCACGGTGACTCTACAAATGACCAGTCTAACAGTCGCGGACACGGCCACCTATTT

CTGTGCGAGAATCAGTGCTGAAAATGGTGGGGACTTGTGGGGCCCAGGCACCCTGG
TCACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCCTGGCCCCCTGCT
GCGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCTC
CCGGAGCCAGTGACCGTGACCTGGAACTCGGGCACCCTCACCAATGGGGTACGCAC
CTTCCCGTCCGTCCGGCAGTCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGT
GACCTCAAGCAGCCAGCCCCGTCACCTGCAACGTGGCCACCCAGCCACCAACACCA
AAGTGGACAAGACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCACCCCCCT
GAACTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCCAAAACCCAAGGACACCCTC
ATGATCTCACGCACCCCCGAGGTCACATGCGTGGTGGTGGACGTGAGCCAGGATGA
CCCCGAGGTGCAGTTACATGGTACATAAACAACGAGCAGGTGCGCACCGCCCCGGC
CGCCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCCTCCCC
ATCGCGCACCAAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAA
GGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCCTGG
AGCCGAAGGTCTACACCATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTTCGGTC
AGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAG
AAGAACGGGAAGGCAGAGGACAACACTACAAGACCACGCCGACCGTGCTGGACAGCG
ACGGCTCCTACTTCTCTACAGCAAGCTCTCAGTGCCACGAGTGAGTGGCAGCGGG
GCGACGTCTTACCTGCTCCGTGATGCACGAGGCCTTGCAACAACACTACACGCAGA
AGTCCATCTCCCGCTCTCCGGGTAAATAG (SEQ ID NO: 67)

A11B1_12F2 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCAGATGTGATGTTGTGATGACCCAGACTCCAGCCTCCGTGGAGGCAGCTGTGGG
AGGCACAGTCACCATCAAGTGCCAGGCCAGTCAGAGCATTAGCAACTACTTTTCTTG
GTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTACAGGGCGTCCACTCT
GGCATCTGGGGTCCCATCGCGGTTACGCGGCAGTGGATCTGGGACAGAGTTCACTCT
CACCATCAGCGACCTGGAGTGTGCCGATTCTGCCACTTACTACTGTCACTGCACTTA
TGGTAGTAGTAGTACTGGTTTTGGTTTCGGCGGAGGGACCGAGGTGGTGGTCAAAG
GTGATCCAGTTGCACCTACTGTCCCCATCTTCCCAACAGCTGCTGATCAGGTGGCAA
CTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTACCCGTCA
CCTGGGAGGTGGATGGCACCAACCCAAACAACCTGGCATCGAGAACAGTAAACACCG
CAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAGCACA
CAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACCTCAGT
CGTCCAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 68)

A11B1_11D10 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACT
CACCTGCATGGCCTCTGGAATCGACTTCAGTAGCGGCTACGGCATGTGGTGGGTCCG
CCAGGCTCCAGGGAAGGGACTGGAGTATATCGGATACATTGATACTGGTGATGATA
ACACATACTACGCGAACTGGGCGAAAGGCCGATTACCATCTCCAAAACCTCGTCG
ACCACGGTGACTCTGCAAATGACCAGTCTGACAGTCGCGGACACGGCCACCTATTTC
TGTGCGAAAGGGGGCGCCATAGACCTCTGGGGCCCAGGGACCCTCGTCACCGTCTC
TTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCTGCTGCGGGGACAC
ACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCTCCCGGAGCCAGT
GACCGTGACCTGGAACCTCGGGCACCCCTACCAATGGGGTACGCACCTTCCCGTCCGT

CCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCA
GCCAGCCCCGTACCTGCAACGTGGCCCCACCCAGCCACCAACACCAAAGTGGACAAG
ACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCCCACCCCCTGAACTCCCGGGG
GGACCGTCTGTCTTCATCTTCCCCCAAAAACCCAAGGACACCCCTCATGATCTCACGC
ACCCCCGAGGTCACATGCGTGGTGGTGGACGTGAGCCAGGATGACCCCGAGGTGCA
GTTACATGGTACATAAAACAACGAGCAGGTGCGCACCGCCCCGGCCGCGCTACGGG
AGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCCTCCCCATCGCGCACCCAG
GACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAGGCACTCCCGGC
CCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCCTGGAGCCGAAGGTCT
ACACCATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTCCGTGAGCCTGACCTGC
ATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAGAAGAACGGGAA
GGCAGAGGACAACATAAGACCACGCCGACCGTGTGGACAGCGACGGCTCCTACT
TCCTCTACAGCAAGCTCTCAGTGCCACGAGTGAGTGGCAGCGGGGCGACGTCTTCA
CCTGCTCCGTGATGCACGAGGCCTTGCACAACCACTACACGCAGAAGTCCATCTCCC
GCTCTCCGGGTAAATAG (SEQ ID NO: 69)

A11B1_11D10 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGACTCCTACTGCTCTGGCTCCCAGGT
GCCAGATGTGCTGACATTGTGATGACCCAGACTCCAGCCTCCGTGGAGGCAGCTGTG
GGAGGCACAGTCACCATCAAGTGCCAGGCCAGTCAGAGCATTAGTAGTTACTTAGC
CTGGTATCAGCAGAAACCAGGGCAGCGTCCCAAGCTCCTGATCTACAGGGCATCCA
CTCTAAAATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGAGTAC
ACTCTCACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTATTATTGTCAAGCG
TATTATCTTAGTAGTAGTATCAGTTATGGTAATACTTTCGGCGGAGGGACCGAGGTG
GTGGTCAAAGGTGATCCAGTTGCACCTACTGTCTCATCTTCCCACCACTGCTGAT
CAGGTGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAAATACTTTCGGAT
GTCACCGTCACCTGGGAGGTGGATGGCACCACCCAAACAACCTGGCATCGAGAACAG
TAAACACCCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACT
GACCAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGC
ACGACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 70)

A11B1_10F9 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCGTCCCTGACACT
CACCTGCACAGCCTCTGGATTCTCCCTCAGTAGCGGGTATGGCATGTGCTGGGTCCG
CCAGGCTCCAGGGAAGGGACTGGAGTGGATCGGATACACTGATACTGCTACTGGTA
CCATTCACTACGCGAGCTGGGCGAAAGGCCGATTACCATCTCCAAAACCTCGTCGA
CCACGGTGACTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATTTCT
GTGCGAAAGGGGGCGCCATGGACCTCTGGGGCCCAGGGACCCCTCGTCACCGTCTCT
TCAGGGCAACCTAAGGCTCCATCAGTCTTCCCACCTGGCCCCCTGCTGCGGGGACACA
CCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCTCCCGGAGCCAGTG
ACCGTGACCTGGAACTCGGGCACCCTACCAATGGGGTACGCACCTTCCCGTCCGTC
CGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCAG
CCAGCCCCGTACCTGCAACGTGGCCCCACCCAGCCACCAACACCAAAGTGGACAAGA
CCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCACCCCCTGAACTCCCGGGGG
GACCGTCTGTCTTCATCTTCCCCCAAAAACCCAAGGACACCCCTCATGATCTCACGCA

CCCCCGAGGTCACATGCGTGGTGGTGGACGTGAGCCAGGATGACCCCCGAGGTGCAG
TTCACATGGTACATAAAACAACGAGCAGGTGCGCACCGCCCCGGCCGCTACGGGA
GCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCCTCCCCATCGCGCACCAAGG
ACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAGGCACTCCCCGGCC
CCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCCTGGAGCCGAAGGTCTA
CACCATGGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTTCGGTCAGCCTGACCTGCA
TGATCAACGGCTTCTACCCCTCCGACATCTCGGTGGAGTGGGAGAAGAACGGGAAG
GCAGAGGACAACTACAAGACCACGCCGACCGTGCTGGACAGCGACGGCTCCTACTT
CCTCTACAGCAAGCTCTCAGTGCCACGAGTGAGTGGCAGCGGGGCGACGTCTTCA
CCTGCTCCGTGATGCACGAGGCCTTGCACAACCACTACACGCAGAAGTCCATCTCCC
GCTCTCCGGGTAAATAG (SEQ ID NO: 71)

A11B1_10F9 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTACTGCTCTGGCTCCCAGGT
GCCAGATGTGCTGACATTGTGATGACCCAGACTCCAGCCTCCGTGGAGGCAGCTGTG
GGAGGCACAGTCACCATCAAGTGCCAGGCCAGTCAGAGCATTAGTAGCTACTTAGC
CTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTACAGGACATCCA
CTCTGGCATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGAGTAC
ACTCTCACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTACTATTGTCAAAGC
TATGCTTATAGTAGTAGTAGCAGTTATGGTAATGCTTTCGGCGGAGGGACCGAGGTG
GTGGTCAAAGGTGATCCAGTTGCACCTACTGTCCTCATCTTCCCACCAGCTGCTGAT
CAGGTGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTCCCAGT
GTCACCGTCACCTGGGAGGTGGATGGCACCACCCAAACAACCTGGCATCGAGAACAG
TAAACACCCGCAGAAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACT
GACCAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGC
ACGACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 72)

A11B1_7H12 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACT
CACCTGCACAGGCTCTGGAATCGACTTCAGTAGCAGCTACTGGATATGCTGGGTCCG
CCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATCGATGGTAGTGATGGTA
ACACTTACTACGCGAGCTGGGCGAGAGGCCGATTACCATCTCCAAAACCTCGTCG
ACCACGGTGACTCTGCAAATGGCCAGTCTGACAGCCGCGGACACGGCCACCTATTTC
TGTACGAGAGATCTCAGGTTGTGGGGCCCAGGCACCCTGGTCACCGTCTCCTCAGGG
CAACCTAAGGCTCCATCAGTCTTCCCCTGGCCCCCTGCTGCGGGGACACACCCAGC
TCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCTCCCGGAGCCAGTGACCGTG
ACCTGGAACCTCGGGCACCTCACCAATGGGGTACGCACCTTCCCGTCCGTCCGGCAG
TCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCAGCCAGCCC
GTCACCTGCAACGTGGCCCACCCAGCCACCAACACCAAAAGTGGACAAGACCGTTGC
GCCCTCGACATGCAGCAAGCCCATGTGCCACCCCTGAACCTCCCGGGGGACCGT
CTGTCTTCATCTTCCCCCAAACCAAGGACACCCTCATGATCTCACGCACCCCCG
AGGTCACATGCGTGGTGGTGGACGTGAGCCAGGATGACCCCGAGGTGCAGTTCACA
TGGTACATAAAACAACGAGCAGGTGCGCACCGCCCCGGCCGCTACGGGAGCAGCA
GTTCAACAGCACGATCCGCGTGGTCAGCACCCCTCCCCATCGCGCACCAAGGACTGGCT
GAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAGGCACTCCCCGGCCCCCATCG

AGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCTGGAGCCGAAGGTCTACACCATG
GGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTTCGGTCAGCCTGACCTGCATGATCAA
CGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAGAAGAACGGGAAGGCAGAGG
ACAACTACAAGACCACGCCGACCGTGCTGGACAGCGACGGCTCCTACTTCCTCTACA
GCAAGCTCTCAGTGCCACGAGTGAGTGGCAGCGGGGCGACGTCTTACCTGCTCC
GTGATGCACGAGGCCTTGCAACAACCTACACGCAGAAAGTCCATCTCCCGCTCTCCG
GGTAAATAG (SEQ ID NO: 73)

A11B1_7H12 Light Chain

ATGGACACGAGGGGCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCAGATGTGCTGACATTGTGCTGACCCAGACTCCAGCCTCGGTGTCTGCAGCTGTG
GGAGGCACAGTCACCATCAACTGCCAGGCCAGTCAGAATGTTTATAGTAACAATGC
CTTAGCCTGGCATCAGCAGAAACCAGGGCAGCGTCCCAACCTCCTGATCTACAAGG
CTTCCACTCTGGCATCTGGGGTCCCATCGCGTTCAAAGGCAGTGGATCTGGGACAC
AGTTTACTCTCACCATCAGCGACGTGCAGTGTGACGATGCTGCCACTTACTACTGTC
TAGGCGAATTTAGTTGTAGTAGTGGTGATTGTTTTGTTTTCGGCGGAGGGACCGAGG
TGGTGGTCAAAGGTGATCCAGTTGCACCTACTGTCTCATCTTCCACCAAGCTGCTG
ATCAGGTGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCG
ATGTCACCGTCACCTGGGAGGTGGATGGCACCACCCAAACAACCTGGCATCGAGAAC
AGTAAACACCGCAGAAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGAC
ACTGACCAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGG
GCACGACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 74)

A11B1_7G12 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACT
CACCTGCATGGCCTCTGGAATCGACTTCAGTAGCGGCTACGGCATGTGGTGGGTCCG
CCAGGCTCCAGGGAAGGGACTGGAGTATATCGGATACATTGATACTGGTGTATGATA
ACACATACTACGCGAACTGGGCGAAAGGCCGATTACCATCTCCAAAACCTCGTCG
ACCACGGTGACTCTGCAAATGACCAGTCTGACAGTCGCGGACACGGCCACCTATTTCT
TGTGCGAAAGGGGGCGCCATAGACCTCTGGGGGCCAGGGACCCTCGTCACCGTCTC
TTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCTGCTGCGGGGACAC
ACCCAGTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCTCCCGGAGCCAGT
GACCGTGACCTGGAACCTCGGGCACCTCACCAATGGGGTACGCACCTTCCCGTCCGT
CCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCA
GCCAGCCCGTCACCTGCAACGTGGCCACCCAGCCACCAACACCAAAGTGGAACAAG
ACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCACCCCTGAACTCCCGGGG
GGACCGTCTGTCTTCATCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCACGC
ACCCCCGAGGTACATGCATGCGTGGTGGTGGACGTGAGCCAGGATGACCCGAGGTGCA
GTTACATGGTACATAAACAACGAGCAGGTGCGCACCGCCCGGCCGCGCTACGGG
AGCAGCAGTTAACAGCACGATCCGCGTGGTCAGCACCTCCCCATCGCGCACCAAG
GACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAGGCACTCCCGGC
CCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCTGGAGCCGAAGGTCT
ACACCATGGGCCCTCCCGGGAGGAGCTGAGCAGCAGGTTCGGTCAGCCTGACCTGC
ATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAGAAGAACGGGAA

GGCAGAGGACAACTACAAGACCACGCCGACCGTGCTGGACAGCGACGGCTCCTACT
TCCTCTACAGCAAGCTCTCAGTGCCCACGAGTGAGTGGCAGCGGGGCGACGTCTTCA
CCTGCTCCGTGATGCACGAGGCCTTGCACAACCACTACACGCAGAAGTCCATCTCCC
GCTCTCCGGGTAAATAG (SEQ ID NO: 75)

A11B1_7G12 Light Chain

ATGGACACGAGGGGCCCCACTCAGCTGCTGGGACTCCTACTGCTCTGGCTCCCAGGT
GCCAGATGTGCTGACATTGTGATGACCCAGACTCCAGCCTCCGTGGAGGCAGCTGTG
GGAGGCACAGTCACCATCAAGTGCCAGGCCAGTCAGAGCATTAGTAGTTACTTAGC
CTGGTATCAGCAGAAACCAGGGCAGCGTCCCAAGCTCCTGATCTACAGGGCATCCA
CTCTAAAATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGAGTAC
ACTCTCACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTATTATTGTCAAGCG
TATTATCTTAGTAGTAGTATCAGTTATGGTAATACTTTTCGGCGGAGGGGACCGAGGTG
GTGGTCAAAGGTGATCCAGTTGCACCTACTGTCTCATCTTCCCACCACTGCTGAT
CAGGTGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGAT
GTCACCGTCACCTGGGAGGTGGATGGCACCACCCAAACAACCTGGCATCGAGAACAG
TAAACACCCGCAGAAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACT
GACCAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGC
ACGACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 76)

A11B1_6G4 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGCAGCAGCTGGAGGAGTCCGGGGGAGGCCTGGTCAAGCCTGGAGGAACCCTGAC
ACTCACCTGCAAAGCCTCTGGAGTCGCCCTCAATCCCTACTACTATATGTGCTGGGT
CCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCGTGGATGCTGATAGTA
GTGGTAGCACTTACTACGCGAGCTGGGCGAAAGGCCGATTACCATCTCCAAAACC
TCGTGACACCGGTGACTCTGAAAATGACCAGTCTGACAGCCGCGGACACGGCCAC
CTATTTCTGTGCGAGAGAATCGGTTGACTATAGTTCTGTTGGTATTGGCTATGTACAT
GGTACGGATGGCTTGTGGGGGCCAGGCACCCTGGTCACCGTCTCCTCAGGGCAACCT
AAGGCTCCATCAGTCTTCCCCTGCCCCCTGCTGCGGGGACACACCCAGCTCCACG
GTGACCTGGGCTGCCTGGTCAAAGGCTACCTCCCGGAGCCAGTGACCGTGACCTG
GAACTCGGGCACCCTCACCAATGGGGTACGCACCTTCCCGTCCGTCCGGCAGTCCTC
AGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCAGCCAGCCCGTCA
CCTGCAACGTGGCCCACCCAGCCACCAACACCAAAGTGGAACAAGACCGTTGCGCCC
TCGACATGCAGCAAGCCCATGTGCCCACCCCCTGAACTCCCGGGGGGACCGTCTGTC
TTCATCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCACGCACCCCGAGGTC
ACATGCGTGGTGGTGGACGTGAGCCAGGATGACCCCGAGGTGCAGTTCACATGGTA
CATAAACAACGAGCAGGTGCGCACCGCCCGGCCGCTACGGGAGCAGCAGTTCA
ACAGCACGATCCGCGTGGTCAGCACCCCTCCCATCGCGCACCAAGACTGGCTGAGG
GGCAAGGAGTTCAAGTGCAAAGTCCACAACAAGGCACTCCCGGCCCCCATCGAGAA
AACCATCTCAAAGCCAGAGGGCAGCCCCCTGGAGCCGAAGGTCTACACCATGGGCC
CTCCCCGGGAGGAGCTGAGCAGCAGGTGCGTCAGCCTGACCTGCATGATCAACGGC
TTCTACCCTTCCGACATCTCGGTGGAGTGGGAGAAGAACGGGAAGGCAGAGGACAA
CTACAAGACCACGCCGACCGTGCTGGACAGCGACGGCTCCTACTTCTCTACAGCAA
GCTCTCAGTGCCACGAGTGAGTGGCAGCGGGGCGACGTCTTACCTGCTCCGTGAT

GCACGAGGCCTTGCACAACCACTACACGCAGAAGTCCATCTCCCGCTCTCCGGGTAA
ATAG (SEQ ID NO: 77)

A11B1_6G4 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCAGATGTGCCGACATCGTGGTGACCCAGACTCCATCCTCCGTGTCTGCAGCTGTG
GGAGGCACAGTCACCATCAAGTGCCAGGCCAGTCAGAGCATTAGCAACTACTTTTCT
TGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTACAGGGCGTCCAC
TCTGGCATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGAGTTTAC
TCTACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTACTACTGTCAATGCAC
TTACGGTAGAAGTAATAGTAATTTTTTTTATGGTTTCGGCGGAGGGACCGAGGTGGT
GGTCAAAGGTGATCCAGTTGCACCTACTGTCCTCATCTTCCCACCAGCTGCTGATCA
GGTGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGT
CACCGTCACCTGGGAGGTGGATGGCACCACCCAAACAACCTGGCATCGAGAACAGTA
AAACACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGA
CCAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACG
ACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTAG (SEQ ID NO: 78)

A11B1_6F9 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCCGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCCTCCCTGACACT
CACCTGCACAGCCTCTGGATCCTCCTTCAGTAGTACCTACTGGAAGTGTGGGTCCG
CCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATTAATGCTGGTAGTGGTA
CCACTTACTACGCGAGCTGGGCGAAAGGCCGATTACCGTCTCCAAAACCTCGTCGA
CCACGGTGACTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATTTCT
GTACGAGAGATAGTGATGGTCGTTTTAGTAGTGGCTACTATTTTAACTTGTGGGGCC
CAGGCACCCTGGTCACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCAC
TGGCCCCCTGCTGCGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCA
AAGGCTACCTCCCGGAGCCAGTGACCGTGACCTGGAAGTCCGGGCACCCTACCAAT
GGGGTACGCACCTTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGC
GTGGTGAGCGTGACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGCCCACCCAGC
CACCAACACCAAAGTGGAACAAGACCGTTGCGCCCTCGACATGCAGCAAGCCCATGT
GCCCCCCCCCTGAACTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCCAAAACCCA
AGGACACCCTCATGATCTCACGCACCCCCGAGGTCACATGCGTGGTGGTGGACGTG
AGCCAGGATGACCCCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAGGTGCG
CACCGCCCGGCCGCCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTGGTCA
GCACCCTCCCCATCGCGCACCAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAA
GTCCACAACAAGGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAGAGG
GCAGCCCCTGGAGCCGAAGGTCTACACCATGGGCCCTCCCGGGAGGAGCTGAGCA
GCAAGTTCGGTCAGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACATCTCG
TGGAGTGGGAGAAGAACGGGAAGGCAGAGGACAACCTACAAGACCACGCCGACCGT
GCTGGACAGCGACGGCTCCTACTTCTCTACAGCAAGCTCTCAGTGCCCACGAGTGA
GTGGCAGCGGGGCGACGTCTTACCTGCTCCGTGATGCACGAGGCCTTGACAACC
ACTACACGCAGAAGTCCATCTCCCGCTCTCCGGGTAAATAG (SEQ ID NO: 79)

A11B1_6F9 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCACATTTGCCCAAGTGCTGACCCAGACTGCATCCCCTGTGTCTGCAGCTGTGGGA
GGCACAGTCACCATCAATTGTCAAGTCCAGTCAGAGTGTTTATGATAACAACTGGTTA
GCCTGGTATCAGCAAAAACCAGGGCAGCCTCCCAAACCTTGATCGACGATGCATC
CAAATTGACATCTGGGGTCTCATCGCGGTTCAAAGGCAGTGGATCTGGGACGCAGTT
CACTCTCACCATCAGCGGCGTGCAAGTGACGATGCTGCCACTTACTACTGTCAAGG
CGCTTATTATAGTAGTGGTTGGTACTGGGCTTTTCGGCGGAGGGACCGAGGTGGTGGT
CAAAGGTGATCCAGTTGCACCTACTGTCTCATCTTCCCACCAGCTGCTGATCAGGT
GGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCAC
CGTCACCTGGGAGGTGGATGGCACCACCCAAACAACCTGGCATCGAGAACAGTAAAA
CACC GCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCA
GCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACC
TCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 80)

A11B1_6C7 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGCAGCAGCTGGAGGAGTCCGGGGGAGGCCTGGTCAAGCCTGGAGGAACCCTGAC
ACTCACCTGCAAAGCCTCTGGAATCGACTTCAGTAGCTACTACTACATGTGTTGGGT
CCGCCAGGCTCCAGGGAAGGGGCTGGAGTTGATCGTATGTATTTATACTAGTAGTGG
TGGCACATGGTACGCGAGCTGGGTGAATGGCCGACTCACCATCTCCAGAAGCACCA
GCCTAAACACGGTGGATCTGAAAATGACCAGTCTGACAGCCGCGGACACGGCCACC
TATTTCTGTGCCAGAGGGGTTTATTCTGGTAGTAGTGATTATCCAACCTCGGTTGGATC
TCTGGGGCCAGGGCACCCCTGGTCACCGTCTCCTTAGGGCAACCTAAGGCTCCATCAG
TCTTCCCCTGAGGGGCTGCTGCGGGGACACACCCAGCTCCACGGTGACCCTGGGCT
GCCTGGTCAAAGGCTACCTCCCGGAGCCAGTGACCGTGACCTGGAACCTCGGGCACC
CTCACCAATGGGGTACGCACCTTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCG
CTGAGCAGCGTGGTGAGCGTGACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGC
CCACCCAGCCACCAACACCAAAGTGGACAAGACCGTTGCGCCCTCGACATGCAGCA
AGCCCATGTGCCACCCCTGAACTCCCGGGGGGACCGTCTGTCTTCATCTTCCCC
CAAAACCAAGGACACCCTCATGATCTCACGCACCCCGAGGTACATGCGTGGTG
GTGGACGTGAGCCAGGATGACCCCGAGGTGCAGTTCACATGGTACATAAACAAACGA
GCAGGTGCGCACCCGCGCCGCGCTACGGGAGCAGCAGTTCACACAGCACGATCC
GCGTGGTCAGCACCCCTCCCCATCGCGCACCCAGGACTGGCTGAGGGGCAAGGAGTTC
AAGTGCAAAGTCCACAACAAGGCACTCCCGGCCCCATCGAGAAAACCATCTCCAA
AGCCAGAGGGCAGCCCCTGGAGCCGAAGGTCTACACCATGGGCCCTCCCCGGGAGG
AGCTGAGCAGCAGGTCCGTGAGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCG
ACATCTCGGTGGAGTGGGAGAGAAGCGGAAGGCAGAGGACAACCTACAAGACCAC
GCCGACCGTGCTGGACAGCGACGGCTCCTACTTCTCTACAGCAAGCTCTCAGTGCC
CACGAGTGAGTGGCAGCGGGGCGACGTCTTACCTGCTCCGTGATGCACGAGGCCT
TGCACAACCACTACACGCAGAAGTCCATCTCCCGCTCTCCGGGTAAATAG (SEQ ID
NO: 81)

A11B1_6C7 Light Chain

ATGGACACGAGCACCTCCACTGCGCTCCTGGGGCTCCTGCTGCTCTGGCTCACAGGT
GCCAGATGTGCCATCGAGATGACCCAGTCTCCACCTCCCTGTCTGCATCTGTGGGA
GAAACTGTCAGGATTAGGTGCCTGGCCAGTGAGGACATTTACAGTGGTATATCCTGG

TACCAACAGAAGCCAGAGAAACCTCCTACACTCCTGATCTCTGGTGCATCCAATTTA
GAATCTGGGGTCCCACCACGGTTCAGTGGCGGTGGATCCGGGACAGATTACACCT
CACCATCGGCGGCGTGCAGGCTGAAGATGTTGCCACCTACTACTGTCTAGGCGGTTA
TAGTTTCAGTAGTACCGGTTTGACTTTTGGAGCTGGCACCAAGGTGGAAATCAAACG
TGATCCAGTTGCGCCTTCTGTCTCCTCTTCCCACCATCTAAGGAGGAGCTGACAAC
TGGAACAGCCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCACCGTCAC
CTGGGAGGTGGATGGCACCACCCAAACAACCTGGCATCGAGAACAGTAAACACCGC
AGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAGCACAC
AGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACCTCAGTC
GTCCAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 82)

A11B1_6B6 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGCAACATCTGGTGGAGTCCGGGGGAGGCCTGGTCAAGCCTGGGGCATCCCTGAC
ACTCACCTGCACAGCCTCTGGATTCTCCTTCACTACCGGCTATCACATGTGCTGGGT
CGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGTTTTGGTGTTTATACTAGT
ACCACTACCTACGCGAGCTGGGCGAAAGGTGATTACCATCTCCAAAACCTCGTCG
ACCACGGTGACTCTACAAATGACCAGTCTAACAGTCGCGGACACGGCCACCTATTT
TGTGCGAGAATCAGTGCTGAAGATGGTGGGGACTTGTGGGGCCCAGGCACCCTGGT
CACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCTGCTG
CGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGTACCTCC
CGGAGCCAGTGACCGTGACCTGGAACCTCGGGCACCTCACCAATGGGGTACGCACC
TTCCCGTCCGTCCGGCAGTCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTG
ACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGCCCACCCAGCCACCAACACCAA
AGTGGACAAGACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCCACCCCTG
AACTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCCAAAACCCAAGGACACCCTCA
TGATCTCACGCACCCCCGAGGTACATGCGTGGTGGTGGACGTGAGCCAGGATGAC
CCCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAGGTGCGCACCGCCCCGGCC
GCCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCCTCCCCA
TCGCGCACCAAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAG
GCACTCCCGGGCCCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCCTGGA
GCCGAAGGTCTACACCATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTCCGTCA
GCCTGACCTGCATGATCAACGGCTTCTACCTTCCGACATCTCGGTGGAGTGGGAGA
AGAACGGGAAGGCAGAGGACAACCTACAAGACCACGCGACCGTGCTGGACAGCGA
CGGCTCCTACTTCTCTACAGCAAGCTCTCAGTGCCACGAGTGAGTGGCAGCGGGG
CGACGTCTTACCTGCTCCGTGATGCACGAGGCCTTGCACAACCACTACACGCAGAA
GTCCATCTCCCGCTCTCCGGGTAAATAG (SEQ ID NO: 83)

A11B1_6B6 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCAGATGTGATGTTGTGATGACCAGACTCCAGCCTCCGTGGAGGCAGCTGTGGG
AGGCACAGTCACCATCACGTGCCAGGCCAGTCAGAGCATTAGCAACTACTTTTCTTG
GTATCAGCAGAAACCAGGGCAGCCTCCCAAGTCTCTGATCTACAGGGCGTCCACTCT
GGCATCTGGGGTCCCATCGCGGTTTACGCGGCAGTGGATCTGGGACACAGTTCACTCT
CACCATCAGCGACCTGGAGTGTGCCGATTCTGCCACTTACGCCTGTCAGTGCACTTA
TGGTAGTAGTAGTACTGGTTTTGGTTTCGGCGGAGGGACCGAGGTGGTGGTCAAAG

GTGATCCAGTTGCACCTACTGTCCTCATCTTCCCACCAGCTGCTGATCAGGTGGCAA
CTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTACACCGTCA
CCTGGGAGGTGGATGGCACCAACCCAAACAACCTGGCATCGAGAACAGTAAAAACACCG
CAGAAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAGCACA
CAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACCTCAGT
CGTCCAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 84)

A11B1_5F7 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACT
CACCTGCAAAGCCTCTGGATTCTCCTTCAGTAGTTACTTCTGGATATGCTGGGTCCGC
CAGGCTCCAGGGAAGGGGCTGGAGTGGAGCGCATGCATCTATGGTGATAGTAGTGG
TAGTAGTTACTACGCGAGCTGGGCGAAAGGCCGATTACCATCTCCAAAACCTCGTC
GACCACGGTGACTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATT
TCTGTGCGAGTTATGGTAGTAGTAGTTATTACTACTCTAATTTATGGGGCCCAGGCA
CCCTGGTCACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCC
CCTGCTGCGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGC
TACCTCCCGGAGCCAGTGACCGTGACCTGGAACCTCGGGCACCCCTACCAATGGGGT
ACGCACCTTCCCGTCCCGTCCGGCAGTCTCAGGCCTCTACTCGCTGAGCAGCGTGGT
GAGCGTGACCTCAAGCAGCCAGCCCGTCACTGCAACGTGGGCCACCCAGCCACCA
ACACCAAAGTGGAACAAGACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCCA
CCCCCTGAACTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCCAAACCCAAAGGAC
ACCCTCATGATCTCACGCACCCCCGAGGTCACATGCGTGGTGGTGGACGTGAGCCA
GGATGACCCCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAGGTGCGCACCG
CCCGGCCCGCGTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACC
CTCCCCATCGCGCACCAAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCA
CAACAAGGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGC
CCCTGGAGCCGAAGGTCTACACCATGGGCCCTCCCGGGAGGAGCTGAGCAGCAGG
TCGGTCAGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAG
TGGGAGAAGAACGGGAAGGCAGAGGACAACCTACAAGACCACGCCGACCGTGCTGG
ACAGCGACGGCTCCTACTTCTCTACAGCAAGCTCTCAGTGCCCAAGAGTGAGTGGC
AGCGGGGCGACGTCTTACCTGCTCCGTGATGCACGAGGCCTTGACACAACCACTACA
CGCAGAAGTCCATCTCCCGCTCTCCGGGTAAATAG (SEQ ID NO: 85)

A11B1_5F7 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCATATGTGACCCTGTGATGACCCAGACTCCATCTTCCACGTCTGCGGCTGTGGGA
GGCACAGTCACCATCAGTTGCCAGTCCAGTCAGAGTGTTTATAATAACAACACTACTTA
GCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAACGCCTGATCTACGAATCATC
CAAACCTGGCATCTGGGGTCCCATCGCGGTTCAGAGGCAGTGGATCTGGGGCACAGT
TCACTCTCACCATCAGCGACCTGGAGTGTGACGATGCTGCCACTTACTACTGTCTAG
GCGCATATTATACTACTCTTGATTTCCGGCGGAGGGACCGAGGTGGTGGTCAGAGGTG
ATCCAGTTGCACCTACTGTCTCATCTTCCCACCAGCTGCTGATCAGGTGGCAACTG
GAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTACACCGTCACCT
GGGAGGTGGATGGCACCAACCCAAACAACCTGGCATCGAGAACAGTAAAAACACCGCA
GAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAGCACACA

GTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACCTCAGTCG
TCCAGAGCTTCAATAGGGGTGACTGTAG (SEQ ID NO: 86)

A11B1_5D7 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGGAGCAGTTGGTGGAGTCCGGGGGAGGCCTGGTCCAGCCTGAGGGATCCCTGAC
ACTCACCTGCAAAGCCTCTGGATTGCACTTCAGTAGCAATGCAATGTGCTGGGTCCG
CCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATTTATAATGGTGATGGCA
GCACATACTACGCGAGCTGGGTGAATGGCCGATTACCATCTCCAAGACCTCGTCGA
CCACGGTGACTCTGCAAATGACCACTGTGACAGCCGCGGACACGGCCACCTATTTCT
GTGCGAGAGGTCTCTCTAATTGGAATAGGGATAACTTATGGGGCCCTGGCACCCCTGG
TCACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCTGCT
GCGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCTC
CCGGAGCCAGTGACCGTGACCTGGAATCGGGCACCTCACCAATGGGGTACGCAC
CTTCCCGTCCGTCCGGCAGTCCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGT
GACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGCCACCCAGCCACCAACACCA
AAGTGGACAAGACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCACCCCT
GAACTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCCAAACCCAAGGACACCTC
ATGATCTCACGCACCCCGAGGTACATGCGTGGTGGTGGACGTGAGCCAGGATGA
CCCCGAGGTGCAGTTACATGGTACATAAACAACGAGCAGGTGCGCACCGCCCGGC
CGCCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCTCCCC
ATCGCGCACCAAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAA
GGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCTGG
AGCCGAAGGTCTACACCATGGGCCCTCCCGGGAGGAGCTGAGCAGCAGGTGCGTC
AGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAG
AAGAACGGGAAGGCAGAGGACAACACTACAAGACCACGCCGACCGTGTGACAGCG
ACGGCTCCTACTTCTCTACAGCAAGCTCTCAGTGCCACGAGTGAGTGGCAGCGGG
GCGACGTCTTACCTGCTCCGTGATGCACGAGGCCTTGCAACAACCTACACGCAGA
AGTCCATCTCCCGCTCTCCGGGTAAATAG (SEQ ID NO: 87)

A11B1_5D7 Light Chain

ATGGACACGAGGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCACATTTGCCCAAGTGCTGACCCAGACTCCATCCTCCGTGTCTGCAGCTGTGGGA
GGCACAGCCACCATCAACTGCCAGGCCAGTCAGAGTCTTTATAGTCCCAAGAATTTA
GCCTGGTATCAGCAGACACCAGGGCAGCCTCCCAAGCTCCTGATCTATTCTGCATCG
AAACTGGCATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACACAGTT
CACTCTCACCATCAGCGGCGTGCAGTGTGACGATGCTGCAATTTACTACTGTCAAGG
CGAATTTAGTTGTACTACTGCTGCTTGTGTTTGGCGGAGGGACCGAGGTGGT
GGTCAAAGGTGATCCAGTTGCACCTACTGTCCTCATCTTCCACCACTGCTGATCA
GGTGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGT
CACCGTCACCTGGGAGGTGGATGGCACCCACCAACAACACTGGCATCGAGAACAGTA
AAACACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGA
CCAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACG
ACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTAG (SEQ ID NO: 88)

A11B1_5A7 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCTTTGGAGGAGTCCGGGGGAGGCCTGGTCCAGCCTGAGGGATCCCTGACACT
CGCCTGCACAGCTTCGGGATTCTCCTTCAGTAGCTACTACTACATCTGCTGGGTCCG
CCAGGCTCCAGGGACGGGGCTGGAGTGGATCGGATGCATTAATACTGGTAGTGATG
ACACTCACTACGCGAGCTGGTTGAAAGGCCGATTACCTTCTCCAAGGCCTCGTCGA
CCACGTTGACTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATTTCT
GTGCGAGATCATCTGGTAGTAGTGATGATGCTTATGATCTCTGGGGCCAGGCACCC
TGGTCACTGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCT
GCTGCGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTAC
CTCCCGGAGCCAGTGACCGTGACCTGGAACCTCGGGCACCCTCACCAATGGGGTACG
CACCTTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAG
CGTGACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGCCCCACCCAGCCACCAACA
CCAAAGTGGAACAAGACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCACCC
CCTGAACCTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCCAAAACCCAAGGACACC
CTCATGATCTCACGCACCCCCGAGGTACATGCGTGGTGGTGGACGTGAGCCAGGA
TGACCCCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAGGTGCGCACCCGCC
GGCCGCCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCCTC
CCATCGCGCACCAAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAA
CAAGGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCC
TGGAGCCGAAGGTCTACACCATGGGCCCTCCCGGGAGGAGCTGAGCAGCAGGTGCG
GTCAGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGG
GAGAAGAACGGGAAGGCAGAGGACAACACTACAAGACCACGCCGACCGTGCTGGACA
GCGACGGCTCCTACTTCTCTACAGCAAGCTCTCAGTGCCCACGAGTGAGTGGCAGC
GGGGCGACGTCTTACCTGCTCCGTGATGCACGAGGCCTTGACAACCACTACACGC
AGAAGTCCATCTCCCGCTCTCCGGGTAAATAG (SEQ ID NO: 89)

A11B1_5A7 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCAGATGTGATGTTGTGATGACCCAGACTCCAGCCTCCGTGTCTGAACCTGTGGGA
GGCGCAGTCACCATCAAGTGCCAGGCCAGTCAGAGCATTGGTAGTAATTTAGCCTG
GTATCAGCACAAACCAGGGCAGCCTCCCAAGCTCCTGATCTATTTTGCATCCAGCCT
GGCATCTGGGGTCTCGTCGCGGTTCAAGGGCGGTAGATCTGGGACACAGTTCACCTCT
CACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTACTACTGTCACTGTACTTA
TTATCCTCTTAGTTATGTTACTTTTCGGCGGAGGGACCGAGGTGGTGGTCAAAGGTGA
TCCAGTTGCACCTACTGTCCTCATCTTCCCACCAGCTGCTGATCAGGTGGCAACTGG
AACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCACCGTCACCTG
GGAGGTGGATGGCACCACCCAAACAACCTGGCATCGAGAACAGTAAACACCGCAG
AATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAGCACACAG
TACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACCTCAGTCGT
CCAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 90)

A11B1_4E1 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGACATCCCTGACACT
CTCCTGCACAGCCTCTGGATTCTCCTTCGGTAGCTATTATTATATGTGCTGGGTCCGC
CAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATTGATGTTGGTAGTAGTGG

TGACACATACTACGCGAGCTGGGTGAATGGCCGATTACCATCTCCAAAACCTCGTC
GACCACGGTGACTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATT
TCTGTGCGAGAGATGATACTGCTGCTGGTGGTTTTGGTAATTTGGAATTGTGGGGCC
CAGGCACCCTGGTCACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCAC
TGGCCCCCTGCTGCGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCA
AAGGCTACCTCCCGGAGCCAGTGACCGTGACCTGGAACCTCGGGCACCCCTACCAAT
GGGGTACGCACCTTCCCGTCCGTCCGGCAGTCTCAGGCCTCTACTCGCTGAGCAGC
GTGGTGAGCGTGACCTCAAGCAGCCAGCCCGTACCTGCAACGTGGGCCACCCAGC
CACCAACACCAAAGTGGAACAAGACCGTTGCGCCCTCGACATGCAGCAAGCCCATGT
GCCCCACCCCTGAACTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCCAAAAACCA
AGGACACCCTCATGATCTCACGCACCCCGAGGTACATGCGTGGTGGTGGACGTG
AGCCAGGATGACCCCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAGGTGCG
CACCGCCCGGCCGCCGTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTGGTCA
GCACCTCCCCATCGCGCACCAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAA
GTCCACAACAAGGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAGAGG
GCAGCCCCTGGAGCCGAAGGTCTACACCATGGGCCCTCCCGGGAGGAGCTGAGCA
GCAGGTGCGTCAGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACATCTCGG
TGGAGTGGGAGAAGAACGGGAAGGCAGAGGACAACATAAGACCACGCCGACCGT
GCTGGACAGCGACGGCTCCTACTTCCTCTACAGCAAGCTCTCAGTGCCACGAGTGA
GTGGCAGCGGGGCGACGTCTTACCTGCTCCGTGATGCACGAGGCCTTGACAACC
ACTACACGCAGAAGTCCATCTCCCGCTCTCCGGGTAAATAG (SEQ ID NO: 91)

A11B1_4E1 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCAGATGTGCATTTCGAATTGACCCAGACTCCATCCTCCGTGTCTGAACCTGTGGGA
GGCACAGTCACCATCAAGTGCCAGGCCAGTCAGAGCATTTACAGCTACTTTTCTCTGG
TATCAGCAGAAACCAGGGCAGCCTCCCAAGCGCCTGATTTACCAGGCATCCACTCTG
GCTTCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGATTTCACTCTC
ACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTACTACTGTCAAAACAATTAT
GGTAGGGGTAGTGGTAGTTATTTTTTTGGTTTTCGGCGGAGGGACCGAGGTGGTGGTC
AAAGGTGATCCAGTTGCACCTACTGTCTCATCTTCCCACCAGCTGCTGATCAGGTG
GCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCACC
GTCACCTGGGAGGTGGATGGCACCACCCAAACAACCTGGCATCGAGAACAGTAAAC
ACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAG
CACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACCT
CAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 92)

A11B1_3H9 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACT
CACCTGCAAAGCCTCTGGAATCGACTTCAGTAGCGGCTACGGCATGTGGTGGGTCCG
CCAGGCTCCAGGGAAGGGACTGGAGTATATCGGATACATTGATACTGGTAGTGTA
GCACTTACTACGCGAACTGGGCGAAAGGCCGATTACCATCTCCAAAACCTCGTCG
ACCATGGTGACTCTGCAAATGACCAGTCTGACAGTCGCGGACACGGCCACCTATTTCT
TGTGCGAAAGGGGGCGCCATAGACCTCTGGGGCCCAGGGACCCTCGTCACCGTCTC
TTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCTGCTGCGGGGACAC

ACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCTCCCCGGAGCCAGT
GACCGTGACCTGGAACCTCGGGCACCCCTACCAATGGGGTACGCACCTTCCCGTCCGT
CCGGCAGTCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCA
GCCAGCCCCGTACCTGCAACGTGGCCCCACCCAGCCACCAACACCAAAGTGGACAAG
ACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCCCACCCCCTGAACTCCCCGGGG
GGACCGTCTGTCTTCATCTTCCCCCCTCAAGGACACCCCTCATGATCTCACGC
ACCCCCGAGGTACATGCGTGGTGGTGGACGTGAGCCAGGATGACCCGAGGTGCA
GTTACATGGTACATAAAACAACGAGCAGGTGCGCACCGCCCCGGCCGCGCTACGGG
AGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCCTCCCCATCGCGCACCCAG
GACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAGGCACTCCCGGC
CCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCTGGAGCCGAAGGTCT
ACACCATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTGCGTCAGCCTGACCTGC
ATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAGAAGAACGGGAA
GGCAGAGGACAACTACAAGACCACGCCGACCGTGCTGGACAGCGACGGCTCCTACT
TCCTCTACAGCAAGCTCTCAGTGCCCACGAGTGAGTGGCAGCGGGGCGACGTCTTCA
CCTGCTCCGTGATGCACGAGGCCTTGCACAACCACTACACGCAGAAGTCCATCTCCC
GCTCTCCGGGTAAATAG (SEQ ID NO: 93)

A11B1_3H9 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGACTCCTACTGCTCTGGCTCCCAGGT
GCCAGATGTGCTGACATTGTGATGACCCAGACTCCAGCCTCCGTGGAGGCAGCTGTG
GGAGGCACAGTCACCATCAAGTGCCAGGCCAGTCAGAGCATTAGTAGTTACTTAGC
CTGGTATCAGCAGAAACCAGGGCAGCGTCCCAAGCTCCTGATCTACAGGGCATCCA
CTCTGGCATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGACTACA
CTCTACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTATTATTGTCATACCTA
TTATCTTAGTAGTAGTATCAGTTATGGTAATACTTTCGGCGGAGGGACCGAGGTGGT
GGTCAAAGGTGATCCAGTTGCACCTACTGTCTCATCTTCCCACCAGCTGCTGATCA
GGTGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGT
CACCGTCACCTGGGAGGTGGATGGCACCAACCAAACTGGCATCGAGAACAGTA
AAACACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGA
CCAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACG
ACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 94)

A11B1_3G2 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGGAGCAGCTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGAGGGATCCCTGAC
ACTCACCTGCAAAGCCTCTGGATTCTCCTTCAGTAGCATCTACTGGATTTGCTGGGTC
CGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCACTACTGTTGTCAAAG
TGGTAGAACTTACTACGCGAACTGGGCGAAAGGCCGATTACCATCTCCAAAACCT
CGTCGACCACGGTGACTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACC
TATTTCTGTGCGAGAGAATTTGTTGATGGTGGTAGTAGTGGTAGGGACTTGTGG
GGCCCAGGCACCCTGGTCACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTTC
CCACTGGCCCCCTGCTGCGGGGACACACCCAGCTCCACGGTGACCTGGGCTGCCTG
GTCAAAGGCTACCTCCCGGAGCCAGTGACCGTGACCTGGAACTCGGGCACCCCTCAC
CAATGGGGTACGCACCTTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGAG
CAGCGTGGTGAGCGTGACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGCCCCACC

CAGCCACCAACACCAAAGTGGACAAGACCGTTGCGCCCTCGACATGCAGCAAGCCC
ATGTGCCACCCCCTGAACTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCCAAAA
CCCAAGGACACCCTCATGATCTCACGCACCCCCGAGGTACATGCGTGGTGGTGGA
CGTGAGCCAGGATGACCCCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAGG
TGCGCACCGCCCCGGCCGCCGCTACGGGAGCAGCAGTTC AACAGCACGATCCGCGTG
GTCAGCACCTCCCCATCGCGCACCAAGGACTGGCTGAGGGGCAAGGAGTTC AAGTG
CAAAGTCCACAACAAGGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCA
GAGGGCAGCCCCTGGAGCCGAAGGTCTACACCATGGGCCCTCCCCGGGAGGAGCTG
AGCAGCAGGTCCGTCAGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACATC
TCGGTGGAGTGGGAGAAGAACGGGAAGGCAGAGGACA ACTACAAGACCACGCCGA
CCGTGCTGGACAGCGACGGCTCCTACTTCTCTACAGCAAGCTCTCAGTGCCACGA
GTGAGTGGCAGCGGGGCGACGTCTTACCTGCTCCGTGATGCACGAGGCCTTGCAC
AACCCTACACGCAGAAAGTCCATCTCCCGCTCTCCGGGTAAATAG (SEQ ID NO: 95)

A11B1_3G2 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCAGATGTGCTATGATATGACCCAGACTCCAGCCTCCGTGGAGGCAGCTGTGGG
AGGCACAGTCACCATCAAGTGCCAGGCCAGTCAGAGCATTAGTAGGGACTTATCCT
GGTATCAGCAGAAACCTGGACAGCCTCCCAAGCGCCTAATCTACAAGGCATCCACT
CTGGCATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGATTTACT
CTCACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTACTACTGTCAACAGGGT
TATAGTAGTATTGATGTTGATAATGATTTTCGGCGGAGGGACCGAGGTGGTGGTCAA
GGTGTATCCAGTTGCACCTACTGTCTCATCTTCCCACCAGCTGCTGATCAGGTGGCA
ACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCACCGTC
ACCTGGGAGGTGGATGGCACCAACCAAACTGGCATCGAGAACAGTAAACACC
GCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAGCAC
ACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACCTCAG
TCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 96)

A11B1_3B1 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGGAGCAGCTGGAGGAGTCCGGGGGAGGCCTGGTCAAGCCTGAGGGATCCCTGAC
ACTCACCTGCAAAGCCTCTGGATTCGACCTCAGTAGCGGCTATGACATGTGCTGGGT
CCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATTTATGCTGATTATA
GTGGTAGCACATACTACGCGAGCTGGGTGAATGGCCGATTACCATCTCCAGCAGC
ACCAGCCTAAACACGGTGGATCTGAAAATGACCAGTCTGACAGCCGCGGACACGGC
CACCTATTTCTGTGCCAGAGGGGCTACTGGTAATGGTGGTTATGGATACTACTTTAA
CTTGTGGGGCCCAGGCACCCTGGTCACCGTCTCCTCAGGGCAACCTAAGGCTCCATC
AGTCTTCCCCTGCTGGCCCCCTGCTGCGGGGACACACCCAGCTCCACGGTGACCCTGGG
CTGCCTGGTCAAAGGCTACCTCCCGGAGCCAGTGACCGTGACCTGGAACCTCGGGCA
CCCTACCAATGGGGTACGCACCTTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACT
CGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCAGCCAGCCCGTCACCTGCAACGTG
GCCCACCCAGCCACCAACACCAAAGTGGACAAGACCGTTGCGCCCTCGACATGCAG
CAAGCCCATGTGCCCACCCCCTGAACTCCCGGGGGGACCGTCTGTCTTCATCTTCCC
CCCAAAACCCAAGGACACCCTCATGATCTCACGCACCCCCGAGGTACATGCGTGG
TGGTGGACGTGAGCCAGGATGACCCCGAGGTGCAGTTCACATGGTACATAAACAAC

GAGCAGGTGCGCACCGCCCGGCCGCGCTACGGGAGCAGCAGTTCAACAGCACGAT
CCGCGTGGTCAGCACCTCCCCATCGCGCACCAAGGACTGGCTGAGGGGCAAGGAGT
TCAAGTGCAAAGTCCACAACAAGGCACTCCCGGCCCCCATCGAGAAAACCATCTCC
AAAGCCAGAGGGCAGCCCCCTGGAGCCGAAGGTCTACACCATGGGCCCCCCCCGGA
GGAGCTGAGCAGCAGGTTCGGTCAGCCTGACCTGCATGATCAACGGCTTCTACCCTTC
CGACATCTCGGTGGAGTGGGAGAAGAACGGGAAGGCAGAGGACAACTACAAGACC
ACGCCGACCGTGCTGGACAGCGACGGCTCCTACTTCCTCTACAGCAAGCTCTCAGTG
CCCACGAGTGAGTGGCAGCGGGGCGACGTCTTCACCTGCTCCGTGATGCACGAGGC
CTTGCAACAACCACTACACGCAGAAGTCCATCTCCCGCTCTCCGGGTAAATAG (SEQ
ID NO: 97)

A11B1_3B1 Light Chain

ATGGACACGAGGGGCCCCCACTCAGCTGCTGGGGCTCCTACTGCTCTGGCTCCCAGGT
GCCAGATGTGCTGACATTGTGATGACCCAGACTCCAGCCTCCGTGTCTGAACCTGTG
GGAGGCACAGTCACCATCAAGTGTGAGGCCAGTCAGAACATTAATAGCGGCTTAGC
CTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTACAAGGCATCCA
CTCTGGCATCTGGGGTCTCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGAATTCA
CTCTACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTACTACTGTCAAACCT
ATTATTATAGTAGTAGTAGTAGTATAATGCTTTCGGCGGAGGGGACCGAGGTGGTGG
TCAAAGGTGATCCAGTTGCACCTACTGTCTCATCTTCCCACCAGCTGCTGATCAGG
TGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCGGATGTCA
CCGTACCTGGGAGGTGGATGGCACCACCCAAACAACCTGGCATCGAGAACAGTAAA
ACACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACC
AGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGA
CCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTAG (SEQ ID NO: 98)

A11B1_2D3 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACT
CACCTGCACAGCTTCTGGATTCTCCTTCAGTAGCAGTTATTGGATATGCTGGGTCCG
CAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGTATTTATGGTGGTAGTAGTGG
TAACATTGCCTACGCGAGCTGGGCGAAAGGCCGATTACCATCTCCAAAACCTCGTC
GACCACGGTGACTCTACAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATT
TCTGTGCGAGAGATATTCCTAGTGATGCTTTCACCTTAGACTTGTGGGGCCCAGGCA
CCCTGGTCACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCCTGGCCC
CCTGCTGCGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGC
TACCTCCCGGAGCCAGTGACCGTGACCTGGAACCTCGGGCACCTCACCAATGGGGT
ACGCACCTTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGT
GAGCGTGACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGGCCACCCAGCCACCA
ACACCAAAGTGGACAAGACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCCA
CCCCCTGAACTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCCCTAAACCAAGGAC
ACCCTCATGATCTCACGCACCCCCGAGGTCACATGCGTGGTGGTGGACGTGAGCCA
GGATGACCCCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAGGTGCGCACCG
CCCGGCCCGCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTGGTACGACCC
CTCCCCATCGCGCACCAAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCA
CAACAAGGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGC

CCCTGGAGCCGAAGGTCTACACCATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGG
TCGGTCAGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAG
TGGGAGAAGAACGGGAAGGCAGAGGACAACACTACAAGACCACGCCGACCGTGCTGG
ACAGCGACGGCTCCTACTTCCTCTACAGCAAGCTCTCAGTGCCACGAGTGAGTGGC
AGCGGGGCGACGTCTTCACCTGCTCCGTGATGCACGAGGCCTTGACAACCACTACA
CGCAGAAGTCCATCTCCCGCTCTCCGGGTAAATAG (SEQ ID NO: 99)

A11B1_2D3 Light Chain

ATGGACACGAGGGGCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCACATTTGCCCAAGTGCTGACCCAGACTCCATCCTCCGTGTCTGCAGCTGTGGGA
AGCACAGTCACCATCAATTGCCAGGCCAGTCAGAGTGTTTATAAAGACAACAATTTA
GCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTACAAGGCTTCC
ACTCTGGCATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACACAGTTC
ACTCTACCATCAGCGGCGTGCAGTGTGAAGATGCTGCCACTTACTACTGTCAAGGC
GAATTCAGTTGTGGTAGTGCTGATTGTATTGCTTTCGGCGGAGGGACCGAGGTGGTG
GTCAAAGGTGATCCAGTTGCACCTACTGTCTCATCTTCCCACCAGCTGCTGATCAG
GTGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTC
ACCGTCACCTGGGAGGTGGATGGCACCACCCAAACAACCTGGCATCGAGAACAGTAA
AACACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGAC
CAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACG
ACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 100)

A11B1_2A7 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACT
CACCTGCAAAGGCTCTGGAATCGACTTCAGTAGCGGCTACGGCATGTGGTGGGTCCG
CCAGGCTCCAGGGAAGGGACTGGAGTATATCGGATACATTGATACTGGTTATGGTA
GCACTTACTACGCGAGCTGGGCGAAAGGCCGATTACCATCTCCAAGACCTCGTCG
ACCACGGTGACTCTGCAAATGACCAGTCTGACAGTCGCGGACACGGCCACCTATTTCT
TGTGCGAAAGGGGGCGCCATAGACCTCTGGGGGCCAGGGACCCTCGTCACCGTCTC
TTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCTGCTGCGGGGACAC
ACCCAGTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCTCCCGGAGCCAGT
GACCGTGACCTGGAACCTCGGGCACCTCACCAATGGGGTACGCACCTTCCCGTCCGT
CCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCA
GCCAGCCCGTCACCTGCAACGTGGGCCACCCAGCCACCAACACCAAAGTGGACAAG
ACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCCACCCCTGAACTCCCGGGG
GGACCGTCTGTCTTCATCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCACGC
ACCCCCGAGGTCACATGCGTGGTGGTGGACGTGAGCCAGGATGACCCGAGGTGCA
GTTACATGGTACATAAACAACGAGCAGGTGCGCACCGCCCGGCCGCTACGGG
AGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCTCCCCATCGCGCACCG
GACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAGGCACTCCCGGC
CCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCTGGAGCCGAAGGTCT
ACACCATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTCCGTGAGCCTGACCTGC
ATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAGAAGAACGGGAA
GGCAGAGGACAACACTACAAGACCACGCCGACCGTGCTGGACAGCGACGGCTCCTACT
TCCTCTACAGCAAGCTCTCAGTGCCCACGAGTGAGTGGCAGCGGGGCGACGTCTTCA

CCTGCTCCGTGATGCACGAGGCCTTGCACAACCACTACACGCAGAAGTCCATCTCCC
GCTCTCCGGGTAAATAG (SEQ ID NO: 101)

A11B1_2A7 Light Chain

ATGGACACGAGGGCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCACATTTGCAGCCGTGCTGACCCAGACTCCGGCTTCCACGTCTGCAGCTGTGGGA
GGCACAGTCACCATCAATTGTCAGTCCAGTCAGAGCGTGTATCGTAGCAACTGGTTA
GCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTATGATGTATTT
AATTTGGCATCTGGGGTCCCATCCCGGTTCAAGGGCAGTGGATCTGGGACACAGTTC
ACTCTCACCATCAGCGGCGTGCAGTGTGCCGATGCTGCCACTTACTACTGTCAAGGC
AGTTATTATAGTGGTAATTGGTACAGTGCTTTCGGCGGAGGGACCGAGGTGGTGGTC
AAAGGTGATCCAGTTGCACCTACTGTCCTCATCTTCCCACCAGCTGCTGATCAGGTG
GCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCACC
GTCACCTGGGAGGTGGATGGCACCACCCAAACAACACTGGCATCGAGAACAGTAAAC
ACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAG
CACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACCT
CAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (SEQ ID NO: 102)

Protein sequences of anti- α 11 β 1 monoclonal antibodies

Rat mAb sequences

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

79E3E3 Heavy Chain Variable Region

MDWLWNLFLMVVAQSAQAQIQLVQSGPEVKKPGESVKISCKASGYTFTD**YAMN**WVKQ
APGNGLKWMGWINT**QTGKPTYADDFKQ**RFVFSLETSARTTYLQINNLNIEDTATYFCT
RLGTGNT**KGFAY**WGQGLVTVSS (SEQ ID NO: 145)

79E3E3 Light Chain Variable Region

MESQTHVLISLLLCVSGTCGDILINQSPASLTVSAGERVTMSCKSSQSLLYSENNQDYLA
WYQQKPGQFPKLLIYGASNRHTGVPDRFTGSGSGTDFTLTISSVQAEDLADYY**CEQTY**
RYPFTFGSGTKLEIK (SEQ ID NO: 146)

24E4G6 Heavy Chain Variable Region

MELELSLIFISLLKDVQCEVQLVESGGSLVQPGGSLKLSCVASGYTFSNYWMDWVRQSP
GKSLEWIGEINTD**GRRTNYAPSIKDR**FTISRDNASTLYLQMSNVKSDDTAIYYCTILR
VYPHYFDYWGGQVMVTVSS (SEQ ID NO: 147)

24E4G6 Light Chain Variable Region

MMSPAQFLFLMLWIQEARGDVVMTQTTPPSLSVAIGQSVSISCKSSQSLVYSDGETYLH
WFLQSPGRSPKRLIYHVSNLGSGVPDRFSGTGSLTDFTLRISRVEAEDLGYYCAQTTH
FPPTFGAGTKLELK (SEQ ID NO: 148)

8H8E9 Heavy Chain Variable Region

*MAVLVLLCLVTFPSCALSQVQLKESGPGVLVQPSQTLSTCTVSGFSLTSNSVSWVRQAPG
KGLEWMGAIWSGGSTDYNSALKSRLSISRDTSKSQVFLKMNSLQTEDTAIFYCTRSHW
EPFDYWGQGVMVTVSS (SEQ ID NO: 149)*

8H8E9 Light Chain Variable Region

*MESQTQALISLLLWVYGTCGDIVMTQSPFSLAVSEGEMVTINCKSSQGLLSSGNQKNYLA
WYQQRPGQSPKLLIYYASTRQSGVPDRFIGGSGTDFTLTISDVQAEDLADYYCLQHYS
YPPTFGSGTKLEIK (SEQ ID NO: 150)*

6E5C11 Heavy Chain Variable Region

*MAVLVLLCLVTFPSCALSQVQLRESGPGVLVQPSQTLSTCTVSGFSLTSNSVTWVRQPPG
KGLEWMGAIWSDGSTDYNSTLKSRLSISRDTSKSQVFLKMSSLQTEDTAIFYCTRSHW
EPFDYWGQGVMVTVSS (SEQ ID NO: 151)*

6E5C11 Light Chain Variable Region

*MESQTQALISLLLWVYGTCGDIVMTQSPSLAVSEGETVTMNCKSSQSLFSSGNQKNYLA
WYQQKPGQSPKLLIYYASTRQSGVPDRFIGSGSGTDFTLTISDVQTEDLADYYCLQHYN
YPPTFGSGTKLEIK (SEQ ID NO: 152)*

7D8B10 Heavy Chain Variable Region

*MDLRLTYVFIVAILKGVLCEVKLEESGGGLVQPGMSVKLSCATSGFIFSDYWMEWVRQAP
GKGLEWVAEIRNKANNYATYYGKSMKGRFTISRDDSKSIVYLQVNSIRSEDTAIYYCA
PNFDYWGQGVMVTVSS (SEQ ID NO: 153)*

7D8B10 Light Chain Variable Region

*MSPVQSLFLLLWILGTHGDVVLTPPTLSATIGQSVSISCRSSQSLLHSTGNTYLNWLL
QRPQPPQLLIYLVSRLESGVPNRFASGSGTDFTLKISGIEAEDLGYYCVQSSHTPYT
FGTGTKLELK (SEQ ID NO: 154)*

18E10F10 Heavy Chain Variable Region

*MDIRLSLVFLVLFMKGVCQEVQLVESGGGLVQPGRSLKLSCAASRFTFSDYNMAWVRQA
PKKGLEWVATIYHDDSGSYRDSVKGRFTISRNNAKSTLYLQMDSLRSRSEDTATYYCA
RHNNGFDYWGQGVMVTVAS (SEQ ID NO: 155)*

18E10F10 Light Chain Variable Region

*MKWPVRLVLFFWIPASGGDVVMTQTPVSLPVRLGGQASISCRSSQSLVHSNGNTYLHW
YLQKPGQSPQLLINRVSNRFSGVPDRFSGSGSGTDFTLKINRVEPEDLDYYCLQSTHFP
LTFGSGTKLETK (SEQ ID NO: 156)*

40G10H11 Heavy Chain Variable Region

*MDIRLSLGLVLFIKGDQCAVQLVESGGGLVQPGRSLKLSCAASRITFTDYMAWVRQA
PTKGLEWVATISSDGGDTFYRDSVKGRFTISRDNKSTLYLQMVSLRSEDTATYYCST
DRGAQFGYWGQGTTLVTVSS (SEQ ID NO: 157)*

40G10H11 Light Chain Variable Region

MAPVQLLGLLLIWLPAMRCDIQMTQSPSFLSASVGDRVSINCKASQNVHENLNWYQQKL
GEAPKRLIYNTNNLQTGIPSRFSGSGSGADYTLTISSLQPEDFATYFCLQHNAFPYTFGP
GTKLELK (SEQ ID NO: 158)

Mouse mAb sequences

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

9-G05 Heavy Chain Variable Region

EVQLQQSGPELVKPGASVKIPCKASGYTFPDYNMDWVKQSHGKSLEWIGYINPDNGGT
IYNQKFKGKATLTVDKSSSTAYMELRSLTSEDVAVYYCARLDSSGYGYAMDYWGQG
TSTVTSS (SEQ ID NO: 103)

9-G05 Light Chain Variable Region

DIVLTQSPASLAVSLGQRATISCRASEVDNYGISFMHWYQQKPGQPPELLIYRASNL
SEIPARFSGSGSRDFTLTIDPVETDDVATYYCQQSYKDPRTFGGGTKLEIK (SEQ ID
NO: 104)

8-P20 Heavy Chain Variable Region

KVMLVESGGALVKPGSLKLSVCVASGFTFSNYAMSWVRQTPEKRLEWVATISSGGYY
TYYPDSVKGRFTISRDNARNTLFLQMSSLRSEDAMFYCAREDDYGRYSYTMIDYWGQ
GTSVTSS (SEQ ID NO: 105)

8-P20 Light Chain Variable Region

DVVMQTPLSLPVSLGDQVSISSCRCSQSLVHSNGNTYLHWYLVKPGQSPQLLIYKISNR
FSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPYTFGGGTELEIK (SEQ ID
NO: 106)

8-G15 Heavy Chain Variable Region

EVQLQQSGPELVKPGASVRISCKASGYTFTDYYIHWVKQKPGQGLECIGEIYPGTDNTY
YSKKFRGKATLTADKSSDTAYMQLSSLTSEDSAVYFCARGDYRGRYFDVWGAGTTVT
VSS (SEQ ID NO: 107)

8-G15 Light Chain Variable Region

DVVMQTSLTSLVTIGQPASISCKSSQSLHNSNGKTYLNWLLQRPGQSPKFLIYLVSKL
ESGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCLQSTHFPWTFGGGTELEIK (SEQ ID
NO: 108)

8-I14 Heavy Chain Variable Region

EVQLQQSGPELVKPGASVKKSCASGYTFTDYYMHWVKQKPGQGLEWIGKIYPGSGN
THYNEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCATNYYGYRAMNYWGQGSS
VTSS (SEQ ID NO: 109)

8-I14 Light Chain Variable Region

DIHLTQSPSSLSASLGERISLTCRASQDIYISLNWFQQKPDGTIKLLIYGTSSLD SGV PKRF
SGSRSGSDYSLTISSLESEDFADYYCLQYASSPYTFGGG TKLEIK (SEQ ID NO: 110)

9-E16 Heavy Chain Variable Region

EVQLQQSGPELVKPGASVKISCKASGYTFTDYMHVWKQKPGQGLEWIGEIYPGSGNP
YYNEKFKGKATLTADKSSSSAYMQLSSLTSEDSAVYFCARTSYGRVGTGFAYWGQGT
LTVSA (SEQ ID NO: 111)

9-E16 Light Chain Variable Region

NFVMTQTPLSLPVSLGDQASISCRSSQSLHSNGNTYLHWYLQKPGQSPKLLIYKVSNR
FSGVPDRFSGSGGTDFTLKINRVETEDLGIYFCSQSSHVPTFGAGTKLELK (SEQ ID
NO: 112)

8-J17 Heavy Chain Variable Region

QVQLQQSGAELAKPGASVKMSCKASGYTFTNYWMHVWKQRPQGLEWIGYINPNNG
YTEYNQRFKDKATLTADRSSTAYMQLSSLTSEDSAVYYCARSDIITTDYWGQGTTLT
VSS (SEQ ID NO: 113)

8-J17 Light Chain Variable Region

DVVMQTQTPLSLPVSLGDQASISCRSSQSLVYSNGNTYLHWYLQKPGQSPKLLIYKVSNR
FSGVPDRFSGSGGTDFTLKISRVEAEDLGVYFCSQSTHVPWTFGGG TKLEIK (SEQ ID
NO: 114)

9-B11 Heavy Chain Variable Region

QVQLQQPGAELVRPGTSVKLSCKASGYTFTSYWMHVWQRPQGLEWIGVIDPSDSY
TNYNQKFKGKATLTVDTSSSSAYMQLSSLTSEDSAVYYCARDVDVMDYWGQGTSTV
SS (SEQ ID NO: 115)

9-B11 Light Chain Variable Region

DIVVTQSPASLAVSLGQRATISCRASESVDSYGNSFIHWYQQKPGQPPKLLIYRASNLKS
GIPARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPYTFGGG TKLEIK (SEQ ID NO:
116)

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

6-O12 Heavy Chain Variable Region

EVKLEESGGGLVQPGGSMKLSCAASGFTFSDAWMDWVRQSPEAGLEWVAEIRNKAHN
PATYYAESVKGRFTISRDDSKSSVYLQMNSLRAEDTGIYY**CTLVAPDAMDYWGQTS**
VTVSS (SEQ ID NO: 117)

6-O12 Light Chain Variable Region

DIVMSLSPSSLAVSVGEKVTMSCKSSQSLLYSRNQKNYLAWYQQKPGQSPKLLIYWAST
RASGVPDRFTGSGSGTDFTLTISSVKAEDLAVYY**CQOYYSYPYTFGGG**TKLEIK (SEQ
ID NO: 118)

10-L15 Heavy Chain Variable Region

QVQLQQSGPELVRPGASVKMSCKASGYTFTSYWMHWVKQRPGQGLEWIGMIDPSNSE
TWLNQKFKDKATLNVDKSSNTAYMQLSSLTSEDSAVYYCARYDGYDYWGQGTTLT
VSS (SEQ ID NO: 119)

10-L15 Light Chain Variable Region

NIVLTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQQKPGQPPKLLIYLASNVES
GVPARFSGSGSRTDFTLTIDPVEADDAATYYCQONNEDPWTFGGGKLEIK (SEQ ID
NO: 120)

7-H14 Heavy Chain Variable Region

QVQLQQPGAELVRPGASVKLSCKPSGYTFTSYWMNWVKQRPGQGLEWIGMIDPSDSET
HYNQMFKDKATLTVDKSSNTAYMQLSSLTSEDSAVYYCAQIYYAYDKAYWGQGTLV
TVSA (SEQ ID NO: 121)

7-H14 Light Chain Variable Region

DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSSHQKNYLAWYQQKPGQSPKLLIYWAST
RESGVPDRFTGSGSGTDFSLTISSVKAEDLAVYYCOEYYSWTFGGGKLEIK (SEQ ID
NO: 122)

6-B21 Heavy Chain Variable Region

EVQLQQSGPELVKPGASVKISCKASGYTFTDYMNWVKQSHGKSLEWIGDINPHNGGT
SFIQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCAPLGRKEGFAYWGQGTLVTV
SA (SEQ ID NO: 123)

6-B21 Light Chain Variable Region

DTVLTQSPASLVVSLGQRATISCRASKSVSTSGYSYMHWYQQKPGQPPKLLIYLASNLES
GVPARFSGSGSGTAFTLNHPVEEEDAATYYCQHSRELPYTFGGGKLEIK (SEQ ID
NO: 124)

10-F23 Heavy Chain Variable Region

QVTLKESGPGILQPSQTLSTCSFSGFSLSTFAMGVGWIRQPSGKGLEWLAHWWDDDK
YYNPALKSRLTISKDTSKNHVFLKIANVDTADTATYYCARMPLTFYFDYWGQGTTLT
VSS (SEQ ID NO: 125)

10-F23 Light Chain Variable Region

DVLLTQTPLSLPVSLGDQASISCRSSQSIVHSNGHTYLEWYLQKPGQSPKLLIYKVSNRFS
GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFGGGKLEIK (SEQ ID
NO: 126)

6-A12 Heavy Chain Variable Region

QVTLKESGPGILQPSQTLSTCSFSGFSLRTFAMGVGWIRQPSGKGLEWLAHWWDDDK
YYNPALKSRLTISKDTSKNQVFLKIANVDTADTATYYCARMPLTFYFDYWGQGTTLT
VSS (SEQ ID NO: 127)

6-A12 Light Chain Variable Region

DVLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSTRF
SGVPDRFSGSGGTDFTLKISRVEAEDLGVIYYCFQGSHPVPTFGGGKLEIK (SEQ ID
NO: 128)

6-M8 Heavy Chain Variable Region

QVQLQQPGAELVMPGASVKLSCKASGYTFTNYWMHWVKQRPGQGLEWIGEIDPSDSY
TNYNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTROGSTYAWGQGTSVTVS
S (SEQ ID NO: 129)

6-M8 Light Chain Variable Region

DIVMTQAAFSNPVTLGTSAISCRSSKSLHNSGITYLYWYLQKPGQSPQLLIYQMSNLA
SGVPDRFSSSGGTDFTLRISRVEAEDVGVIYYCAQNLLELPPTFGGGKLEIK (SEQ ID
NO: 130)

2-A3 Heavy Chain Variable Region

EVQLQQSGPELVKPGASVKMSCKASGYTFTDYMMWVKQSHGKSLEWIGDINPYNGG
SSYNPKFKGRATLTVDKSSSTAYMQLNSLTSEDSAVYYCARGTYWGQGTLLTVSA
(SEQ ID NO: 131)

2-A3 Light Chain Variable Region

DVVMQTQPLTSLVTIGQPASISCKSSQSLLDSAGKTYLNLWLLQRPGQSPKRLMYLVSKL
DSGVPDRFTGSGGTDFTLKISRVEAEDLGVIYYCWQGTHTFPYTFGGGKLEIK (SEQ
ID NO: 132)

6-O17 Heavy Chain Variable Region

QVQLQQPGAELVMPGASVKLSCKASGYTFTSYWMHWIKQRPGQGLEWIGEINPSNGGS
NYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYHCKSRGYWGQGTLLTVSS (SEQ
ID NO: 133)

6-O17 Light Chain Variable Region

DVVMQTQPLTSLVTIGQPASISCKSSQSLLDSYGKTYLNLWLLQRPGQSPKRLIYLVSKLD
SGVPDRFTGSGGTDFTLKISRVEAEDLGIYYCWQGTHTFPHTFGSGTKLEIK (SEQ ID
NO: 134)

3-G5 Heavy Chain Variable Region

QVQLQQSGAELARPGASVKLSCKASGYTFTSYGISWVKQRTGQGLEWIGEIFPRSSNTY
YNEKFKGKATLTADKSSSTVYMEFRSLTSEDSAVYFCAREGGLAWFAYWGQGTLLTVS
SA (SEQ ID NO: 135)

3-G5 Light Chain Variable Region

DVVMQTQPLTSLVTIGQPASISCKSSQSLLYTNNGNTYLNWLLQRPGQSPKRLIYLVSKLD
SGIPDRFSGSGGTDFTLRISRVEAEDLGVIYYCLQSTHTFPPTFGSGTKLEIK (SEQ ID
NO: 136)

6-A15 Heavy Chain Variable Region

EVQLQQSGPELVKPGASVKMSCKASGYTITDYYMMWLKQSHGKSLEWIGDINPYTGGT
SYNQKFKGKATLTVDKSSSTAYLQLHSLTSEDSAVYYCARGAYWGQGTTTLTVSS (SEQ
ID NO: 137)

6-A15 Light Chain Variable Region

DVVMQTPTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLD
SGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTTHFPYTFGGGGTKLEIK (SEQ ID
NO: 138)

10-K10 Heavy Chain Variable Region

EVQLQQSGPELVKPGASVKMSCKASGYTITDYYMMWLKQSHGKSLEWIGDINPYTGGT
SYNQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARGAYWGQGTTTLTVSS
(SEQ ID NO: 139)

10-K10 Light Chain Variable Region

DVVMQTPTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLD
SGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTTHFPYTFGGGGTKLEIK (SEQ ID
NO: 140)

6-P20 Heavy Chain Variable Region

EVQLQQSGPELVKPGASVKISCKASGYTFTDYYMNWVKQSHGRSLELIGDINPNNGGSN
FNQKFRGKATLTVDKSSSTAYMELRSLTSEDSAIYYCARMGYWGQGTTLTVSA (SEQ
ID NO: 141)

6-P20 Light Chain Variable Region

DVVMQTPTPLTSLVTIGQPASISCKSSQSLHSDGKTYLNWMFQRPQGSPKRLIYLVSKLD
SGVPYRFTGGSGTDFTLQISRVETEDLGVYYCWQGTTHFPRTFGGGGTKLEIK (SEQ ID
NO: 142)

7-08 Heavy Chain Variable Region

EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYIHWVKQKPGQGLEIYIGEIYPGSGNT
YYNGKFRGKATLTADKSSSTAYMQLSSLTSEDSAVYFCGSGYFDYWGQGTTTLTVSS
(SEQ ID NO: 143)

7-08 Light Chain Variable Region

DVVMQTPTPLTSLVTIGQPASISCKSSQSLLYSNGKTYLNWLLQSPGQSPKLLIYLVSKLES
GVPDRFSGSGSGTDFTLKLSRVEAEDLGVYYCVQGTTHFPFTFGSGGTKLEIK (SEQ ID
NO: 144)

Rabbit mAb sequences

A11B1_16G7 Heavy Chain

METGLRWLLLVAVFKGVQCQEQLVESGGDLVKPGASLTLTCTASGFSFNKNYWMCWV
RQAPGKGLEWIGCIYNGDGNTYYASWVNGRFTISKTSSTTVTLQMTSLTVADTAIFYCA
RLNLMWGPGLTVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLPEPVTVTWNS
GTLTNGVRTFSPVRQSSGLYSLSSVSVTSSSQPVTCNVAHPATNTKVDKTVAPSTCSKP
MCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRTA
RPPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEPK
VYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSDGSYFL
YSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO: 159)

A11B1_16G7 Light Chain

MDTRAPTQLLGLLLLWLPGARCAIVMTQTPASVEAAVGGTVTIKCQASESIGNALAW
YQKPGQPPKLLIYTAATLASGVPSRFSGSGSGTEFTLTISGVQCDDAATYYCQSYFYTS
VSSYGNAFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWE
VDGTTQTGTIENSKTPQNSADCTYNLSSLTLTSTQYNHKEYTCKVTQGTTSVVQSFNR
GDC* (SEQ ID NO: 160)

A11B1_16E10 Heavy Chain

METGLRWLLLVAVLKGVQCQSLEESGGDLVKPGASLTLTCRVSGFSFSSSYMCWVRQ
APGKGLEWIIACIGTTRGSTYYATWAKGRFTISKISSTTVTLQMTSLTDADTATYFCARDA
TGYRINTIGLYFNLWGPGLTVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLPE
PVTVTWNSGTLTNGVRTFSPVRQSSGLYSLSSVSVTSSSQPVTCNVAHPATNTKVDKT
VAPSTCSKPMCAPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYI
NNEQVRTARPPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKA
RGQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVL
DSDGSYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO:
161)

A11B1_16E10 Light Chain

MDTRAPTQLLGLLLLWLPGARCAFELTQTPSSVEAAVGGTPTIKCQASQTIYSYLSWYQ
QKPGQPPKLLIYEASKLASGVPSRFSGSGSGTDYTLTISDLECADAAATYYCQSYHGTAST
EYNTFGGGTEVVVRGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVDG
TTQTGTIENSKTPQNSADCTYNLSSLTLTSTQYNHKEYTCKVTQGTTSVVQSFNRGDC
* (SEQ ID NO: 162)

A11B1_15G10 Heavy Chain

METGLRWLLLVAVLKGVQCQQQLVESGGGLVKPGAALTFTCTASGFSFSGNYWICWV
RQAPGKGLEWIIACIGTITSRTYYASWAKGRFTISKTSSTTVTLQMTSLTAADTATYFCAR
GAVVSSGNAPYYFTLWGPGLTVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYL
PEPVTVTWNSGTLTNGVRTFSPVRQSSGLYSLSSVSVTSSSQPVTCNVAHPATNTKVD
KTVAPSTCSKPMCAPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFT
WYINNEQVRTARPPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTI
SKARGQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPT
TVLDSDGSYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID
NO: 163)

A11B1_15G10 Light Chain

MDTRAPTQLLGLLLLWLPGARCAFELTQTPSSVEAAVGGTVTIKCQASQSISSYLSWYQ
QKPGQPPKLLIYRASTLESGVPSRFKGS GSGTEFTLTISDLECADAAATYFCQSYYGVTFSG
FAFGGGTEVVVKGDPVAPTIVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVDGTT
QTTGIENSKTPQNSADCTYNLSSLTLTSTQYNHKEYTCKVTQGTTSVVQSFNRGDC*
(SEQ ID NO: 164)

A11B1_14H1 Heavy Chain

METGLRWLLLVAVLKGVQCQSLEESGGDLVKPGASLTLTCKASGIDFNWYITWVRQA
PGKGLEWIACIYVGITGRWYANWAKGRFTISKASSTVDLKMSTLTAADTATYFCARN
GDGGIYALNLWPGTLTVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLPEPVT
VTWNSGTLTNGVRTFPSPVRQSSGLYSLSSVSVTSSSQPVTCNVAHPATNTKVVDKTVAP
STCSKPMCPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNE
QVRTARPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKISKARGQ
PLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSGD
SYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO: 165)

A11B1_14H1 Light Chain

MDTRAPTQLLGLLLLWLPGATFAQVLTQTASSVSAAVGGTVTISCQSSQSVYNNWLA
WYQQKPGQPPKLLIYRASTLTSGVPSRFKGS GSGTQFTLTISDLECDAAATYYCAGGYS
GNIYVNDFFGGGTEVVVKGDPVAPTIVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWE
VDGTTQTTGIENSKTPQNSADCTYNLSSLTLTSTQYNHKEYTCKVTQGTTSVVQSFNR
GDC* (SEQ ID NO: 166)

A11B1_13G4 Heavy Chain

METGLRWLLLVAVLKGVQCQEQLLEESGGDLVKPGGSLTLTCKASGFSFSNTYWACWV
RQAPGKGLEWIACMNPASSGSSYYASWAKGRFTISKSTSTTVTLHMPSLTAADTATYFC
AKWDTAFDVWPGTLTVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLPEPVT
TWNSGTLTNGVRTFPSPVRQSSGLYSLSSVSVTSSSQPVTCNVAHPATNTKVVDKTVAPS
TCSKPMCPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNE
QVRTARPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKISKARGQ
PLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSGD
SYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO: 167)

A11B1_13G4 Light Chain

MDTRAPTQLLGLLLLWLPGARCAADVMTQTPSSVEAAVGGTVTIKCQASQSISSYLAW
YQQKPGQPPKLLIYGASNLESGVPSRFKGS GSGTEYTLTISGVQCDDAAATYYCQNYAI
DTYGHAFGGGTEVVVKGDPVAPTIVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEV
DGTTQTTGIENSKTPQNSADCTYNLSSLTLTSTQYNHKEYTCKVTQGTTSVVQSFNRG
DC* (SEQ ID NO: 168)

A11B1_13C3 Heavy Chain

METGLRWLLLVAVLKGVQCQEQLLEESGGDLVKPGASLTLTCTASGFSFSSNYHICWVR
QAPGKGLELIACIYVGDGSTYYASWAKGRFTISKSSSTVALQMTSLTAADTATYFCGR
MFNLWPGTLTVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLPEPVTVTWNSG
TLTNGVRTFPSPVRQSSGLYSLSSVSVTSSSQPVTCNVAHPATNTKVVDKTVAPSTCSKPM
CPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRTAR

PLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEPKVY
TMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSDGSYFLYSK
LSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO: 169)

A11B1_13C3 Light Chain

MDTRAPTQLLGLLLLWLPGAICDPVLTQTPSSVSAAVGVTVTINCQSSPSVYSNYLSWY
QQKPGQPPKLLIYLASTLASGVPSRFKGSFGSGTQFTLTISDVQCDDAATYYCAGTYSNGI
WSFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVDGTT
QTTGIENSKTPQNSADCTYNLSSSTLTLTSTQYNHKEYTCKVTQGTTSVVQSFNRGDC*
(SEQ ID NO: 170)

A11B1_12F2 Heavy Chain

METGLRWLLLVAVLKGVQCQQQLVESGGGLVKPGASLTLTCTASGFSFSSGYHMCWV
RQAPGKGLEWIACFGVYTGTTYASWAKGRFTISKTSSTTVTLQMTSLTVADTATYFCA
RISAENGGDLWPGTLTVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLPEPVTY
TWNSGTLTNGVRTFPSVRQSSGLYSLSSVSVTSSSQPVTCNV AHPATNTKV DKT VAP S
TCKPMCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSDDDPEVQFTWYINNE
QVRTARPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQ
PLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSDG
SYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO: 171)

A11B1_12F2 Light Chain

MDTRAPTQLLGLLLLWLPGARCDVVMVTQTPASVEAAVGGTVTIKCQASQSSISNYFSWY
QQKPGQPPKLLIYRASTLASGVPSRFGSGSGTEFTLTISDLECADSATYYCQCTYGSST
GFGFGGGTEVVVKGDPVAPTVPFPPAADQVATGTVTIVCVANKYFPDVTVTWEVDGT
TQTTGIENSKTPQNSADCTYNLSSSTLTLTSTQYNHKEYTCKVTQGTTSVVQSFNRGDC*
(SEQ ID NO: 172)

A11B1_11D10 Heavy Chain

METGLRWLLLVAVLKGVQCQSLEESGGDLVKPGASLTLTCMASGIDFSSGYGMWWVR
QAPGKGLEIYGYIDTGDDNTYYANWAKGRFTISKTSSTTVTLQMTSLTVADTATYFCAK
GGAIDLWPGTLTVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLPEPVTVTWN
SGTLTNGVRTFPSVRQSSGLYSLSSVSVTSSSQPVTCNV AHPATNTKV DKT VAP STCK
PMCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSDDDPEVQFTWYINNEQVRT
ARPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEP
KVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSDGSYF
LYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO: 173)

A11B1_11D10 Light Chain

MDTRAPTQLLGLLLLWLPGARCAIVMTQTPASVEAAVGGTVTIKCQASQSISSYLAWY
QQKPGQRPKLLIYRASTLKSQVPSRFKGSFGSGTEYTLTISDLECADAAATYYCQAYYLS
ISYGNTFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVD
GTTQTTGIENSKTPQNSADCTYNLSSSTLTLTSTQYNHKEYTCKVTQGTTSVVQSFNRGD
C* (SEQ ID NO: 174)

A11B1_10F9 Heavy Chain

METGLRWLLLVAVLKGVQCQSLEESGGDLVKPGASLTLTCTASGFSLSGGYGMCWVR
QAPGKGLEWIGYTDATGTIHYASWAKGRFTISKTSSTTVTLQMTSLTAADTATYFCAK
GGAMDWGPGLTVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLPEPVTVTW
NSGTLTNGVRTFPSVRQSSGLYSLSSVSVTSSSQPVTCNV AHPATNTKV DKT VAPSTCS
KPMC PPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVR
TARPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEP
KVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWENKGAEDNYKTTPTVLDSDGSYF
LYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO: 175)

A11B1_10F9 Light Chain

MDTRAPTQLLGLLLLWLP GARCADIVMTQTPASVEAAVGGTVTIKQASQSISSYLAWY
QQKPGQPPKLLIYRTSTLASGVPSRFKGS GSGTEYTLTISDLECA DAATYYCQSYAYSSSS
SYGNAFGGGTEVVVKGDPVAPT VLI FPPAADQVATGTVTIVCVANKYFPDVTVTWEVD
GTTQTGTIENSKTPQNSADCTYNLSSTLTLTSTQYN SHKEYTCKVTQGTTSVVQSFNRGD
C* (SEQ ID NO: 176)

A11B1_7H12 Heavy Chain

METGLRWLLLVAVLKGVQCQSLEESGGDLVKPGASLTLTCTGSGIDFSSSYWICWVRQ
APGKGLEWIAIDGSDGNTYYASWARGRFTISKTSSTTVTLQMASLTAADTATYFCTRD
LRLWGPGLTVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLPEPVTVTWNSGT
LTNGVRTFPSVRQSSGLYSLSSVSVTSSSQPVTCNV AHPATNTKV DKT VAPSTCSKPM
CPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRTAR
PLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEPKVY
TMGPPREELSSRSVSLTCMINGFYPSDISVEWENKGAEDNYKTTPTVLDSDGSYFLYSK
LSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO: 177)

A11B1_7H12 Light Chain

MDTRAPTQLLGLLLLWLP GARCADIVLTQTPASVSAAVGGTVTINCQASQNVYSNNAL
AWHQKPGQRPNNLIYKASTLASGVPSRFKGS GSGTQFTLTISDVQCDDAATYYCLGEF
SCSSGDCFVFGGGTEVVVKGDPVAPT VLI FPPAADQVATGTVTIVCVANKYFPDVTVTW
EVDGTTQTGTIENSKTPQNSADCTYNLSSTLTLTSTQYN SHKEYTCKVTQGTTSVVQSFN
RGDC* (SEQ ID NO: 178)

A11B1_7G12 Heavy Chain

METGLRWLLLVAVLKGVQCQSLEESGGDLVKPGASLTLTCMASGIDFSSGYGMWWVR
QAPGKGLEYIGYIDTGDDNTYYANWAKGRFTISKTSSTTVTLQMTSLTVADTATYFCAK
GGAILWGPGLTVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLPEPVTVTWN
SGTLTNGVRTFPSVRQSSGLYSLSSVSVTSSSQPVTCNV AHPATNTKV DKT VAPSTCSK
PMC PPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRT
ARPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEP
KVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWENKGAEDNYKTTPTVLDSDGSYF
LYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO: 179)

A11B1_7G12 Light Chain

MDTRAPTQLLGLLLLWLP GARCADIVMTQTPASVEAAVGGTVTIKQASQSISSYLAWY
QQKPGQRPKLLIYRASTL KSGVPSRFKGS GSGTEYTLTISDLECA DAATYYCQAYYLSSS

ISYGNTFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVD
GTTQTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNHKEYTCKVTQGTTSVVQSFNRGD
C* (SEQ ID NO: 180)

A11B1_6G4 Heavy Chain

METGLRWLLLVAVLKGVQCQQQLEESGGGLVKPGGTLTLTCKASGVALNPYYMYMCW
VRQAPGKGLEWVACVDADSSGSTYYASWAKGRFTISKTSSTTVTLKMTSLTAADTATYF
CARESDYSSVGIGYVHGTDGLWGPGLTVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLG
CLVKGYLPEPVTVTWNSGTLTNGVRTFPSVRQSSGLYSLSSVSVTSSSQPVTCNVAHP
ATNTKVDKTVAPSTCSKPMCPPELPGGPSVFIFPPKPKDTLMISRTPPEVTCVVVDVSQD
DPEVQFTWYINNEQVRTARPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKAL
PAPIEKTISKARGQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAED
NYKTTPTVLDSDGSYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK*
(SEQ ID NO: 181)

A11B1_6G4 Light Chain

MDTRAPTQLLGLLLLWLPGARCAIVVTQTPSSVSAAVGGTVTIKQASQSSISNYFSWY
QQKPGQPPKLLIYRASTLASGVPSRFKGSSTGTEFTLTISDLECAATAATYYCQCTYGRSN
SNFFYGFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEV
DGTTQTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNHKEYTCKVTQGTTSVVQSFNRG
DC* (SEQ ID NO: 182)

A11B1_6F9 Heavy Chain

METGLRWLLLVAVLKGVQCQSLEESGGDLVKPGASLTLTCTASGSSFSSTYWNCWVRQ
APGKGLEWVACINAGSGTYYASWAKGRFTVSKTSSTTVTLQMTSLTAADTATYFCTRD
SDGRFSSGYFNLWGPGLTVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLPEP
VTVTWNSGTLTNGVRTFPSVRQSSGLYSLSSVSVTSSSQPVTCNVAHPATNTKVDKTV
APSTCSKPMCPPELPGGPSVFIFPPKPKDTLMISRTPPEVTCVVVDVSQDDPEVQFTWYIN
NEQVRTARPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKAR
GQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSD
DGSYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO:
183)

A11B1_6F9 Light Chain

MDTRAPTQLLGLLLLWLPGATFAQVLTQTASPVSAAVGGTVTINCQSSQSVYDNNWLA
WYQQKPGQPPKLLIDDASKLTSGVSSRFKGSSTGQFTLTISGVQCDDAATYYCQGAYY
SSGWYWAFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWE
VDGTTQTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNHKEYTCKVTQGTTSVVQSFNR
GDC* (SEQ ID NO: 184)

A11B1_6C7 Heavy Chain

METGLRWLLLVAVLKGVQCQQQLEESGGGLVKPGGTLTLTCKASGIDFSSYYMYMCW
RQAPGKGLELIVCIYTSSGGTWYASWVNGRLTISRSTSLNTVDLKMTSLTAADTATYFC
ARGVYSGSSDYPTRLDLWGQGLTVTVSLGQPKAPSVFPLAPCCGDTSPSTVTLGCLVK
YLPEPVTVTWNSGTLTNGVRTFPSVRQSSGLYSLSSVSVTSSSQPVTCNVAHPATNTK
VDKTVAPSTCSKPMCPPELPGGPSVFIFPPKPKDTLMISRTPPEVTCVVVDVSQDDPEVQF

TWYINNEQVRTARPPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKT
ISKARGQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTTP
TVLDSGSDGSYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID
NO: 185)

A11B1_6C7 Light Chain

MDTSTSTALLGLLLLWLTGARCAIEMTQSPPSLSASVGETVRIRCLASEDIYSGISWYQQ
KPEKPPTLLISGASNLESGVPPRFSGGGSGTDYTLTIGGVQAEDVATYYCLGGYSFSSTG
LTFGAGTKVEIKRDPVAPSVLLFPPSKEELTTGTATIVCVANKYFPDVTVTWEVDGTTQT
TGIENSKTPQNSADCTYNLSSSTLTLTSTQYNHKEYTCKVTQGTTSVVQSFNRGDC*
(SEQ ID NO: 186)

A11B1_6B6 Heavy Chain

METGLRWLLLVAVLKGVQCQQHLVESGGGLVKPGASLTLTCTASGFSFTTGYHMCWV
RQAPGKGLEWIACFGVYTSTTTYASWAKGRFTISKTSSTTVTLQMTSLTVADTATYFCA
RISAEDGGDLWPGTLTVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLPEPVTV
TWNSGTLTNGVRTFPVSRQSSGLYSLSSVSVTSSSQPVTCNV AHPATNTKV DKT VAPS
TCSKPMC PPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVDVVSQDDPEVQFTWYINNE
QVRTARPPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQ
PLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSG
SYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO: 187)

A11B1_6B6 Light Chain

MDTRAPTQLLGLLLLWLPGARCDVVMQTTPASVEAAVGGTVTITCQASQSSISNYFSWY
QQKPGQPPKLLIYRASTLASGVPSRFGSGSGTQFTLTISDLECADSATYACQCTYGSST
GFGFGGGTEVVVKGDPVAPT VLIFFPAADQVATGTVTIVCVANKYFPDVTVTWEVDGT
TQTGTIENSKTPQNSADCTYNLSSSTLTLTSTQYNHKEYTCKVTQGTTSVVQSFNRGDC*
(SEQ ID NO: 188)

A11B1_5F7 Heavy Chain

METGLRWLLLVAVLKGVQCQSLEESGGDLVKPGASLTLTCKASGFSFSSYFWICWVRQ
APGKGLEWSACIYGDSSGSSYYASWAKGRFTISKTSSTTVTLQMTSLTAADTATYFCAS
YGSSSYYYSNLWPGTLTVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLPEPVTV
TWNSGTLTNGVRTFPVSRQSSGLYSLSSVSVTSSSQPVTCNV AHPATNTKV DKT VAP
STCSKPMC PPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVDVVSQDDPEVQFTWYINNE
QVRTARPPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQ
PLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSG
SYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO: 189)

A11B1_5F7 Light Chain

MDTRAPTQLLGLLLLWLPGAICDPVMTQTTPSSTSAAVGGTVTISCQSSQSVYNNNYLAW
YQKPGQPPKRLIYESSKLASGVPSRFRGSGGAQFTLTISDLECDDAATYYCLGAYYTT
LDFGGGTEVVVRGDPVAPT VLIFFPAADQVATGTVTIVCVANKYFPDVTVTWEVDGTT
QTTGTIENSKTPQNSADCTYNLSSSTLTLTSTQYNHKEYTCKVTQGTTSVVQSFNRGDC*
(SEQ ID NO: 190)

A11B1_5D7 Heavy Chain

METGLRWLLLVAVLKGVQCQEQLVESGGGLVQPEGSLTLTCKASGFDSSNAMCWVR
QAPGKGLEWIACIYNGDGSTYYASWVNGRFTISKTSSTTVTLQMTSLTAADTATYFCAR
GLSNWNRDNLWGPGTLTVVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLPEPVT
VTWNSGTLTNGVRTFPSVRQSSGLYSLSSVSVTSSSQPVTCNVAHPATNTKVDKTAP
STCSKPMCPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNE
QVRTARPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQ
PLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSDG
SYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO: 191)

A11B1_5D7 Light Chain

MDTRAPTQLLGLLLLWLPGATFAQVLTQTPSSVSAAVGGTATINCQASQSLYSPKNLAW
YQQTGQPPKLLIYASKLASGVPSRFKSGSGTQFTLTISGVQCDDAAIYYCQGEFSCTT
AACFAFGGGTEVVVKGDPVAPTFLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVD
GTTQTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNHKEYTCKVTQGTTSVVQSFNRGD
C* (SEQ ID NO: 192)

A11B1_5A7 Heavy Chain

METGLRWLLLVAVLKGVQCQSLEESGGGLVQPEGSLTLACTASGFSFSSYYYICWVRQ
APGTGLEWIGCINTGSDDTHYASWLKGRFTFSKASSTTLTLQMTSLTAADTATYFCARS
SGSSDDAYDLWGPGTLTVVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLPEPVT
VTWNSGTLTNGVRTFPSVRQSSGLYSLSSVSVTSSSQPVTCNVAHPATNTKVDKTAP
STCSKPMCPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNE
QVRTARPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQ
PLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSDG
SYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO: 193)

A11B1_5A7 Light Chain

MDTRAPTQLLGLLLLWLPGARCDVVMTPASVSEPVGGAVTIKCQASQSIGSNLAWY
QHKPGQPPKLLIYFASSLASGVSSRFKGRSGTQFTLTISDLECAADAATYYCHCTYYPLS
YVTFGGGTEVVVKGDPVAPTFLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVDGT
TQTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNHKEYTCKVTQGTTSVVQSFNRGDC*
(SEQ ID NO: 194)

A11B1_4E1 Heavy Chain

METGLRWLLLVAVLKGVQCQSLEESGGDLVKPGTSLTSLCTASGFSFGSYYMYMCWVRQ
APGKGLEWIAIDVGSSGDTYYASWVNGRFTISKTSSTTVTLQMTSLTAADTATYFCAR
DDTAAGGFGNLELWGPGTLTVVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLPE
PVTVTWNSGTLTNGVRTFPSVRQSSGLYSLSSVSVTSSSQPVTCNVAHPATNTKVDKT
VAPSTCSKPMCPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYI
NNEQVRTARPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKA
RGQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVL
DSDGSYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO:
195)

A11B1_4E1 Light Chain

MDTRAPTQLLGLLLLWLPGARCAFELTQTPSSVSEPVGGTVTIKCQASQSIYSYFSWYQ
QKPGQPPKRLIYQASTLASGVPSRFKGSSTGDTFTLTISDLECADAATYYCQNNYGRGS
GSYFFGGGGTEVVVKGDPVAPTIVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEV
DGTQTGTGIENSKTPQNSADCTYNLSSSTLTSTQYNHKEYTCKVTQGTTSVVQSFNRG
DC* (SEQ ID NO: 196)

A11B1_3H9 Heavy Chain

METGLRWLLLVAVLKGVQCQSLEESGGDLVKPGASLTLTCKASGIDFSSGYGMWWVR
QAPGKGLEIYIGYIDTGSGSTYYANWAKGRFTISKTSSTMVTLQMTSLTVADTATYFCAK
GGAIDLWGPGLTVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLPEPVTVTWN
SGTLTNGVRTFPSVRQSSGLYSLSSVSVTSSSQPVTCNVAHPATNTKVDKTVAPSTCSK
PMCPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSDDDPEVQFTWYINNEQVRT
ARPPLEQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEP
KVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSDGSYF
LYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO: 197)

A11B1_3H9 Light Chain

MDTRAPTQLLGLLLLWLPGARCADIVMTQTPASVEAAVGGTVTIKCQASQSISSYLAWY
QQKPGQRPKLLIYRASTLASGVPSRFKGSSTGDTFTLTISDLECADAATYYCHTYLSSS
ISYGNFTGGGTEVVVKGDPVAPTIVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVD
GTTQTGTGIENSKTPQNSADCTYNLSSSTLTSTQYNHKEYTCKVTQGTTSVVQSFNRGD
C* (SEQ ID NO: 198)

A11B1_3G2 Heavy Chain

METGLRWLLLVAVLKGVQCQEQLLEESGGDLVKPEGSLTLTCKASGFSFSSIYWICWVRQ
APGKGLEWIACTTVVKSGRTYYANWAKGRFTISKTSSTTVTLQMTSLTAADTATYFCA
REFVDGGGSSGRDLWGPGLTVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLP
EPVTVTWNSGTLTNGVRTFPSVRQSSGLYSLSSVSVTSSSQPVTCNVAHPATNTKVDK
TVAPSTCSKPMCPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSDDDPEVQFTW
YINNEQVRTARPPLEQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTIS
KARGQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPT
VLDSDGSYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID
NO: 199)

A11B1_3G2 Light Chain

MDTRAPTQLLGLLLLWLPGARCAYDMTQTPASVEAAVGGTVTIKCQASQSISRDLRWY
QQKPGQPPKRLIYKASTLASGVPSRFKGSSTGDTFTLTISDLECADAATYYCQQGYSSID
VDNDFGGGTEVVVKGDPVAPTIVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVDG
TTQTGTGIENSKTPQNSADCTYNLSSSTLTSTQYNHKEYTCKVTQGTTSVVQSFNRGDC
* (SEQ ID NO: 200)

A11B1_3B1 Heavy Chain

METGLRWLLLVAVLKGVQCQEQLLEESGGGLVKPEGSLTLTCKASGFDLSSGYDMCWV
RQAPGKGLEWIACIYADYSGSTYYASWVNGRFTISSSTSLNTVDLKMSTLTAADTATYF
CARGATNGGGYGYFNLWGPGLTVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVK
GYLPEPVTVTWNSGTLTNGVRTFPSVRQSSGLYSLSSVSVTSSSQPVTCNVAHPATNT

KVDKTVAPSTCSKPMCPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEV
QFTWYINNEQVRTARPPLEQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIE
KTISKARGQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWENGKAEDNYKT
TPTVLDSDGSYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ
ID NO: 201)

A11B1_3B1 Light Chain

MDTRAPTQLLGLLLLWLPGARCAIVMTQTPASVSEPVGGTVTIKCQASQNINSGLAWY
QQKPGQPPKLLIYKASTLASGVSSRFKSGSGTEFTLTISDLECAATYYCQTYYYSSS
SSDNAFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVD
GTTQTGTIENSKTPQNSADCTYNLSSTLTLTSTQYNHKEYTCKVTQGTTSVVQSFNRGD
C* (SEQ ID NO: 202)

A11B1_2D3 Heavy Chain

METGLRWLLLVAVLKGVQCQSLEESGGDLVKPGASLTLTCTASGFSFSSSYWICWVRQ
APGKGLEWIAICYGGSSGNIA YASWAKGRFTISKTSSTTVTLQMTSLTAADTATYFCAR
DIPSDAFTLDLWGPGLTVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLPEPVT
VTWNSGTLTNGVRTFPSVRQSSGLYSLSSVSVTSSSQPVTCNV AHPATNTKV DKT VAP
STCSKPMCPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNE
QVRTARPPLEQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQ
PLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWENGKAEDNYKTTPTVLDSDG
SYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO: 203)

A11B1_2D3 Light Chain

MDTRAPTQLLGLLLLWLPGATFAQVLTQTPSSVSAAVGSTVTINCQASQSVYKDNLA
WYQQKPGQPPKLLIYKASTLASGVPSRFKSGSGTQFTLTISGVQCEDAATYYCQGEFS
CGSADCIAFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWE
VDGTTQTGTIENSKTPQNSADCTYNLSSTLTLTSTQYNHKEYTCKVTQGTTSVVQSFNR
GDC* (SEQ ID NO: 204)

A11B1_2A7 Heavy Chain

METGLRWLLLVAVLKGVQCQSLEESGGDLVKPGASLTLTCKGSGIDFSSGYGMWWVR
QAPGKLEYIGYIDTGYGSTYYASWAKGRFTISKTSSTTVTLQMTSLTVADTATYFCAK
GGAILDWGPGLTVTVSSGQPKAPSVFPLAPCCGDTSPSTVTLGCLVKGYLPEPVTVTWN
SGTLTNGVRTFPSVRQSSGLYSLSSVSVTSSSQPVTCNV AHPATNTKV DKT VAPSTCSK
PMCPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRT
ARPPLEQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEP
KVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWENGKAEDNYKTTPTVLDSDGSYF
LYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (SEQ ID NO: 205)

A11B1_2A7 Light Chain

MDTRAPTQLLGLLLLWLPGATFAAVLTQTPASTSAAVGGTVTINCQSSQSVYRSNWLA
WYQQKPGQPPKLLIYDVFNLASGVPSRFKSGSGTQFTLTISGVQCADAATYYCQGSYY
SGNWYSAFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWE
VDGTTQTGTIENSKTPQNSADCTYNLSSTLTLTSTQYNHKEYTCKVTQGTTSVVQSFNR
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	MNWVRQAPGKGLEWVSY (SEQ ID NO: 210)
Heavy Chain CDR2	ISSSGSTV (SEQ ID NO: 211)
Heavy Chain FR3	YYADSVKGRFTISRDNAKNSLYLQMNSLRDEDTAVYYCAS (SEQ ID NO: 212)
Heavy Chain CDR3	GQLDTSDAFDI (SEQ ID NO: 213)
Heavy Chain FR4	WGQGTLLTVSS (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	SLQSGVPSRFGSGSGTDFTLTISSLQPEDFATYYC (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	YYADSVKGRFTISRDNKAENSLYLQMNSLRAEDTAVYYCAR (SEQ ID NO: 226)
Heavy Chain CDR3	DLGHFDSGSSYFDY (SEQ ID NO: 442)
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	QGISNY (SEQ ID NO: 228)
Light Chain FR2	LAWYQQKPGKVPKLLIY (SEQ ID NO: 229)
Light Chain CDR2	AAS (SEQ ID NO: 218)
Light Chain FR3	TLQSGVPSRFGSGSGTDFTLTISSLQPEDFATYYC (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	ISSSSTI (SEQ ID NO: 233)
Heavy Chain FR3	YYADSVKGRFTISRDNKNSLYLQMNSLRDEDTAVYYCAS (SEQ ID NO: 212)
Heavy Chain CDR3	GQXDXSDAFDI (SEQ ID NO: 234)
Heavy Chain FR4	WGQGTLVTVSS (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	SLQSGVPSRFGSGSGTDFLTISLQPEDXATYYC (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: 436)
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	ATRYDILTGYS DGVDYFDY (SEQ ID NO: 240)
Heavy Chain FR4	WGQGTLVTVSS (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	SLQSGVPSRFGSGSGTDFLTISLQPEDFATYYC

	(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: 437)
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	WGRGTLTVTVSS (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	QSYSTPLT (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: 438)
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	WGRGTLTVTVSS (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	QSTDSSGTYQV (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	QVQLVQSGAEVKKPGASVKVSKAS (SEQ ID NO: 263)
Heavy Chain CDR1	GYTFTSYG (SEQ ID NO: 439)
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	WGQGTMTVTVSS (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	SLESGVPSRFSGSGSGTEFTLTISLQPDDFAVYYC (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: 440)
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	WGRGTLTVTVSS (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: 440)
Heavy Chain FR2	MHWVRQAPGKGLEWVAV (SEQ ID NO: 286)
Heavy Chain CDR2	ISYDGSNK (SEQ ID NO: 287)
Heavy Chain FR3	YYADSVKGRFAISRDN SKNTLYLQMNSLRAEDTAVYYCAR (SEQ ID NO: 288)
Heavy Chain CDR3	DRDVGPTYYYYGMDV (SEQ ID NO: 289)
Heavy Chain FR4	WGQGTMTVTVSS (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	lamdba

2004_03_G10

Heavy Chain FR1	EVQLLES GGGVVPGRSLRLSCAAS (SEQ ID NO: 232)
Heavy Chain CDR1	GFTFSSYA (SEQ ID NO: 440)
Heavy Chain FR2	MSWVRQAPGKGLEWVSA (SEQ ID NO: 274)
Heavy Chain CDR2	ISGSGGST (SEQ ID NO: 275)
Heavy Chain FR3	YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAK (SEQ ID NO: 295)
Heavy Chain CDR3	DREYIAVAADY (SEQ ID NO: 296)
Heavy Chain FR4	WGQGTTVTVSS (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	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

2002_02_B05

Heavy Chain FR1	EVQLLESGGGVVQPGRSLRLSCAAS (SEQ ID NO: 232)
Heavy Chain CDR1	GFTFSTYG (SEQ ID NO: 436)
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	ATRYDILTGYS DGVDYFDY (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	SLQSGVPSRFSGSGSGTDFLTISLQPEDFATYYC (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: 441)
Heavy Chain FR2	MHWVRQAPGQGLEWMGI (SEQ ID NO: 303)
Heavy Chain CDR2	INPSGGST (SEQ ID NO: 304)
Heavy Chain FR3	IYAQKFQGRVTMTRDTSTSTVYMELSSLRSED TAVYYCAR (SEQ ID NO: 305)
Heavy Chain CDR3	SLRDGYNYIGSLGY (SEQ ID NO: 306)
Heavy Chain FR4	WGQGTLLTVSS (SEQ ID NO: 214)
Heavy Chain V Gene Segment	IGHV1-46
Light Chain FR1	QSELTQPPSASGTPGQRVTISCSGS (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	QRPSGVPDRFSGSGSGTSASLAIRGLQSEDEAGYYC (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	YYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAG (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	NLETGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC (SEQ ID NO: 317)
Light Chain CDR3	QOSYHTPYT (SEQ ID NO: 318)
Light Chain FR4	FGQGTKVEIK (SEQ ID NO: 272)
Light Chain Locus	kappa

1994_01_A09

Heavy Chain FR1	QMQLVQSGAEVKKPGSSVKVCKAS (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	NYAQKFQGRVTITADKSTSTAYMELSSLRSEDVAVYYCAR (SEQ ID NO: 323)
Heavy Chain CDR3	DINRYNWNFRAFDI (SEQ ID NO: 324)
Heavy Chain FR4	WGQGTLLTVSS (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	TRESGVPDRFSGNGSGTDFTLTISSLQAEDVAAYYC (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	QVQLVQSGAEVKKPGSSVKVSCAS (SEQ ID NO: 330)
Heavy Chain CDR1	GYTFTSYG (SEQ ID NO: 439)
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	SLQSGVPSRFSGSGSGTDFTLTISLQPEDAATYYC (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	EVQLVESGGGVVQPGRSLRLSCAAS (SEQ ID NO: 335)
Heavy Chain CDR1	GFTFSSYA (SEQ ID NO: 440)
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	VSWYQQHPGKAPKLMYI (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)
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Heavy Chain CDR1	GFTFSSYA (SEQ ID NO: 440)
Heavy Chain FR2	MSWVRQAPGKGLEWVSA (SEQ ID NO: 274)
Heavy Chain CDR2	ISGSGGST (SEQ ID NO: 275)
Heavy Chain FR3	YYADSVKGRFTISRDN SKNALYLQMNSLRAEDTAVYYCRG (SEQ ID NO: 347)
Heavy Chain CDR3	YCSSTSCYGRRGAFDI (SEQ ID NO: 348)
Heavy Chain FR4	SGQGTLVTVSS (SEQ ID NO: 349)
Light Chain FR1	QAVLTQPPSASGTPGQRTVITSCSGR (SEQ ID NO: 350)
Light Chain CDR1	NSNIGSNN (SEQ ID NO: 351)
Light Chain FR2	VNWYQHLPGTAPKLLIY (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	QVQLVESGGGLVQP GGSRLRLSCAAS (SEQ ID NO: 243)
Heavy Chain CDR1	GFTFSSYW (SEQ ID NO: 437)
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	WGQGTITVTVSS (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	TLQGGVPSRFSGSGSGTDFLTITSLQPEDFATYYC (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	EVQLVESGGGVVQPGRSLRLSCAAS (SEQ ID NO: 335)
Heavy Chain CDR1	GFTFSSYA (SEQ ID NO: 440)
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	WGQGTITVTVSS (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: 443)
Light Chain CDR3	SSYANNPWV (SEQ ID NO: 369)
Light Chain FR4	FGGGTKVTVLG (SEQ ID NO: 370)
Light Chain Locus	lambda

2002_02_E01

Heavy Chain FR1	QVQLVQSGAEVRKPGASVKVCKAS (SEQ ID NO: 371)
Heavy Chain CDR1	GYTFTSYG (SEQ ID NO: 439)
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	NLETGVPSRFSGSGSGTDFTFTISSLPEDIATYYC (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	QSISSF (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: 440)
Heavy Chain FR2	MHWVRQAPGKGLEWVAV (SEQ ID NO: 286)
Heavy Chain CDR2	ISYDGSNK (SEQ ID NO: 287)
Heavy Chain FR3	YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR (SEQ ID NO: 276)
Heavy Chain CDR3	DKELSY (SEQ ID NO: 385)
Heavy Chain FR4	WGQGT LTVSS (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	NRPSGVPDRFSGSKSGNTASLTISGLQAEDEADYYC (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	YYADSVKGRFTISRDN AKNSLYLQMNSLRDEDTAVYYCAS (SEQ ID NO: 212)
Heavy Chain CDR3	GQLDTSDAFDI (SEQ ID NO: 213)
Heavy Chain FR4	WGQGT TTVSS (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	KTS (SEQ ID NO: 389)
Light Chain FR3	NLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC (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: 440)
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	DRPYSYGKNDAFDI (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	SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC (SEQ ID NO: 219)
Light Chain CDR3	QSYSTPLT (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	GYTFTSY (SEQ ID NO: 396)
Heavy Chain FR2	MHWVRQAPGQGLEWMGI (SEQ ID NO: 303)
Heavy Chain CDR2	INPSGGST (SEQ ID NO: 304)
Heavy Chain FR3	SYAQKFQGRVTMTTRDTSTSTVYMELSSLRSEDTAVYYCAR (SEQ ID NO: 397)
Heavy Chain CDR3	SPWLITFGGVAMGY (SEQ ID NO: 402)
Heavy Chain FR4	WGQGTTLTVSS (SEQ ID NO: 214)
Light Chain FR1	QSVLTQPPSASGTPGQRTVISCSS (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: 439)
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	WGQGTTLTVSS (SEQ ID NO: 214)
Light Chain FR1	DIVMTQSPSSLSASVGDRVTITCRAS (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	NLETGVPSRFSGSGSGTDFLTISLQPEDFATYYC (SEQ ID NO: 317)
Light Chain CDR3	QQFNYYPLT (SEQ ID NO: 408)
Light Chain FR4	FGGGTKLEIK (SEQ ID NO: 394)
Light Chain Locus	kappa

1997_02_B03

Heavy Chain FR1	QVQLVESGAIEVKKPGASVKVSKAS (SEQ ID NO: 409)
Heavy Chain CDR1	GYTFTSY (SEQ ID NO: 396)
Heavy Chain FR2	MHWVRQAPGQGLEWMGI (SEQ ID NO: 303)
Heavy Chain CDR2	INPSGGST (SEQ ID NO: 304)
Heavy Chain FR3	SYAQKFQGRVTMTTRDTSTSTVYMELSSLRSEDATVYYCAR (SEQ ID NO: 397)
Heavy Chain CDR3	AGGYYYMDV (SEQ ID NO: 398)
Heavy Chain FR4	WGQGTLLTVSS (SEQ ID NO: 214)
Light Chain FR1	QSGLTQPPSASGTPGQRTISCSGS (SEQ ID NO: 399)
Light Chain CDR1	GPNIQNNY (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
YSPSFQGGFIFSLDTSINTTYLQWSSLKASDTAIYFCTRLGTGNTKGFAYWGQGTITVTS
S (SEQ ID NO: 413)

Humanized 79E3E3 Light Chain Variable Region

DIQITQSPSSLSASLGDKVTITCRSSQSLYSENNDYLAQYQQKPGKAPKLLIYGASNL
QSGVPSRFSGRGSGTDFLTISLQPEDFATYYCEQTYRYPFTFGPGTKVDIKR (SEQ ID
NO: 414)

Humanized 9-G05 Heavy Chain VH_1

Leader sequence-VH-hIgG1CH-Stop codon*

MGWSCILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSKASGYTFPDYNMDWVR
QAPGQRLEWMGYINPDNGGTIYNQKFKGRVTLTVDTASTAYMELSSLRSEDATVYYC
ARLDSSGYGYAMDYWGQGTSTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGLVKD

YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK
PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV
VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNG
KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
HEALHNHYTQKSLSLSPGK* (SEQ ID NO: 415)

Humanized 9-G05 Heavy Chain VH_2

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

MGWSCILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFPDYNMDWVR
QAPGQRLEWIGYINPDNGGTIYNQKFKGRVTLTVDTASTAYMELSSLRSEDTAVYYCA
RLDSSGYGYAMDYWGQGTSTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS
NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGK
EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE
ALHNHYTQKSLSLSPGK* (SEQ ID NO: 416)

Humanized 9-G05 Heavy Chain VH_3

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

MGWSCILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFPDYNMDWVR
QAPGQRLEWIMGYINPDNGGTIYNQKFKGRATLTVDTSASTAYMELSSLRSEDTAVYYC
ARLDSSGYGYAMDYWGQGTSTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK
PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV
VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNG
KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
HEALHNHYTQKSLSLSPGK* (SEQ ID NO: 417)

Humanized 9-G05 Heavy Chain VH_4

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

MGWSCILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFPDYNMDWVR
QAPGQSLEWIGYINPDNGGTIYNQKFKGRATLTVDTSASTAYMELSSLRSEDTAVYYCA
RLDSSGYGYAMDYWGQGTSTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS
NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGK
EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE
ALHNHYTQKSLSLSPGK* (SEQ ID NO: 418)

Humanized 9-G05 Light Chain VL_1

Leader sequence-VL-hIgKCL-Stop codon*

**MGWSCILFLVATATGVHSDIVMTQSPDSLAVSLGERATINCRASESVDNYGISFMHWY
QQKPGQPPKLLIYRASNLDSGVPDRFSGSGSGTDFTLTISSLQAEDVATYYCQQSYKDPR
TFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN
RGE*** (SEQ ID NO: 419)

Humanized 9-G05 Light Chain VL_2

Leader sequence-VL-hIgKCL-Stop codon*

**MGWSCILFLVATATGVHSDIVLTQSPASLA VSPGQRATITCRASESVDNYGISFMHWYQ
QKPGQPPKLLIYRASNLDSVDPARFSGSGSRDFTLTINPVEANDTATYYCQQSYKDPR
TFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN
RGE*** (SEQ ID NO: 420)

16E10 Heavy Chain Variable Region

**QSLEESGGDLVKPGASLTLCRVSGFSFSSSYMCWVRQAPGKGLEWVSCIGTTRGSTY
YATWAKGRFTISKISSTTVTLQMTSLTDADTATYFCARDATGYRINTIGLYFNLWGPGTL
VTVSS** (SEQ ID NO: 421)

Humanized 16E10 Heavy Chain Variable Region VH_1

**QSLLESGGGLVKPGSLRLSCAVSGFSFSSSYMCWVRQAPGKGLEWVSCIGTTRGSTY
YADSAKGRFTISKISKNTVYLQMTSLRAEDTAVYFCARDATGYRINTIGLYFNLWGPGT
LTVSS** (SEQ ID NO: 422)

Humanized 16E10 Heavy Chain Variable Region VH_2

**EVQLLESGGGLVKPGSLRLSCAVSGFSFSSSYMCWVRQAPGKGLEWVSCIGTTRGST
YYADSAKGRFTISKDNSKNTVYLQMTSLRAEDTAVYFCARDATGYRINTIGLYFNLWG
QGTLVTVSS** (SEQ ID NO: 423)

Humanized 16E10 Heavy Chain Variable Region VH_3

**QSLLESGGGLVKPGSLRLSCAVSGFSFSSSYMCWVRQAPGKGLEWVSCIGTTRGSTY
YADSAKGRFTISKESKNTVYLQMSSLRAEDTAVYFCARDATGYRINTIGLYFNLWGPGT
LTVSS** (SEQ ID NO: 424)

Humanized 16E10 Heavy Chain Variable Region VH_4

**EVQLLESGGGLVKPGSLRLSCAVSGFSFSSSYMCWVRQAPGKGLEWVSCIGTTRGST
YYADSAKGRFTISKDNSKNTVYLQMSSLRAEDTAVYFCARDATGYRINTIGLYFNLWG
QGTLVTVSS** (SEQ ID NO: 425)

Humanized 16E10 Heavy Chain Variable Region VH_5

**QSLLESGGGLVKPGSLRLSCAVSGFSFSSSYMCWVRQAPGKGLEWVSCIGTTRGSTY
YADSAKGRFTISKESKNTVYLQMSSLRAEDTAVYFCARDATGYRIQTIGLYFNLWGPGT
LTVSS** (SEQ ID NO: 426)

Humanized 16E10 Heavy Chain Variable Region VH_6

EVQLLES G GGLVKPGGSLRLSCA VSGFSFSSSYMCWVRQAPGKGLEWVSCIGTTRGST
YYADSAKGRFTISKDNSKNTVYLQMSSLRAEDTAVYFCARDATGYRIQTIGLYFNLWG
QGTLVTVSS (SEQ ID NO: 427)

16E10 Light Chain Variable Region

ELTQTPSSVEAAVGGTPTIKCQASQTIYSYLSWYQQKPGQPPKLLIYEASKLASGVPSRFS
GSGSGTDYTLTISDLECA DAATYYCQSYHGTASTEYNTFGGGTEVVVK (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

[0149] 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: 103-443.
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 413-443.
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 312-443.
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 413-443.
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 chronic kidney disease, 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 chronic kidney disease is or comprises Primary Glomerular Disease (including, but not limited to, IgA Nephropathy and focal segmental glomerular sclerosis), Secondary Glomerular Disease (including, but not limited to, lupus nephritis), Thrombotic Microangiopathy, Tubulointerstitial Diseases (including, but not limited to, Obstructive Uropathy), Diabetic Nephropathy, Hypertensive Nephropathy, Ischemic Nephropathy, Cardiorenal Syndromes in CKD, Inherited Disorders of the Glomerulus (including, but not limited to, Alport syndrome), Cystic Diseases of the Kidney (including, but not limited to, Polycystic Kidney Disease), or Inherited Disorders of the Renal Tubule.
19. The method of claim 17 or 18, wherein administering the therapeutically effective amount of the antibody, or antigen-binding fragment thereof results in a reduction in a measured marker, sign and/or symptom by at least about 10%, 15%, 20%, 25%, 30%, 35%, 40%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85% or 90% relative to a control.
20. The method of claim 19, wherein the control comprises a level of measured marker, sign and/or symptom in the subject prior to administration of the antibody.
21. The method of claim 19, wherein the control comprises a level of measured marker, sign and/or symptom in a subject suffering from the kidney-related disorder.
22. The method of claim 19, wherein the control comprises an average level of measured marker, sign and/or symptom in a population of subjects suffering from the kidney-related disorder.

23. The method of any one of claims 19-22, wherein the measured marker, sign and/or symptom is or comprises: COL1A1, Fibronectin, PAI-1, IL-11, CXCL1, MCP-1, IL-6, TIMP-1, Hyaluronic acid, TGF β , CTGF, PDGF, MMP9, or a combination thereof.