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(54) **Title:** ANTIBODIES AGAINST INTEGRIN ALPHA 11 BETA 1

(57) **Abstract:** The present disclosure includes antibodies that specifically bind integrin alpha 11 beta 1 (α11β1), as well as methods of making and using such antibodies.

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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-α11β1 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-α11β1 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-α11β1 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-α11β1 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-α11β1 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-α11β1 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-α11β1 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-α11β1 antibody, or antigen-binding fragment thereof, is a monoclonal antibody, or antigen-binding fragment thereof. In some embodiments, an anti-α11β1 antibody, or antigen-binding fragment thereof, is a humanized antibody, or antigen-binding fragment thereof. In some embodiments, an anti-α11β1 antibody, or antigen-binding fragment thereof, reduces interaction of α11β1 with collagen in human α11β1-expressing cells. In some embodiments, an anti-α11β1 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, TGFβ, 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 α11β1.

[0015] **Figure 2B** shows a chart illustrating an exemplary ELISA analysis of binding of mouse monoclonal antibodies to mouse α11β1.

[0016] **Figure 3A** shows a graph illustrating an ELISA analysis of binding of exemplary rat monoclonal antibodies to a human α11β1 I domain.

[0017] **Figure 3B** shows a graph illustrating an ELISA analysis of binding of exemplary mouse monoclonal antibodies to a human α11β1 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 α11β1.

[0019] **Figure 4B** shows a graph illustrating an FACS analysis of binding of exemplary mouse monoclonal antibodies to CHO-K1 cells expressing human α11β.

[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 α11 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 α11 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 α11 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 αSMA 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 αSMA 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 αSMA upregulation.

[0027] **Figure 8** shows graphs illustrating the ability of exemplary monoclonal antibodies to inhibit CHO-K1 human α11-mediated rat tail type I collagen gel contraction.

[0028] **Figure 9** shows graphs illustrating the affinity of exemplary monoclonal antibodies for human α11β1 via surface plasmon resonance (SPR).

[0029] **Figure 10A** and **Figure 10B** show graphs illustrating the affinity of exemplary monoclonal antibodies for human α11β1 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 α11β1 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 α11β1 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 α11 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 Col1a1 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 α11β1. 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 anfd, 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 α11 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 α1β1, α2β1, α10β1, and α11β1 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 (Mg2+) 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. α11β1 integrin is specifically expressed on a subset of fibroblasts and myofibroblasts (i.e., terminal scar producing cells). Recent literature has provided strong evidence that α11β1 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 α11β1 function may inhibit myofibroblast differentiation and extracellular matrix deposition (i.e., the major event in scar formation) and blocking α11β1 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-α11β1 antibody, or antigen-binding fragment thereof, of the present disclosure reduces interaction of α11β1 with collagen in human α11β1-expressing cells. In some embodiments, reducing interaction of α11β1 with collagen in human α11β1-expressing cells comprises an anti-α11β1 antibody, or antigen-binding fragment thereof, interacting with α11β1 that is in a resting, low affinity state (bent conformation). In some embodiments, reducing interaction of α11β1 with collagen in human α11β1-expressing cells comprises an anti-α11β1 antibody, or antigen-binding fragment thereof, interacting with α11β1 that is in an extended, intermediate affinity state. In some embodiments, reducing interaction of α11β1 with collagen in human α11β1-expressing cells comprises an anti-α11β1 antibody, or antigen-binding fragment thereof, interacting with α11β1 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 (α11β1) antibody, or antigen-binding fragment thereof. In some embodiments, an α11β1 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-α11β1 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-α11β1 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-α11β1 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-α11β1 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-α11β1 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-α11β1 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-α11β1 antibody, or antigen-binding fragment thereof, is a monoclonal antibody, or antigen-binding fragment thereof. In some embodiments, an anti-α11β1 antibody, or antigen-binding fragment thereof, is a humanized antibody, or antigen-binding fragment thereof. In some embodiments, an anti-α11β1 antibody, or antigen-binding fragment thereof, reduces interaction of α11β1 with collagen in human α11β1-expressing cells. In some embodiments, the present disclosure provides an anti-α11β1 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-α11β1 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-α11β1 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-α11β1 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-α11β1 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-α11β1 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 chai 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-α11β1 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-α11β1 antibody, or antigen-binding fragment thereof, wherein the anti-α11β1 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 α11β1. In some embodiments, the present disclosure provides an anti-α11β1 antibody, or antigen-binding fragment thereof, comprising between 1 and 30 additions, deletions, or substitutions relative to an anti-α11β1 antibody, or antigen-binding fragment thereof, wherein the anti-α11β1 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 α11β1. In some embodiments, the present disclosure provides an anti-α11β1 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 α11β1. In some embodiments, the present disclosure provides an anti-α11β1 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 α11β1.

[0063] In some embodiments, the present disclosure provides an anti-α11β1 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-α11β1 antibody, or antigen-binding fragment thereof, wherein the anti-α11β1 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 α11β1. In some embodiments, the present disclosure provides an anti-α11β1 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 α11β1.

[0064] In some embodiments, the disclosure provides an antibody or fragment thereof that selectively binds α11β1, 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 α11β1, 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 α11β1, 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 α11β1, 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-α11β1 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 α11β1

[0070] The binding properties of an antibody described herein to α11β1 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 α11β1 can be analyzed using surface plasmon resonance (SPR). SPR or Biomolecular Interaction Analysis (BIA) detects bio-specific interactions in real time, without labeling any of the interactants. Changes in the mass at the binding surface (indicative of a binding event) of the BIA chip result in alterations of the refractive index of light near the surface. The changes in the refractivity generate a detectable signal, which are measured as an indication of real-time reactions between biological molecules. Methods for using SPR are described, for example, in U.S. Pat. No. 5,641,640; Raether (1988) Surface Plasmons Springer Verlag; Sjolander and Urbaniczky (1991) Anal. Chem. 63:2338-2345; Szabo et al. (1995) Curr. Opin. Struct. Biol. 5:699-705 and on-line resources provide by BIAcore International AB (Uppsala, Sweden). Additionally, a KinExA® (Kinetic Exclusion Assay) assay, available from Sapidyne Instruments (Boise, Id.) can also be used.

[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 α11β1. 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 α11β1. In various embodiments, K_D of an antibody as described herein for α11β1 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 α11β1 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-α11β1 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-α11β1 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-α11β1 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-α11β1 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, TGFβ, CTGF, PDGF, and MMP9. In some embodiments, upon administration to a subject, an anti-α11β1 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-α11β1 antibody described herein reduces levels of COL1A1, IL-6, TIMP-1, Hyaluronic acid, TGFβ, 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-α11β1 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, mytomycin C, plicamycin, and dactinomycin), taxanes (e.g., paclitaxel and docetaxel), antimetabolites (e.g., 5-fluorouracil, cytarabine, premetrexed, thioguanine, floxuridine, capecitabine, and methotrexate), nucleoside analogues (e.g., fludarabine, clofarabine, cladribine, pentostatin, and nelarabine), topoisomerase inhibitors (e.g., topotecan and irinotecan), hypomethylating agents (e.g., azacitidine and decitabine), proteosome inhibitors (e.g., bortezomib), epipodophyllotoxins (e.g., etoposide and teniposide), DNA synthesis inhibitors (e.g., hydroxyurea), vinca alkaloids (e.g., vicristine, 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, bicaluatmide, granisetron, and flutamide), aromatase inhibitors (e.g., letrozole and anastrozole), arsenic trioxide, tretinoin, nonselective cyclooxygenase inhibitors (e.g., nonsteroidal anti-inflammatory agents, salicylates, aspirin, piroxicam, ibuprofen, indomethacin, naprosyn, diclofenac, tolmetin, ketoprofen, nabumetone, and oxaprozin), selective cyclooxygenase-2 (COX-2) inhibitors, or any combination thereof.

[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-OOl, 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-α11β1 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-α11β1 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-α11β1 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-α11β1 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^{TM}, 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 $CaPO_4$ 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 LD_{50} (the dose lethal to 50% of the population) and the ED_{50} (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 LD_{50}/ED_{50}. 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 ED_{50} 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 IC_{50} (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 α11β1

Rat Immunization

[0111] Wistar rats were immunized with recombinant human α11β1 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 α11β1. Positive clones were counter-screened against human α1β1, α2β1 and α10β1. Clones that specifically bound to human and mouse α11β1 and did not bind to α1β1, α2β1 and α10β1 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 α11β1 protein. Splenocytes from the immunized rabbits were sorted and selected against human β1, in order to reduce the number of β1-specific B cell clones. Sorted splenocytes were then cultured for approximately 1 week and culture supernatants were screened for binding to human α11β1. 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 α11β1, mouse α11β1 and tolerance breaking protein. Plasma titers were evaluated by

ELISA against a mixture of human and mouse α11β1. Popliteal, inguinal, and iliac lymph nodes were collected. ELISA-positive anti-human/mouse α11β1 hybridomas were expanded and subjected to a secondary screen against human and mouse α11β1, control HIS protein, and a counter-screen was performed against human α11β1, α2β1 and α10β1. 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 α11β1 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-α11β1 antibodies. Fully human anti-α11β1 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 α11β1 antigen as well as deselection against α10β1, to enrich for α11 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 μg/mL of target antigen (recombinant human or mouse α11β1) 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 α11) 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/cm^2 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 TGFβ-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 Inactived Fetal Bovine Serum (Gibco) for 30 minutes at 4°C. Cells were then incubated with anti-α11 antibodies at the doses described in each figure for 30 minutes at 4°C. A human anti-α11 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-α11 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 α11β1 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 α11β1 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 α11β1. 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 α11β1 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 house at room temperature. After washing the plate with PBS, cell and antibody mixture was added to the wells and the plate was places 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 TGFβ-1 (R&D Systems) with or without anti-α11 antibodies. A polyclonal rabbit anti-human α11 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-αSMA (α-smooth muscle actin) (Invitrogen). Cells were acquired on a FACS Verse (Benton Dickson) to determine expression levels of αSMA. 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 α11 were harvested and resuspended at $1.25x10^6$ 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 400µL 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 $2.5x10^6$ 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 µL/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 ($5x10^6$ cells/mouse) subcutaneously in the flank. Once tumor volume reached ~$100mm^3$, animals were randomized amongst 7 groups of 8 mice each. Mice were then treated intraperitonealy 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 α11β1 and Determination of Binding Affinity

[0127] Antibody discovery was performed by immunizing rats and rabbits with recombinant human α11β1, and by immunizing mice with both human and mouse α11β1. 51 novel anti-human α11β1 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 α11β1 are shown in **Figure 2A**. Three of those mAbs also bound to mouse α11β1, as shown in **Figure 2B**.

[0129] Data was also collected to determine whether antibodies of interest bind to the I domain of α11β1. An in-house generated I domain of α11β1 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 α11β1 I domain. **Figures 3A** and **3B** show graphs illustrating binding data from exemplary mAbs.

[0130] α11β1 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 α1β1, α2β1 and/or α10β1. **Table 2** includes results of cross-reactivity to the other receptors.

Table 2. Data summary of tested monoclonal antibodies

	Clone ID	Human α11β1 ELISA	Murine α11β1 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 (α10β1)	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 α11β1. A CHO-K1 cell line that endogenously expressed high levels of the β1 subunit was engineered to stably express human α11 (CHO-K1 hu α11).

[0132] **Figures 4A** and **4B** show selected rat and mouse mAbs that bound human α11β1 (as tested by ELISA) and also demonstrated binding ability to α11β1 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 α11β1 expressed on the surface of CHO cells. Additionally, **Figure 14** shows selected fully human mAbs that demonstrated binding ability to α11β1 expressed on the surface of CHO cells. However, as shown in **Table 1**, there were several mAbs that were shown to bind α11β1 by ELISA, but did not bind cell-expressed α11β1.

[0133] Binding EC_{50} was estimated using data from Fluorescence-activated cell sorting (FACS) performed with CHO-K1 hu α11β1 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 EC50 for mouse mAbs

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

[0134] As shown in **Figure 9**, when antibodies 16E10, 79E3E3, 9G05 and 1994_01_C07 were tested for their affinity to human α11β1 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 α11β1, which indicates that both might act as allosteric inhibitors by not binding to the ligand binding domain but still inhibiting α11β1 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 α11β1 Headpiece and α11β1 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 TGFβ treatment were used to induce a fibroblast-to-myofibroblast transition (FMT), giving rise to myofibroblasts (MF). While HPFs do not express α11β1, significant expression of α11β1 is exhibited by MFs. Additionally, HPFs express α1β1 and α2β1, 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 α11β1

[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-α11β1 antibodies to inhibit the fibroblast-to-myofibroblast transition. Typical functional inhibitors of a receptor block ligand binding, and while preventing the binding of α11β1 to type I collagen is a desired feature of anti-α11β1 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 α11β1 in a way that affects the structure of α11β1 in a way that prevents inside-out signaling and FMT, but does not affect the ability of α11β1 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 α11 cell line was used to assess the ability of mAbs to block α11β1-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 α11 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 (α1β1,

α2β1 and α10β1). 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 α11β1 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-α11 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-α11β1 mAbs were found to strongly bind human α11β1 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 α11β1) was found to not be necessary for blocking the interaction of α11β1 with type I collagen.

[0138] In addition to the binding abilities described above, it is important for an anti-α11β1 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. TGFβ is one of the potent factors that potentiates this process and alpha smooth muscle actin (αSMA) is one of the main markers that becomes overexpressed when fibroblasts are undergoing the transition to becoming myofibroblasts. The presence of αSMA enhances fibroblast contraction and guides myofibroblast activation through an intracellular feedback loop. Because αSMA is the main molecular marker of myofibroblasts, the ability of the novel anti-α11β1 mAbs to inhibit αSMA expression in TGFβ-induced FMT was tested.

[0139] As shown in **Figure 7A**, two rat mAbs (40G10H11 and 24E4G6) significantly inhibited αSMA 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 αSMA expression (a surrogate for myofibroblast generation). As shown in **Figure 7B**, two rabbit mAbs significantly inhibited αSMA 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 αSMA 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 αSMA 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 α11β1-mediated, and a more recent study showed that α11β1-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 α11-mediated collagen gel contraction. Of note, CHO-hu α11 cells were able to contract collagen gel without the addition of TGFβ, 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 α11 knockout SCID mice to be significantly impeded compared to wild-type mice. In this example, studies were performed to determine if inhibition of α11β1 function with mAb results in xenograft growth inhibition. As shown in **Figure 16** and **Table 4**, blocking α11β1 on mouse CAFs impeded xenograft growth in SCID mice. Specifically, 79E3E3, an effectorless mAb that cross-reacts with mouse α11β1, significantly inhibited tumor growth compared to isotype control, while 16E10, a mAb that does not bind mouse α11β1, showed no significant inhibition of tumor growth. Inhibition of tumor-expressed α11β1 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-α11β1 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-α11-β1 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-α11β1 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-α11β1 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, TGFβ, CTGF, PDGF, and MMP9) and also at the transcriptional level (including, but not limited to, COL1A1, IL-6, TIMP-1, Hyaluronic acid, TGFβ, CTGF, aSMA, 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-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.

[0147] As shown in **Figures 18A-18C**, for each anti-α11-β1 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-α11β1 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-α11β1 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-α11β1 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

*ATGGATTGGTTGTGGAACTTGCTATTCCTGATGGTAGTTGCCCAAAGTGCTCAAGCA*CAG
ATCCAGTTGGTACAGTCTGGACCTGAAGTAAAGAAGCCTGGAGAGTCAGTGAAGAT
CTCCTGCAAGGCCTCTGGGTATACCTTCACA**GACTATGCAATGAAC**TGGGTGAAAC
AGGCTCCAGGAAATGGCCTGAAGTGGATGGGC**TGGATCAACACCCAAACTGGAAA**
GCCAACATATGCGGATGATTTCAAACAACGGTTTGTCTTCTCTTTGGAAACTTCTG
CCAGAACTACATATTTGCAGATCAACAACCTCAATATTGAAGACACAGCTACATATT
TCTGTACGAGA**TTGGGTACAGGTAATACGAAGGGGTTTGCTTAC**TGGGGCCAAG
GCACTCTGGTCACTGTCTCTTCA (**SEQ ID NO: 1**)

79E3E3 Light Chain Variable Region

*ATGGAATCACAGACGCATGTCCTCATTTCCCTTCTGCTCTGTGTATCAGGTACCTGTGGG*G
ACATTTTGATAAACCAGTCTCCAGCCTCTCTGACTGTGTCAGCAGGAGAGAGGGTCA
CTATGAGCTGC**AAGTCCAGTCAGAGTCTTCTATACAGTGAAAACAACCAGGACT**
ATTTGGCTTGGTACCAGCAGAAACCAGGACAGTTTCCTAAATTGCTTATCTAT**GGG**
GCATCCAACCGGCACACTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGA
CAGACTTCACTCTGACCATCAGCAGTGTGCAGGCTGAAGACCTGGCTGATTATTATT
GT**GAGCAGACCTACAGATATCCATTCACG**TTCGGCTCAGGGACGAAGTTGGAAAT
AAAA (**SEQ ID NO: 2**)

24E4G6 Heavy Chain Variable Region

*ATGGAGTTGGAATTGAGCTTAATTTTTATTTTTTCTCTTTTAAAAGATGTCCAGTGT*GAAGT
ACAGCTGGTGGAGTCTGGAGGAAGCTTGGTTCAACCTGGGGGTTCTCTGAAACTCTC
CTGTGTAGCCTCAGGATACACTTTCAGT**AACTACTGGATGGAC**TGGGTTCGGCAGT
CTCCTGGAAAGTCCCTGGAATGGATTGGA**GAGATTAACACGGATGGCAGAAGGAC**
CAACTATGCACCATCCATAAAGGATCGATTCACAATCTCCAGAGACAATGCCAAG
AGCACCCTGTATCTGCAGATGAGCAATGTGAAATCAGATGACACAGCCATTTATTAC
TGTACCATA**CTACGGGTATACCCCCACTACTTTGATTAC**TGGGGCCAAGGAGTCA
TGGTCACAGTCTCCTCA (**SEQ ID NO: 3**)

24E4G6 Light Chain Variable Region

ATGATGAGTCCTGCCCAGTTCCTGTTTCTGCTAATGCTCTGGATCCAGGAAGCCCGC
GGAGATGTTGTGATGACCCAGACACCACCGTCTTTGTCGGTTGCCATTGGACAATCA
GTCTCCATCTCTTGC**AAGTCAAGTCAGAGCCTCGTATATAGTGATGGAGAGACAT**
ATTTGCATTGGTTTTTACAGAGTCCTGGCAGGTCTCCGAAGCGCCTAATTTAT**CACG**
TGTCTAATCTGGGCTCTGGAGTCCCTGACAGGTTCAGTGGCACTGGATCACTGACA

GATTTTACACTTAGAATCAGCAGAGTGGAGGCTGAGGATTTGGGAGTTTATTACTGC
GCGCAAACTACACATTTTCCTCCCACGTTTGGAGCTGGGACCAAGCTGGAACTGA
AA (**SEQ ID NO: 4**)

8H8E9 Heavy Chain Variable Region
*ATGGCTGTCCTGGTGCTGTTGCTCTGCCTGGTGACATTTCCAAGCTGTGCCCTGTCC*CAG
GTGCAGTTGAAGGAGTCAGGACCTGGTCTGGTGCAGCCCTCACAGACCCTGTCCCTC
ACCTGCACTGTCTCTGGGTTCTCATTAACC**AGCAATAGTGTTAGC**TGGGTTCGCCA
GGCTCCGGGAAAGGGTCTGGAGTGGATGGGA**GCAATATGGAGTGGTGGAAGCAC**
AGATTATAATTCAGCTCTCAAATCCCGACTGAGCATCAGCAGGGACACCTCCAAG
AGCCAAGTTTTCTTAAAAATGAACAGTCTGCAAACTGAAGACACAGCCATTTACTTC
TGTACCAGA**TCTCACTGGGAGCCCTTTGATTAC**TGGGGCCAAGGAGTCATGGTCA
CAGTCTCCTCA (**SEQ ID NO: 5**)

8H8E9 Light Chain Variable Region
ATGGAATCACAAACTCAGGCCCTCATATCCCTGCTGCTCTGGGTATATGGTACCTGTGGG
GACATTGTGATGACCCAGTCTCCATTCTCCCTGGCTGTGTCAGAAGGAGAGATGGTC
ACTATAAACTGC**AAGTCCAGTCAGGGTCTTTTATCCAGTGGAAACCAAAAGAAC**
TACTTGGCCTGGTACCAGCAGAGACCAGGGCAGTCTCCTAAACTACTGATCTAC**TA**
TGCATCCACTAGGCAATCAGGGGTCCCTGATCGCTTCATAGGCGGTGGATCTGGGA
CAGACTTCACTCTGACCATCAGCGATGTGCAGGCTGAAGACCTGGCAGATTATTACT
GC**CTGCAGCATTACAGCTATCCTCCCACG**TTCGGTTCTGGGACCAAGCTGGAGAT
CAAA (**SEQ ID NO: 6**)

6E5C11 Heavy Chain Variable Region
*ATGGCTGTCCTGGTGCTGTTGCTCTGCCTGGTGACATTTCCAAGCTGTGCCCTGTCC*CAG
GTGCAGCTGAGGGAGTCAGGACCTGGTCTGGTGCAGCCCTCACAGACCCTGTCCCTC
ACCTGCACTGTCTCTGGGTTCTCATTGACC**AGCAATAGTGTGACC**TGGGTTCGCCA
GCCTCCGGGAAAGGGTCTGGAGTGGATGGGA**GCGATATGGAGTGATGGAAGCAC**
AGATTATAATTCAACTCTCAAATCCCGACTGAGCATCAGTAGGGACACCTCCAAG
AGCCAAGTTTTCTTAAAAATGAGCAGTCTGCAAACTGAAGACACAGCCATTTACTTC
TGTACCAGA**TCCCACTGGGAGCCCTTTGATTAC**TGGGGCCAAGGAGTCATGGTCA
CAGTCTCCTCA (**SEQ ID NO: 7**)

6E5C11 Light Chain Variable Region
ATGGAATCACAAACTCAGGCCCTCATATCCCTGCTGCTCTGGGTATATGGTACCTGTGGG
GACATTGTGATGACCCAGTCTCCACTCTCCCTGGCTGTGTCAGAAGGAGAGACGGTC
ACTATGAACTGC**AAGTCCAGTCAGAGTCTTTTTTCCAGTGGAAATCAAAAGAAC**
TACTTGGCCTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTACTGATCTAC**TA**
TGCATCCACTAGGCAATCAGGGGTCCCTGATCGCTTCATAGGCAGTGGATCTGGGA
CAGACTTCACTCTGACCATCAGCGATGTGCAGACTGAAGACCTGGCAGATTATTACT
GC**CTGCAGCATTACAACTATCCTCCCACG**TTCGGTTCTGGGACCAAGCTGGAGA
(SEQ ID NO: 8)

7D8B10 Heavy Chain Variable Region

*ATGGACTTGCGACTGACTTATGTCTTTATTGTTGCTATTTTAAAAGGTGTCTTGTGT*GAGGT
GAAACTGGAGGAATCTGGGGGAGGTTTGGTGCAACCTGGAATGTCCGTGAAACTCT
CTTGTGCAACCTCTGGATTCATTTTCAGT**GACTACTGGATGGAA**TGGGTCCGCCAG
GCTCCAGGGAAGGGGCTAGAATGGGTAGCC**GAAATTAGAAACAAAGCTAATAATT**
ATGCAACATACTATGGGAAGTCTATGAAAGGCAGATTCACCATCTCAAGAGATGA
TTCCAAAAGTATAGTCTACCTACAAGTGAACAGCATAAGATCTGAAGATACTGCTAT
TTATTACTGTGCACCG**AATTTTGATTAC**TGGGGCCAAGGAGTCATGGTCACGGTCTC
CTCA (**SEQ ID NO: 9**)

7D8B10 Light Chain Variable Region
*ATGAGTCCTGTCCAGTCCCTGTTTTTGCTATTGCTTTGGATTCTGGGAACCCATGGT*GATG
TTGTGCTGACCCAGACTCCACCCACTTTATCGGCTACCATTGGACAATCAGTCTCTAT
CTCTTGC**AGGTCAAGTCAGAGTCTCTTACATAGTACTGGAAACACCTATTTAAAT**
TGGTTGCTACAGAGGCCAGGCCAACCTCCGCAACTTCTAATTTAT**TTGGTTTCCAG**
ACTGGAATCTGGGGTCCCCAACAGGTTCAGTGCCAGTGGGTCAGGAACTGATTTCA
CACTCAAAATCAGTGGAATAGAGGCTGAGGATTTGGGGGTTTATTACTGC**GTGCAA**
AGTTCCCATACTCCGTACACGTTTGGGACTGGGACCAAGCTGGAACTGAAA (**SEQ**
ID NO: 10)

18E10F10 Heavy Chain Variable Region
*ATGGACATCAGGCTCAGCTTGGTTTTCCTTGTCCTTTTTATGAAAGGTGTCCAGTGT*GAGG
TGCAGTTGGTGGAGTCTGGGGGAGGCTTAGTGCAGCCTGGAAGGTCCCTGAAACTCT
CCTGTGCAGCCTCACGATTCACTTTTAGT**GACTATAACATGGCC**TGGGTCCGCCAG
GCTCCAAAGAAGGGTCTGGAGTGGGTCGCA**ACCATTTATCATGATGATAGTGGTT**
CTTACTATCGAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAAATAATGCAAA
AAGCACTCTGTACCTGCAGATGGACAGTCTGAGGTCTGAGGACATGGCCACTTATTA
CTGTGCAAGA**CATAACAATGGCTTTGATTAC**TGGGGCCAAGGAGTCATGGTCACA
GTCGCCTCA (**SEQ ID NO: 11**)

18E10F10 Light Chain Variable Region
*ATGAAGTGGCCTGTTAGGCTGTTGGTGCTGTTCTTCTGGATTCCTGCTTCCGGGGGGT*GAT
GTTGTGATGACACAAACTCCAGTCTCCCTGCCTGTCCGCCTTGGAGGTCAAGCCTCT
ATCTCTTGC**CGGTCAAGTCAGAGCCTGGTACACAGTAATGGAAACACCTACTTG**
CATTGGTACCTACAGAAGCCAGGCCAGTCTCCACAGCTCCTCATCAAT**CGGGTTTC**
CAACAGATTTTCTGGGGTGCCAGACAGGTTCAGTGGCAGTGGGTCAGGGACAGATT
TCACCCTCAAGATCAACAGAGTAGAGCCTGAGGACTTGGGAGATTATTACTGC**TTA**
CAAAGTACACATTTTCCACTCACGTTCGGTTCTGGGACCAAGCTGGAGACCAAA
(SEQ ID NO: 12)

40G10H11 Heavy Chain Variable Region
*ATGGACATCAGGCTCAGCTTGGGTTTCCTTGTCCTTTTCATAAAAGGTGACCAGTGT*GCGG
TGCAACTGGTGGAGTCTGGGGGAGGCTTAGTGCAGCCTGGAAGGTCCCTGAAACTC
TCCTGTGCAGCCTCAAGAATCACTTTCACT**GACTATTACATGGCC**TGGGTCCGCCA
GGCTCCAACGAAGGGTCTGGAGTGGGTCGCA**ACCATTAGTTCTGATGGTGGTGAC**
ACTTTCTATCGAGACTCCGTGAAGGGCCGATTTACTATCTCCAGAGACAATGCAA
AAAGCACCCTATATTTGCAAATGGTCAGTCTGAGGTCTGAGGACACGGCCACTTATT

ACTGTTCAACA**GATCGGGGAGCTCAGTTTGGTTAC**TGGGGCCAAGGCACTCTGGT
CACTGTCTCTTCA (**SEQ ID NO: 13**)

40G10H11 Light Chain Variable Region
*ATGGCTCCAGTCCAGCTCTTAGGGCTGCTGCTGATTTGGCTCCCAGCCATGAGATGT*GAC
ATCCAGATGACCCAGTCTCCTTCATTCCTGTCTGCATCTGTGGGAGACAGAGTCTCT
ATCAACTGC**AAAGCAAGTCAGAATGTTCACGAGAACCTAAAC**TGGTATCAGCAAA
AGCTTGGAGAAGCTCCCAAACGCCTGATATAT**AATACAAACAATTTGCAAACA**GG
CATCCCATCAAGGTTCAGTGGCAGTGGATCTGGTGCAGATTACACACTCACCATCAG
CAGCCTGCAGCCTGAAGATTTTGCCACATATTTCTGT**TTGCAGCATAATGCTTTTC**
CGTACACGTTTGGACCTGGGACGAAGCTGGAACTGAAA (**SEQ ID NO: 14**)

Mouse mAb sequences

9-G05 Heavy Chain Variable Region
GAGGTCCAGCTGCAACAGTCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAA
GATACCCTGCAAGGCTTCTGGATACACATTCCCTGACTACAACATGGACTGGGTGAA
GCAGAGCCATGGAAAGAGCCTTGAGTGGATTGGATATATTAATCCTGACAATGGTG
GTACTATCTACAACCAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAGTCC
TCCAGCACAGCCTACATGGAGCTCCGCAGCCTGACATCTGAGGACACTGCAGTCTAT
TACTGTGCAAGATTAGACAGCTCAGGCTACGGTTACTATGCTATGGACTACTGGGGT
CAAGGAACCTCAGTCACCGTCTCCTCA (**SEQ ID NO: 15**)

9-G05 Light Chain Variable Region
GACATTGTGCTGACCCAATCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCC
ACCATCTCCTGCAGAGCCAGCGAAAGTGTTGATAATTATGGCATTAGTTTTATGCAC
TGGTACCAGCAGAAACCAGGACAGCCACCCAAACTCCTCATCTATCGTGCATCCAA
CCTAGACTCTGAGATCCCTGCCAGGTTCAGTGGCAGTGGGTCTAGGACAGACTTCAC
CCTCACCATTGATCCTGTGGAGACTGATGATGTTGCAACCTATTACTGTCAGCAAAG
TTATAAGGATCCTCGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA (**SEQ ID NO: 16**)

8-P20 Heavy Chain Variable Region
AAAGTGATGCTGGTGGAGTCTGGGGGAGCCTTAGTGAAGCCTGGAGGGTCCCTGAA
ACTCTCCTGTGTAGCCTCTGGATTCACTTTCAGTAACTATGCCATGTCTTGGGTTCGC
CAGACTCCAGAGAAGAGGCTGGAGTGGGTCGCAACCATTAGTAGTGGTGGTTATTA
CACTTACTATCCAGACAGTGTGAAGGGTCGATTCACCATCTCCAGAGACAATGCCAG
GAACACCCTGTTCCTGCAAATGAGCAGTCTGAGGTCTGAGGACACGGCCATGTTTTA
CTGTGCAAGAGAGGATGATTACGGAAGATATTCCTATACTATGGACTACTGGGGTCA
AGGAACCTCAGTCACCGTCTCCTCA (**SEQ ID NO: 17**)

8-P20 Light Chain Variable Region
GATGTTGTGATGACCCAAACTCCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGTC
TCCATCTCTTGCAGATGTAGTCAGAGCCTTGTACACAGTAATGGAAACACCTATTTA
CATTGGTACCTGCAGAAGCCAGGCCAGTCTCCACAGCTCCTGATCTACAAAATTTCC

AACCGATTTTCTGGGGTCCCAGACAGGTTCAGTGGCAGTGGATCAGGGACAGATTTC
ACACTCAAGATCAGCAGAGTGGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAA
AGTACACATGTTCCGTACACGTTCGGAGGGGGGACCGAGCTGGAAATAAAA (**SEQ ID NO: 18**)

8-G15 Heavy Chain Variable Region

GAGGTCCAGCTGCAGCAGTCTGGACCTGAGCTGGTAAAGCCTGGGGCTTCAGTGAG
GATATCCTGCAAGGCTTCTGGATACACATTCACTGACTACTACATACACTGGGTGAA
GCAGAAGCCTGGGCAGGGCCTTGAATGCATTGGAGAGATTTATCCTGGAACTGATA
ATACTTACTACAGTAAAAAATTCAGGGGCAAGGCCACACTGACTGCAGACAAATCC
TCCGACACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCAGTCTAT
TTCTGTGCAAGAGGAGACTACTATAGGGGGTACTTCGATGTCTGGGGCGCAGGGAC
CACGGTCACCGTCTCCTCA (**SEQ ID NO: 19**)

8-G15 Light Chain Variable Region

GATGTTGTGATGACTCAGACCTCACTCACTTTGTCGGTTACCATTGGACAACCAGCC
TCCATCTCTTGCAAGTCAAGTCAGAGCCTCTTACATAGTAATGGAAAGACATATTTG
AATTGGTTATTACAGAGGCCAGGCCAGTCTCCAAAGTTCCTAATCTATCTGGTGTCT
AAACTGGAATCTGGAGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGGACAGATTT
CACACTGAAAATCAGCAGAGTGGAGGCTGAGGATTTGGGGGTTTATTACTGCTTGCA
ATCTACACATTTTCCTTGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA (**SEQ ID NO: 20**)

8-I14 Heavy Chain Variable Region

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

8-I14 Light Chain Variable Region

GACATCCATTTGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAATC
AGTCTCACTTGCCGGGCAAGTCAGGACATTTATATTAGCTTAAACTGGTTTCAGCAG
AAACCAGATGGAACTATTAAACTCCTGATCTACGGCACATCCAGTTTAGATTCTGGT
GTCCCCAAAAGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGC
AGCCTTGAGTCTGAAGATTTTGCAGACTATTACTGTCTACAATATGCTAGTTCTCCGT
ACACGTTCGGAGGGGGGGACCAAGCTGGAAATAAAA (**SEQ ID NO: 22**)

9-E16 Heavy Chain Variable Region

GAGGTCCAGCTGCAGCAGTCTGGACCTGAGCTGGTAAAGCCTGGGGCTTCAGTGAA
GATATCCTGCAAGGCTTCTGGATACACATTCACTGACTACTACATGCACTGGGTGAA
GCAGAAGCCTGGGCAGGGCCTTGAGTGGATTGGAGAGATTTATCCTGGAAGTGGTA
ATCCTTACTACAATGAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGACAAATCA
TCCAGCTCAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCAGTCTAT

TTCTGTGCAAGAACCTCCTACGGTAGAGTAGGGACAGGGTTTGCTTACTGGGGCCAA
GGGACTCTGGTCACTGTCTCTGCA (**SEQ ID NO: 23**)

9-E16 Light Chain Variable Region

AATTTTGTGATGACCCAAACTCCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCCT
CCATCTCTTGCAGATCTAGTCAGAGCCTTCTACACAGTAACGGAAACACCTATTTAC
ATTGGTACCTGCAGAAGCCAGGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCA
ACCGATTTTCTGGGGTCCCAGACAGGTTCAGTGGCAGTGGATCAGGGACAGATTTCA
CACTCAAGATCAACAGAGTGGAGACTGAGGATCTGGGAATTTATTTCTGCTCTCAAA
GTTCACATGTTCCCACGTTCGGTGCTGGGACCAAGCTGGAGCTGAAA (**SEQ ID NO: 24**)

8-J17 Heavy Chain Variable Region

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

8-J17 Light Chain Variable Region

GATGTTGTGATGACCCAAACTCCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCC
TCCATCTCTTGCAGATCTAGTCAGAGCCTTGTATATAGTAATGGAAATACCTATTTAC
ATTGGTACCTGCAGAAGCCAGGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCA
ACCGATTTTCTGGGGTCCCAGACAGGTTCAGTGGCAGTGGATCAGGGACAGATTTCA
CACTCAAGATAAGCAGAGTGGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAA
GTACACATGTTCCGTGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA (**SEQ ID NO: 26**)

6-O12 Heavy Chain Variable Region

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

6-O12 Light Chain Variable Region

GACATTGTGATGTCACTGTCTCCATCCTCCCTAGCTGTGTCAGTTGGAGAGAAGGTT
ACTATGAGCTGCAAGTCCAGTCAGAGCCTTTTATATAGTCGCAATCAAAAGAACTAC
TTGGCCTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATTTACTGGGCA
TCCACTAGGGCATCTGGAGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGAT
TTCACTCTCACCATCAGCAGTGTGAAGGCTGAAGACCTGGCAGTTTATTACTGTCAG

CAATATTATAGCTATCCGTACACGTTCGGAGGGGGGACCAAGCTGGAAATAAAA **(SEQ ID NO: 28)**

10-L15 Heavy Chain Variable Region

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

10-L15 Light Chain Variable Region

AACATTGTGCTGACCCAATCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCC ACCATATCCTGCAGAGCCAGTGAAAGTGTTGATAGTTATGGCAATAGTTTTATGCAC TGGTACCAGCAGAAACCAGGACAGCCACCCAAACTCCTCATCTATCTTGCATCCAAC GTAGAATCTGGGGTCCCTGCCAGGTTCAGTGGCAGTGGGTCTAGGACAGACTTCACC CTCACCATTGATCCTGTGGAGGCTGATGATGCTGCAACCTATTACTGTCAGCAAAAT AATGAGGATCCGTGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA (**SEQ ID NO: 30**)

7-H14 Heavy Chain Variable Region

CAGGTCCAACTGCAGCAGCCTGGGGCTGAGCTGGTGAGGCCTGGGGCTTCAGTGAA GCTGTCCTGCAAGCCTTCTGGCTACACCTTCACCAGCTACTGGATGAACTGGGTGAA GCAGAGGCCTGGACAAGGCCTTGAATGGATTGGTATGATTGATCCTTCAGACAGTG AAACTCACTACAATCAAATGTTCAAGGACAAGGCCACATTGACTGTTGACAAATCCT CCAACACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATT ACTGTGCGCAGATCTACTATGCTTACGACAAGGCTTACTGGGGCCAAGGGACTCTGG TCACTGTCTCTGCA (**SEQ ID NO: 31**)

7-H14 Light Chain Variable Region

GACATTGTGATGTCACAGTCTCCATCCTCCCTAGCTGTGTCAGTTGGAGAGAAGGTT ACTATGAGCTGCAAGTCCAGTCAGAGCCTTTTATATAGTAGCCATCAAAAGAACTAC TTGGCCTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTGCTGATTTACTGGGCA TCCACTAGGGAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGAT TTCAGTCTCACCATCAGCAGTGTGAAGGCTGAAGACCTGGCAGTTTATTACTGTCAG GAATATTATAGCTGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA (**SEQ ID NO: 32**)

6-B21 Heavy Chain Variable Region

GAGGTCCAGCTGCAACAATCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAA GATATCCTGTAAGGCTTCTGGATACACGTTCACTGACTACTACATGAACTGGGTGAA GCAGAGCCATGGAAAGAGCCTTGAGTGGATTGGAGATATTAATCCTCACAATGGTG GTACTAGCTTCATCCAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAGTCCT CCAGCACAGCCTACATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCAGTCTATT

ATTGTGCCCCTCTGGGACGAAAGGAGGGGTTTGCTTACTGGGGCCAAGGGACTCTG
GTCACTGTCTCTGCA (**SEQ ID NO: 33**)

6-B21 Light Chain Variable Region
GACACTGTGCTGACACAGTCTCCTGCTTCCTTAGTTGTATCTCTGGGGCAGAGGGCC
ACCATCTCATGCAGGGCCAGCAAAAGTGTCAGTACATCTGGCTATAGTTATATGCAC
TGGTACCAACAGAAACCAGGACAGCCACCCAAACTCCTCATCTATCTTGCATCCAAC
CTAGAATCTGGGGTCCCTGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGCCTTCACC
CTCAACATCCATCCTGTGGAGGAGGAGGATGCTGCAACCTATTACTGTCAGCACAGT
AGGGAGCTTCCGTACACGTTCGGAGGGGGGACCAAGCTGGAAATAAAA (**SEQ ID NO: 34**)

10-F23 Heavy Chain Variable Region
CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCCAGACCCTCAGT
CTGACTTGTTCTTTCTCTGGGTTTTCACTGAGCACTTTTGCTATGGGTGTAGGCTGGA
TTCGTCAGCCTTCAGGGAAGGGTCTGGAGTGGCTGGCACACATTTGGTGGGATGATG
ATAAGTACTATAACCCAGCCCTGAAGAGCCGGCTCACAATCTCCAAGGATACCTCC
AAAAACCATGTATTCCTCAAGATCGCCAATGTGGACACTGCAGATACTGCCACATAC
TACTGTGCTCGAATGCCGCTAACTTTCTACTTTGACTACTGGGGCCAAGGCACCACT
CTCACAGTCTCCTCA (**SEQ ID NO: 35**)

10-F23 Light Chain Variable Region
GATGTTTTGCTGACCCAAACTCCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCCT
CCATCTCTTGCAGATCTAGTCAGAGCATTGTACATAGTAATGGACACACCTATTTAG
AATGGTACCTGCAGAAACCAGGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCA
ACCGATTTTCTGGGGTCCCAGACAGGTTCAGTGGCAGTGGATCAGGGACAGATTTCA
CACTCAAGATCAGCAGAGTGGAGGCTGAGGATCTGGGAGTTTATTACTGCTTTCAAG
GTTCACATGTTCCGTTCACGTTCGGAGGGGGGACCAAGCTGGAAATAAAA (**SEQ ID NO: 36**)

6-A12 Heavy Chain Variable Region
CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCCAGACCCTCAGT
CTGACTTGTTCTTTCTCTGGGTTTTCACTGAGAACTTTTGCTATGGGTGTAGGCTGGA
TTCGTCAGCCTTCAGGGAAGGGTCTGGAGTGGCTGGCACACATTTGGTGGGATGATG
ATAAGTACTATAACCCAGCCCTGAAGAGCCGGCTCACAATCTCCAAGGATACCTCC
AAAAACCAGGTATTCCTCAAGATCGCCAATGTGGACACTGCAGATACTGCCACATA
CTACTGTGCTCGAATGCCGCTAACTTTCTACTTTGACTACTGGGGCCAAGGCACCAC
TCTCACAGTCTCCTCA (**SEQ ID NO: 37**)

6-A12 Light Chain Variable Region
GATGTTTTGATGACCCAAACTCCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCCT
CCATCTCTTGTAGATCTAGTCAGAGCATTGTACATAGTAATGGAAACACCTATTTAG
AATGGTACCTGCAGAAACCAGGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCA
CCCGATTTTCTGGGGTCCCAGACAGGTTCAGTGGCAGTGGATCAGGGACAGATTTCA
CACTCAAGATCAGCAGAGTGGAGGCTGAGGATCTGGGAGTTTATTACTGCTTTCAAG

GTTCACATGTTCCGTTCACGTTCGGAGGGGGGACCAAGCTGGAAATAAAA (**SEQ ID NO: 38**)

6-M8 Heavy Chain Variable Region

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

6-M8 Light Chain Variable Region

GATATTGTGATGACGCAGGCTGCATTCTCCAATCCAGTCACTCTTGGAACATCAGCT TCCATCTCCTGCAGGTCTAGTAAGAGTCTCCTACATAGTAATGGCATCACTTATTTGT ATTGGTATCTGCAGAAGCCAGGCCAGTCTCCTCAGCTCCTGATTTATCAGATGTCCA ACCTTGCCTCAGGAGTCCCAGACAGGTTCAGTAGCAGTGGGTCAGGAACTGATTTCA CACTGAGAATCAGCAGAGTGGAGGCTGAGGATGTGGGTGTTTATTACTGTGCTCAA AATCTAGAACTTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA (**SEQ ID NO: 40**)

2-A3 Heavy Chain Variable Region

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

2-A3 Light Chain Variable Region

GATGTTGTGATGACCCAGACTCCACTCACTTTGTCGGTTACCATTGGACAACCAGCC TCCATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGCTGGAAAGACATATTTG AATTGGTTGTTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATGTATCTGGTGTCT AAACTGGACTCTGGAGTCCCTGACAGGTTCACTGGCAGCGGATCAGGGACAGATTT CACACTGAAAATCAGCAGAGTGGAGGCTGAGGATTTGGGAGTTTATTATTGCTGGC AAGGTACACATTTTCCGTACACGTTCGGAGGGGGGACCAAGCTGGAAATAAAA (**SEQ ID NO: 42**)

6-O17 Heavy Chain Variable Region

CAGGTCCAACTGCAGCAGCCTGGGGCTGAGCTTGTGAAGCCTGGGGCTTCAGTGAA GTTGTCCTGCAAGGCTTCTGGCTACACCTTCACCAGCTACTGGATGCACTGGATAAA GCAGAGACCTGGACAAGGCCTTGAGTGGATTGGAGAGATTAACCCTAGCAATGGTG GTTCTAACTACAATGAGAAGTTCAAGAGCAAGGCCACACTGACTGTAGACAAATCC TCCAGCACAGCCTACATGCAACTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTAT

CACTGTAAAAGCAGAGGCTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA (**SEQ ID NO: 43**)

6-O17 Light Chain Variable Region

GATGTTGTGATGACCCAGACTCCACTCACTTTGTCGGTTACCATTGGACAACCAGCC TCCATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTTATGGAAAGACATATTTG AATTGGTTGTTACAGCGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGGTGTCT AAATTGGACTCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTC ACACTGAAAATCAGCAGAGTGGAGGCTGAGGATTTGGGAATTTATTATTGCTGGCA AGGTACACATTTTCCTCACACGTTCGGCTCGGGGACAAAGTTGGAAATAAAA (**SEQ ID NO: 44**)

3-G5 Heavy Chain Variable Region

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

3-G5 Light Chain Variable Region

GATGTTGTGATGACCCAGACTCCACTCACTTTGTCGGTTACCATTGGACAACCAGCT TCCATCTCTTGCAAGTCAAGTCAGAGCCTCTTATATACTAATGGAAACACCTATTTG AATTGGTTATTACAGAGGCCAGGCCAGTCTCCAAAACGCCTAATCTATCTGGTGTCT AAATTGGACTCTGGAATCCCTGACAGGTTCAGTGGCAGTGGATCAGGGACAGATTTC ACACTGAGAATCAGCAGAGTGGAGGCTGAGGATTTGGGAGTTTATTACTGCTTGCA GAGTACACATTTTCCATTCACGTTCGGCTCGGGGACAAAGTTGGAAATAAAA (**SEQ ID NO: 46**)

6-A15 Heavy Chain Variable Region

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

6-A15 Light Chain Variable Region

GATGTTGTGATGACCCAGACTCCACTCACTTTGTCGGTTACCATTGGACAACCAGCC TCCATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGATGGAAAGACATATTTG AATTGGTTGTTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGGTGTCT AAACTGGACTCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTC ACACTGAAAATCAGCAGAGTGGAGGCTGAGGATTTGGGAGTTTATTATTGCTGGCA

AGGTACACATTTTCCGTACACGTTCGGAGGGGGGACCAAGCTGGAAATAAAA (**SEQ ID NO: 48**)

10-K10 Heavy Chain Variable Region
GAGGTCCAGCTGCAACAATCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAA
GATGTCCTGTAAGGCTTCTGGATACACAATCACTGACTACTACATGATGTGGTTGAA
GCAGAGTCATGGAAAGAGCCTTGAATGGATTGGAGATATTAATCCTTACACTGGTG
GTACTAGCTACAACCAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAATCC
TCCAGCACAGCCTACATGCAGCTCAACAGCCTGACATCTGAGGACTCTGCAGTCTAT
TACTGTGCAAGAGGGGCCTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA
(**SEQ ID NO: 49**)

10-K10 Light Chain Variable Region
GATGTTGTGATGACCCAGACTCCACTCACTTTGTCGGTTACCATTGGACAACCAGCC
TCCATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGATGGAAAGACATATTTG
AATTGGTTGTTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGGTGTCT
AAACTGGACTCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTC
ACACTGAAAATCAGCAGAGTGGAGGCTGAGGATTTGGGAGTTTATTATTGCTGGCA
AGGTACACATTTTCCGTACACGTTCGGAGGGGGGACCAAGCTGGAAATAAAA (**SEQ ID NO: 50**)

6-P20 Heavy Chain Variable Region
GAGGTCCAGCTGCAACAATCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAA
GATATCCTGTAAGGCTTCTGGATACACGTTCACTGACTACTACATGAACTGGGTGAA
GCAGAGCCATGGCAGGAGCCTTGAGTTGATTGGAGATATTAATCCTAACAATGGTG
GTTCTAACTTCAACCAGAAGTTCAGGGGCAAGGCCACATTGACTGTAGACAAGTCCT
CCAGCACAGCCTATATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCAATCTATT
ACTGTGCAAGAATGGGTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCA (**SEQ ID NO: 51**)

6-P20 Light Chain Variable Region
GATGTTGTGATGACCCAGACTCCACTCACTTTGTCGGTTACCATTGGACAACCAGCC
TCCATCTCTTGCAAGTCAAGTCAGAGCCTCTTACATAGTGATGGAAAGACATATTTG
AATTGGATGTTCCAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGGTGTCT
AAACTGGACTCTGGAGTCCCTTACAGGTTCACTGGCGGTGGATCAGGGACAGATTTC
ACACTGCAAATCAGCAGAGTGGAGACTGAGGATTTGGGAGTTTATTATTGCTGGCA
AGGTACACATTTTCCTCGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA (**SEQ ID NO: 52**)

7-O8 Heavy Chain Variable Region
GAGGTCCAGCTGCAGCAGTCTGGACCTGAACTGGTCAAGCCTGGGGCTTCAGTGAA
GATGTCCTGCAAGGCTTCTGGATACACATTCACTGACTACTACATACACTGGGTGAA
GCAGAAGCCTGGGCAGGGCCTTGAGTACATTGGAGAGATTTATCCTGGAAGTGGTA
ATACTTACTACAATGGGAAGTTCAGGGGCAAGGCCACACTGACTGCAGACAAGTCC
TCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCAGTCTAT

TTCTGTGGTAGTGGCTACTTTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCC
TCA (**SEQ ID NO: 53**)

7-O8 Light Chain Variable Region
GATGTTGTGATGACCCAGACTCCACTCACTTTGTCTGTTACCATTGGACAGCCAGCTT
CCATTTCTTGCAAGTCAAGTCAGAGCCTCTTATATAGTAATGGAAAAACCTATTTGA
ATTGGTTATTACAGAGTCCAGGCCAGTCTCCAAAGCTCCTAATCTATCTGGTGTCTA
AACTGGAATCTGGAGTCCCTGACAGATTCAGTGGCAGTGGATCAGGGACAGATTTT
ACACTGAAACTCAGCAGAGTGGAGGCTGAGGATTTGGGAGTATATTACTGCGTGCA
AGGTACACATTTCCCATTCACGTTCGGCTCGGGGACAAAGTTGGAAATAAAA (**SEQ ID NO: 54**)

Rabbit mAb sequences

A11B1_16G7 Heavy Chain
ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGTTCAAAGGTGTCCAGTGT
CAGGAGCAACTGGTGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGAC
ACTCACCTGCACAGCCTCTGGATTCTCCTTCAATAAGAATTATTGGATGTGCTGGGT
CCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGATGCATTTATAATGGTGATG
GCAACACATACTACGCGAGCTGGGTGAATGGCCGATTCACCATCTCCAAAACCTCGT
CGACCACGGTGACTCTGCAAATGACCAGTCTGACAGTCGCGGACACGGCCATCTATT
TCTGTGCGAGACTACTTAATATGTGGGGCCCAGGCACCCTGGTCACCGTCTCCTCAG
GGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCTGCTGCGGGGACACACCCA
GCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCTCCCGGAGCCAGTGACC
GTGACCTGGAACTCGGGCACCCTCACCAATGGGGTACGCACCTTCCCGTCCGTCCGG
CAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCAGCCA
GCCCGTCACCTGCAACGTGGCCCACCCAGCCACCAACACCAAAGTGGACAAGACCG
TTGCGCCCTCGACATGCAGCAAGCCCATGTGCCCACCCCCTGAACTCCCGGGGGGAC
CGTCTGTCTTCATCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCACGCACCC
CCGAGGTCACATGCGTGGTGGTGGACGTGAGCCAGGATGACCCCGAGGTGCAGTTC
ACATGGTACATAAACAACGAGCAGGTGCGCACCGCCCGGCCGCCGCTACGGGAGCA
GCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCTCCCCATCGCGCACCAGGACT
GGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAGGCACTCCCGGCCCCC
ATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCTGGAGCCGAAGGTCTACAC
CATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTCGGTCAGCCTGACCTGCATGA
TCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAGAAGAACGGGAAGGCA
GAGGACAACTACAAGACCACGCCGACCGTGCTGGACAGCGACGGCTCCTACTTCCT
CTACAGCAAGCTCTCAGTGCCCACGAGTGAGTGGCAGCGGGGCGACGTCTTCACCT
GCTCCGTGATGCACGAGGCCTTGCACAACCACTACACGCAGAAGTCCATCTCCCGCT
CTCCGG GTAAATAG (**SEQ ID NO: 55**)

A11B1_16G7 Light Chain
ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTACTGCTCTGGCTCCCAGGT
GCCAGATGTGCTGACATTGTGATGACCCAGACTCCAGCCTCCGTGGAGGCAGCTGTG
GGAGGCACAGTCACCATCAAGTGCCAGGCCAGTGAGAGCATTGGCAATGCATTAGC

CTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTATACTGCAGCCAC
TCTGGCATCTGGGGTCCCATCGCGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCAC
TCTCACCATCAGTGGCGTGCAGTGTGACGATGCTGCCACTTACTACTGTCAAAGCTA
TTATTTTACTAGTGTTAGTAGTTATGGCAATGCTTTCGGCGGAGGGACCGAGGTGGT
GGTCAAAGGTGATCCAGTTGCACCTACTGTCCTCATCTTCCCACCAGCTGCTGATCA
GGTGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGT
CACCGTCACCTGGGAGGTGGATGGCACCACCCAAACAACTGGCATCGAGAACAGTA
AAACACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGA
CCAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACG
ACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (**SEQ ID NO: 56**)

A11B1_16E10 Heavy Chain
ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACT
CACCTGCAGAGTCTCTGGATTCTCCTTCAGTAGCAGTTATTATATGTGTTGGGTCCGC
CAGGCTCCAGGGAAGGGGCTGGAATGGATCGCATGTATTGGTACTACTCGTGGTAG
CACTTACTACGCGACCTGGGCGAAAGGCCGATTCACCATTTCTAAAATCTCGTCGAC
CACGGTGACTCTACAAATGACCAGTCTGACAGACGCGGACACGGCCACCTATTTCTG
TGCGAGAGATGCTACTGGTTATAGGATTAACACGATTGGCCTCTATTTTAATTTGTG
GGGCCCAGGCACCCTGGTCACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTT
CCCACTGGCCCCCTGCTGCGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCT
GGTCAAAGGCTACCTCCCGGAGCCAGTGACCGTGACCTGGAACTCGGGCACCCTCA
CCAATGGGGTACGCACCTTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGA
GCAGCGTGGTGAGCGTGACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGCCCAC
CCAGCCACCAACACCAAAGTGGACAAGACCGTTGCGCCCTCGACATGCAGCAAGCC
CATGTGCCCACCCCCTGAACTCCCGGGGGGGACCGTCTGTCTTCATCTTCCCCCCAAA
ACCCAAGGACACCCTCATGATCTCACGCACCCCCGAGGTCACATGCGTGGTGGTGG
ACGTGAGCCAGGATGACCCCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAG
GTGCGCACCGCCCGGCCGCCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGT
GGTCAGCACCCTCCCCATCGCGCACCAGGACTGGCTGAGGGGCAAGGAGTTCAAGT
GCAAAGTCCACAACAAGGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCC
AGAGGGCAGCCCCTGGAGCCGAAGGTCTACACCATGGGCCCTCCCCGGGAGGAGCT
GAGCAGCAGGTCGGTCAGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACAT
CTCGGTGGAGTGGGAGAAGAACGGGAAGGCAGAGGACAACTACAAGACCACGCCG
ACCGTGCTGGACAGCGACGGCTCCTACTTCCTCTACAGCAAGCTCTCAGTGCCCACG
AGTGAGTGGCAGCGGGGCGACGTCTTCACCTGCTCCGTGATGCACGAGGCCTTGCA
CAACCACTACACGCAGAAGTCCATCTCCCGCTCTCCGGGTAAATAG (**SEQ ID NO: 57**)

A11B1_16E10 Light Chain
ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCAGATGTGCGTTCGAATTGACCCAGACTCCATCCTCCGTGGAGGCTGCTGTGGGA
GGCACGCCCACCATCAAGTGCCAGGCCAGTCAGACCATTTACAGTTACTTATCCTGG
TATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTATGAAGCGTCCAAACT
GGCCTCTGGGGTCCCATCGCGGTTCAGCGGCAGTGGATCTGGGACAGACTACACTCT
CACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTACTACTGTCAAAGCTATCA

TGGTACTGCTAGTACTGAATATAATACTTTCGGCGGGGGGACCGAGGTGGTGGTCAG
AGGTGATCCAGTTGCACCTACTGTCCTCATCTTCCCACCAGCTGCTGATCAGGTGGC
AACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCACCGT
CACCTGGGAGGTGGATGGCACCACCCAAACAACTGGCATCGAGAACAGTAAAACAC
CGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAGCA
CACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACCTCA
GTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (**SEQ ID NO: 58**)

A11B1_15G10 Heavy Chain
ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGCAGCAGCTGGTGGAGTCCGGGGGAGGCCTGGTCAAGCCTGGGGCAGCCCTGAC
ATTCACCTGCACAGCCTCTGGATTCTCCTTCAGTGGCAATTATTGGATATGCTGGGTC
CGCCAGGCTCCAGGGAAGGGGTTGGAGTGGATCGCGTGCATTGGTACTATTACTAGT
AGGACATACTACGCGAGCTGGGCGAAAGGCCGATTCACCATTTCCAAAACCTCGTC
GACCACGGTGACTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACGTATT
TCTGTGCGAGAGGTGCGGTTGTTAGTAGTGGTAATGCTCCCTACTACTTTACCTTGTG
GGGCCCAGGCACCCTGGTCACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTT
CCCACTGGCCCCCTGCTGCGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCT
GGTCAAAGGCTACCTCCCGGAGCCAGTGACCGTGACCTGGAACTCGGGCACCCTCA
CCAATGGGGTACGCACCTTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGA
GCAGCGTGGTGAGCGTGACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGCCCAC
CCAGCCACCAACACCAAAGTGGACAAGACCGTTGCGCCCTCGACATGCAGCAAGCC
CATGTGCCCACCCCCTGAACTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCCCAAA
ACCCAAGGACACCCTCATGATCTCACGCACCCCCGAGGTCACATGCGTGGTGGTGG
ACGTGAGCCAGGATGACCCCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAG
GTGCGCACCGCCCGGCCGCCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGT
GGTCAGCACCCTCCCCATCGCGCACCAGGACTGGCTGAGGGGCAAGGAGTTCAAGT
GCAAAGTCCACAACAAGGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCC
AGAGGGCAGCCCCTGGAGCCGAAGGTCTACACCATGGGCCCTCCCCGGGAGGAGCT
GAGCAGCAGGTCGGTCAGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACAT
CTCGGTGGAGTGGGAGAAGAACGGGAAGGCAGAGGACAACTACAAGACCACGCCG
ACCGTGCTGGACAGCGACGGCTCCTACTTCCTCTACAGCAAGCTCTCAGTGCCCACG
AGTGAGTGGCAGCGGGGCGACGTCTTCACCTGCTCCGTGATGCACGAGGCCTTGCA
CAACCACTACACGCAGAAGTCCATCTCCCGCTCTCCGGGTAAATAG (**SEQ ID NO: 59**)

A11B1_15G10 Light Chain
ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCAGATGTGCATTCGAATTGACGCAGACTCCATCCTCCGTGGAGGCAGCTGTGGGA
GGCACAGTCACCATCAAGTGCCAGGCCAGTCAGAGCATTAGTAGTTACTTATCCTGG
TATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTACAGGGCATCCACTCTG
GAATCTGGGGTCCCATCGCGGTTTAAAGGCAGTGGATCTGGGACAGAGTTCACTCTC
ACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTACTTCTGTCAAAGCTATTAT
GGTGTTACTTTTAGTGGTTTTGCTTTCGGCGGAGGGACCGAGGTGGTGGTCAAAGGT
GATCCAGTTGCACCTACTGTCCTCATCTTCCCACCAGCTGCTGATCAGGTGGCAACT
GGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCACCGTCACC

TGGGAGGTGGATGGCACCACCCAAACAACTGGCATCGAGAACAGTAAAACACCGCA
GAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAGCACACA
GTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACCTCAGTCG
TCCAGAGCTTCAATAGGGGTGACTGTTAG (**SEQ ID NO: 60**)

A11B1_14H1 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACT
CACCTGCAAAGCCTCTGGAATCGACTTCAATAACTATTGGATAACCTGGGTCCGCCA
GGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATTTATGTTGGAATTACCGGCC
GCACATGGTACGCGAACTGGGCGAAAGGCCGATTCACCATCTCCAAGGCCTCGAGC
ACGGTGGATCTGAAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATTTCTGT
GCGAGGAATGGTGATGGTGGTATTTATGCTCTTAACTTGTGGGGCCCAGGCACCCTG
GTCACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCTGC
TGCGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCT
CCCGGAGCCAGTGACCGTGACCTGGAACTCGGGCACCCTCACCAATGGGGTACGCA
CCTTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCG
TGACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGCCCACCCAGCCACCAACACC
AAAGTGGACAAGACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCCACCCCC
TGAACTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCCCAAAACCCAAGGACACCCT
CATGATCTCACGCACCCCCGAGGTCACATGCGTGGTGGTGGACGTGAGCCAGGATG
ACCCCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAGGTGCGCACCGCCCGG
CCGCCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCTCCC
CATCGCGCACCAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACA
AGGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCTG
GAGCCGAAGGTCTACACCATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTCGGT
CAGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGA
GAAGAACGGGAAGGCAGAGGACAACTACAAGACCACGCCGACCGTGCTGGACAGC
GACGGCTCCTACTTCCTCTACAGCAAGCTCTCAGTGCCCACGAGTGAGTGGCAGCGG
GGCGACGTCTTCACCTGCTCCGTGATGCACGAGGCCTTGCACAACCACTACACGCAG
AAGTCCATCTCCCGCTCTCCGGGTAAATAG (**SEQ ID NO: 61**)

A11B1_14H1 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCACATTTGCACAAGTGCTGACCCAGACTGCATCGTCCGTGTCTGCAGCTGTGGGA
GGCACAGTCACCATCAGTTGCCAGTCCAGTCAGAGTGTTTATAATAATAATTGGTTA
GCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTACAGGGCATC
CACTCTGACATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACACAGTT
CACTCTCACCATCAGCGACCTGGAGTGTGACGATGCTGCCACTTACTACTGTGCAGG
CGGTTATAGTGGTAATATTTACGTAAATGATTTCGGCGGAGGGACCGAGGTGGTGGT
CAAAGGTGATCCAGTTGCACCTACTGTCCTCATCTTCCCACCAGCTGCTGATCAGGT
GGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCAC
CGTCACCTGGGAGGTGGATGGCACCACCCAAACAACTGGCATCGAGAACAGTAAAA
CACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCA
GCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACC
TCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (**SEQ ID NO: 62**)

A11B1_13G4 Heavy Chain
ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGGAGCAGCTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGGATCCCTGAC
ACTCACCTGCAAAGCCTCTGGATTCTCCTTCAGTAATACCTACTGGGCATGCTGGGT
CCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATGAATCCTGCTAGTA
GTGGTAGCTCTTACTACGCGAGCTGGGCGAAAGGCCGATTCACCATCTCCAAAACCT
CGTCGACCACGGTGACTCTGCACATGCCCAGTCTGACAGCCGCGGACACGGCCACC
TATTTCTGTGCGAAATGGGATACTGCTTTCGATGTGTGGGGCCCAGGCACCCTGGTC
ACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCTGCTGC
GGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCTCCC
GGAGCCAGTGACCGTGACCTGGAACTCGGGCACCCTCACCAATGGGGTACGCACCT
TCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTGA
CCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGCCCACCCAGCCACCAACACCAAA
GTGGACAAGACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCCACCCCCTGA
ACTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCCCAAAACCCAAGGACACCCTCAT
GATCTCACGCACCCCCGAGGTCACATGCGTGGTGGTGGACGTGAGCCAGGATGACC
CCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAGGTGCGCACCGCCCGGCCG
CCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCTCCCCAT
CGCGCACCAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAG
GCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCTGGA
GCCGAAGGTCTACACCATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTCGGTCA
GCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAGA
AGAACGGGAAGGCAGAGGACAACTACAAGACCACGCCGACCGTGCTGGACAGCGA
CGGCTCCTACTTCCTCTACAGCAAGCTCTCAGTGCCCACGAGTGAGTGGCAGCGGGG
CGACGTCTTCACCTGCTCCGTGATGCACGAGGCCTTGCACAACCACTACACGCAGAA
GTCCATCTCCCGCTCTCCGGGTAAATAG (**SEQ ID NO: 63**)

A11B1_13G4 Light Chain
ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCAGATGTGCCGATGTTGTGATGACCCAGACTCCATCCTCCGTGGAGGCAGCTGTG
GGAGGCACAGTCACCATCAAGTGCCAGGCCAGTCAGAGCATTAGTAGCTACTTAGC
CTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTATGGTGCATCCAA
TCTGGAGTCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGAGTACA
CTCTCACCATCAGCGGCGTGCAGTGTGACGATGCTGCCACTTACTACTGTCAAAACT
ATTATGCTATTGATACTTATGGTCATGCTTTCGGCGGAGGGACCGAGGTGGTGGTCA
AAGGTGATCCAGTTGCACCTACTGTCCTCATCTTCCCACCAGCTGCTGATCAGGTGG
CAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCACCG
TCACCTGGGAGGTGGATGGCACCACCCAAACAACTGGCATCGAGAACAGTAAAACA
CCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAGC
ACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACCTC
AGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (**SEQ ID NO: 64**)

A11B1_13C3 Heavy Chain
ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGGAGCAGCTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGAC

ACTCACCTGCACAGCCTCTGGATTCTCCTTTAGTAGCAACTATCACATCTGCTGGGTC
CGCCAGGCTCCAGGAAAGGGGCTGGAGTTGATCGCATGCATTTATGTTGGTGATGGC
AGCACATACTACGCGAGCTGGGCGAAAGGCCGATTCACCATCTCCAAATCCTCGTC
GACCACGGTAGCTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATT
TCTGTGGGAGAATGTTTAACTTGTGGGGCCCAGGCACCCTGGTCACCGTCTCCTCAG
GGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCTGCTGCGGGGACACACCCA
GCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCTCCCGGAGCCAGTGACC
GTGACCTGGAACTCGGGCACCCTCACCAATGGGGTACGCACCTTCCCGTCCGTCCGG
CAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCAGCCA
GCCCGTCACCTGCAACGTGGCCCACCCAGCCACCAACACCAAAGTGGACAAGACCG
TTGCGCCCTCGACATGCAGCAAGCCCATGTGCCCACCCCCTGAACTCCCGGGGGGAC
CGTCTGTCTTCATCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCACGCACCC
CCGAGGTCACATGCGTGGTGGTGGACGTGAGCCAGGATGACCCCGAGGTGCAGTTC
ACATGGTACATAAACAACGAGCAGGTGCGCACCGCCCGGCCGCCGCTACGGGAGCA
GCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCTCCCCATCGCGCACCAGGACT
GGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAGGCACTCCCGGCCCCC
ATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCTGGAGCCGAAGGTCTACAC
CATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTCGGTCAGCCTGACCTGCATGA
TCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAGAAGAACGGGAAGGCA
GAGGACAACTACAAGACCACGCCGACCGTGCTGGACAGCGACGGCTCCTACTTCCT
CTACAGCAAGCTCTCAGTGCCCACGAGTGAGTGGCAGCGGGGCGACGTCTTCACCT
GCTCCGTGATGCACGAGGCCTTGCACAACCACTACACGCAGAAGTCCATCTCCCGCT
CTCCGGGTAAATAG (**SEQ ID NO: 65**)

A11B1_13C3 Light Chain
ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCATATGTGACCCTGTGCTGACCCAGACTCCATCCTCCGTGTCTGCGGCTGTGGGA
GTCACAGTCACCATCAACTGCCAGTCCAGTCCGAGTGTTTATAGTAACTACTTATCC
TGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTCATCTATCTGGCATCTACT
CTGGCATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACACAGTTCACT
CTCACCATCAGCGACGTGCAGTGTGACGATGCTGCCACTTACTACTGTGCAGGCACT
TATAGTGGTAATATTTGGTCTTTCGGCGGAGGGACCGAGGTGGTGGTCAAAGGTGAT
CCAGTTGCACCTACTGTCCTCATCTTCCCACCAGCTGCTGATCAGGTGGCAACTGGA
ACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCACCGTCACCTGG
GAGGTGGATGGCACCACCCAAACAACTGGCATCGAGAACAGTAAAACACCGCAGA
ATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAGCACACAGT
ACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACCTCAGTCGTC
CAGAGCTTCAATAGGGGTGACTGTTAG (**SEQ ID NO: 66**)

A11B1_12F2 Heavy Chain
ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGCAGCAGCTGGTGGAGTCCGGGGGAGGCCTGGTCAAGCCTGGGGCATCCCTGAC
ACTCACCTGCACAGCCTCTGGATTCTCCTTCAGTAGCGGCTATCACATGTGCTGGGT
CCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCTTTGGTGTTTATACTGG
TACCACTACCTACGCGAGCTGGGCGAAAGGTCGATTCACCATCTCCAAAACCTCGTC
GACCACGGTGACTCTACAAATGACCAGTCTAACAGTCGCGGACACGGCCACCTATTT

CTGTGCGAGAATCAGTGCTGAAAATGGTGGGGACTTGTGGGGCCCAGGCACCCTGG
TCACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCTGCT
GCGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCTC
CCGGAGCCAGTGACCGTGACCTGGAACTCGGGCACCCTCACCAATGGGGTACGCAC
CTTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGT
GACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGCCCACCCAGCCACCAACACCA
AAGTGGACAAGACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCCACCCCCT
GAACTCCCGGGGGGGACCGTCTGTCTTCATCTTCCCCCCAAAACCCAAGGACACCCTC
ATGATCTCACGCACCCCCGAGGTCACATGCGTGGTGGTGGACGTGAGCCAGGATGA
CCCCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAGGTGCGCACCGCCCGGC
CGCCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCTCCCC
ATCGCGCACCAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAA
GGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCTGG
AGCCGAAGGTCTACACCATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTCGGTC
AGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAG
AAGAACGGGAAGGCAGAGGACAACTACAAGACCACGCCGACCGTGCTGGACAGCG
ACGGCTCCTACTTCCTCTACAGCAAGCTCTCAGTGCCCACGAGTGAGTGGCAGCGGG
GCGACGTCTTCACCTGCTCCGTGATGCACGAGGCCTTGCACAACCACTACACGCAGA
AGTCCATCTCCCGCTCTCCGGGTAAATAG (**SEQ ID NO: 67**)

A11B1_12F2 Light Chain
ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCAGATGTGATGTTGTGATGACCCAGACTCCAGCCTCCGTGGAGGCAGCTGTGGG
AGGCACAGTCACCATCAAGTGCCAGGCCAGTCAGAGCATTAGCAACTACTTTTCTTG
GTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTACAGGGCGTCCACTCT
GGCATCTGGGGTCCCATCGCGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCT
CACCATCAGCGACCTGGAGTGTGCCGATTCTGCCACTTACTACTGTCAGTGCACTTA
TGGTAGTAGTAGTACTGGTTTTGGTTTCGGCGGAGGGACCGAGGTGGTGGTCAAAG
GTGATCCAGTTGCACCTACTGTCCCCATCTTCCCACCAGCTGCTGATCAGGTGGCAA
CTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCACCGTCA
CCTGGGAGGTGGATGGCACCACCCAAACAACTGGCATCGAGAACAGTAAAACACCG
CAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAGCACA
CAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACCTCAGT
CGTCCAGAGCTTCAATAGGGGTGACTGTTAG (**SEQ ID NO: 68**)

A11B1_11D10 Heavy Chain
ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACT
CACCTGCATGGCCTCTGGAATCGACTTCAGTAGCGGCTACGGCATGTGGTGGGTCCG
CCAGGCTCCAGGGAAGGGACTGGAGTATATCGGATACATTGATACTGGTGATGATA
ACACATACTACGCGAACTGGGCGAAAGGCCGATTCACCATCTCCAAAACCTCGTCG
ACCACGGTGACTCTGCAAATGACCAGTCTGACAGTCGCGGACACGGCCACCTATTTC
TGTGCGAAAGGGGGCGCCATAGACCTCTGGGGCCCAGGGACCCTCGTCACCGTCTC
TTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCTGCTGCGGGGACAC
ACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCTCCCGGAGCCAGT
GACCGTGACCTGGAACTCGGGCACCCTCACCAATGGGGTACGCACCTTCCCGTCCGT

CCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCA
GCCAGCCCGTCACCTGCAACGTGGCCCACCCAGCCACCAACACCAAAGTGGACAAG
ACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCCACCCCCTGAACTCCCGGGG
GGACCGTCTGTCTTCATCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCACGC
ACCCCCGAGGTCACATGCGTGGTGGTGGACGTGAGCCAGGATGACCCCGAGGTGCA
GTTCACATGGTACATAAACAACGAGCAGGTGCGCACCGCCCGGCCGCCGCTACGGG
AGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCTCCCCATCGCGCACCAG
GACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAGGCACTCCCGGC
CCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCTGGAGCCGAAGGTCT
ACACCATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTCGGTCAGCCTGACCTGC
ATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAGAAGAACGGGAA
GGCAGAGGACAACTACAAGACCACGCCGACCGTGCTGGACAGCGACGGCTCCTACT
TCCTCTACAGCAAGCTCTCAGTGCCCACGAGTGAGTGGCAGCGGGGCGACGTCTTCA
CCTGCTCCGTGATGCACGAGGCCTTGCACAACCACTACACGCAGAAGTCCATCTCCC
GCTCTCCGGGTAAATAG (**SEQ ID NO: 69**)

A11B1_11D10 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGACTCCTACTGCTCTGGCTCCCAGGT
GCCAGATGTGCTGACATTGTGATGACCCAGACTCCAGCCTCCGTGGAGGCAGCTGTG
GGAGGCACAGTCACCATCAAGTGCCAGGCCAGTCAGAGCATTAGTAGTTACTTAGC
CTGGTATCAGCAGAAACCAGGGCAGCGTCCCAAGCTCCTGATCTACAGGGCATCCA
CTCTAAAATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGAGTAC
ACTCTCACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTATTATTGTCAAGCG
TATTATCTTAGTAGTAGTATCAGTTATGGTAATACTTTCGGCGGAGGGACCGAGGTG
GTGGTCAAAGGTGATCCAGTTGCACCTACTGTCCTCATCTTCCCACCAGCTGCTGAT
CAGGTGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGAT
GTCACCGTCACCTGGGAGGTGGATGGCACCACCCAAACAACTGGCATCGAGAACAG
TAAAACACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACT
GACCAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGC
ACGACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (**SEQ ID NO: 70**)

A11B1_10F9 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCGTCCCTGACACT
CACCTGCACAGCCTCTGGATTCTCCCTCAGTAGCGGGTATGGCATGTGCTGGGTCCG
CCAGGCTCCAGGGAAGGGACTGGAGTGGATCGGATACACTGATACTGCTACTGGTA
CCATTCACTACGCGAGCTGGGCGAAAGGCCGATTCACCATCTCCAAAACCTCGTCGA
CCACGGTGACTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATTTCT
GTGCGAAAGGGGGCGCCATGGACCTCTGGGGCCCAGGGACCCTCGTCACCGTCTCT
TCAGGGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCTGCTGCGGGGACACA
CCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCTCCCGGAGCCAGTG
ACCGTGACCTGGAACTCGGGCACCCTCACCAATGGGGTACGCACCTTCCCGTCCGTC
CGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCAG
CCAGCCCGTCACCTGCAACGTGGCCCACCCAGCCACCAACACCAAAGTGGACAAGA
CCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCCACCCCCTGAACTCCCGGGGG
GACCGTCTGTCTTCATCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCACGCA

CCCCCGAGGTCACATGCGTGGTGGTGGACGTGAGCCAGGATGACCCCGAGGTGCAG
TTCACATGGTACATAAACAACGAGCAGGTGCGCACCGCCCGGCCGCCGCTACGGGA
GCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCTCCCCATCGCGCACCAGG
ACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAGGCACTCCCGGCC
CCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCTGGAGCCGAAGGTCTA
CACCATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTCGGTCAGCCTGACCTGCA
TGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAGAAGAACGGGAAG
GCAGAGGACAACTACAAGACCACGCCGACCGTGCTGGACAGCGACGGCTCCTACTT
CCTCTACAGCAAGCTCTCAGTGCCCACGAGTGAGTGGCAGCGGGGCGACGTCTTCA
CCTGCTCCGTGATGCACGAGGCCTTGCACAACCACTACACGCAGAAGTCCATCTCCC
GCTCTCCGGGTAAATAG (**SEQ ID NO: 71**)

A11B1_10F9 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTACTGCTCTGGCTCCCAGGT
GCCAGATGTGCTGACATTGTGATGACCCAGACTCCAGCCTCCGTGGAGGCAGCTGTG
GGAGGCACAGTCACCATCAAGTGCCAGGCCAGTCAGAGCATTAGTAGCTACTTAGC
CTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTACAGGACATCCA
CTCTGGCATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGAGTAC
ACTCTCACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTACTATTGTCAAAGC
TATGCTTATAGTAGTAGTAGCAGTTATGGTAATGCTTTCGGCGGAGGGACCGAGGTG
GTGGTCAAAGGTGATCCAGTTGCACCTACTGTCCTCATCTTCCCACCAGCTGCTGAT
CAGGTGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGAT
GTCACCGTCACCTGGGAGGTGGATGGCACCACCCAAACAACTGGCATCGAGAACAG
TAAAACACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACT
GACCAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGC
ACGACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (**SEQ ID NO: 72**)

A11B1_7H12 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACT
CACCTGCACAGGCTCTGGAATCGACTTCAGTAGCAGCTACTGGATATGCTGGGTCCG
CCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATCGATGGTAGTGATGGTA
ACACTTACTACGCGAGCTGGGCGAGAGGCCGATTCACCATCTCCAAAACCTCGTCG
ACCACGGTGACTCTGCAAATGGCCAGTCTGACAGCCGCGGACACGGCCACCTATTTC
TGTACGAGAGATCTCAGGTTGTGGGGCCCAGGCACCCTGGTCACCGTCTCCTCAGGG
CAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCTGCTGCGGGGACACACCCAGC
TCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCTCCCGGAGCCAGTGACCGTG
ACCTGGAACTCGGGCACCCTCACCAATGGGGTACGCACCTTCCCGTCCGTCCGGCAG
TCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCAGCCAGCCC
GTCACCTGCAACGTGGCCCACCCAGCCACCAACACCAAAGTGGACAAGACCGTTGC
GCCCTCGACATGCAGCAAGCCCATGTGCCCACCCCCTGAACTCCCGGGGGGGACCGT
CTGTCTTCATCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCACGCACCCCCG
AGGTCACATGCGTGGTGGTGGACGTGAGCCAGGATGACCCCGAGGTGCAGTTCACA
TGGTACATAAACAACGAGCAGGTGCGCACCGCCCGGCCGCCGCTACGGGAGCAGCA
GTTCAACAGCACGATCCGCGTGGTCAGCACCCTCCCCATCGCGCACCAGGACTGGCT
GAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAGGCACTCCCGGCCCCCATCG

AGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCTGGAGCCGAAGGTCTACACCATG
GGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTCGGTCAGCCTGACCTGCATGATCAA
CGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAGAAGAACGGGAAGGCAGAGG
ACAACTACAAGACCACGCCGACCGTGCTGGACAGCGACGGCTCCTACTTCCTCTACA
GCAAGCTCTCAGTGCCCACGAGTGAGTGGCAGCGGGGCGACGTCTTCACCTGCTCC
GTGATGCACGAGGCCTTGCACAACCACTACACGCAGAAGTCCATCTCCCGCTCTCCG
GGTAAATAG (**SEQ ID NO: 73**)

A11B1_7H12 Light Chain
ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCAGATGTGCTGACATTGTGCTGACCCAGACTCCAGCCTCGGTGTCTGCAGCTGTG
GGAGGCACAGTCACCATCAACTGCCAGGCCAGTCAGAATGTTTATAGTAACAATGC
CTTAGCCTGGCATCAGCAGAAACCAGGGCAGCGTCCCAACCTCCTGATCTACAAGG
CTTCCACTCTGGCATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACAC
AGTTTACTCTCACCATCAGCGACGTGCAGTGTGACGATGCTGCCACTTACTACTGTC
TAGGCGAATTTAGTTGTAGTAGTGGTGATTGTTTTGTTTTCGGCGGAGGGACCGAGG
TGGTGGTCAAAGGTGATCCAGTTGCACCTACTGTCCTCATCTTCCCACCAGCTGCTG
ATCAGGTGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCG
ATGTCACCGTCACCTGGGAGGTGGATGGCACCACCCAAACAACTGGCATCGAGAAC
AGTAAAACACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGAC
ACTGACCAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGG
GCACGACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (**SEQ ID NO: 74**)

A11B1_7G12 Heavy Chain
ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACT
CACCTGCATGGCCTCTGGAATCGACTTCAGTAGCGGCTACGGCATGTGGTGGGTCCG
CCAGGCTCCAGGGAAGGGACTGGAGTATATCGGATACATTGATACTGGTGATGATA
ACACATACTACGCGAACTGGGCGAAAGGCCGATTCACCATCTCCAAAACCTCGTCG
ACCACGGTGACTCTGCAAATGACCAGTCTGACAGTCGCGGACACGGCCACCTATTTC
TGTGCGAAAGGGGGCGCCATAGACCTCTGGGGCCCAGGGACCCTCGTCACCGTCTC
TTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCTGCTGCGGGGACAC
ACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCTCCCGGAGCCAGT
GACCGTGACCTGGAACTCGGGCACCCTCACCAATGGGGTACGCACCTTCCCGTCCGT
CCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCA
GCCAGCCCGTCACCTGCAACGTGGCCCACCCAGCCACCAACACCAAAGTGGACAAG
ACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCCACCCCCTGAACTCCCGGGG
GGACCGTCTGTCTTCATCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCACGC
ACCCCCGAGGTCACATGCGTGGTGGTGGACGTGAGCCAGGATGACCCCGAGGTGCA
GTTCACATGGTACATAAACAACGAGCAGGTGCGCACCGCCCGGCCGCCGCTACGGG
AGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCTCCCCATCGCGCACCAG
GACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAGGCACTCCCGGC
CCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCTGGAGCCGAAGGTCT
ACACCATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTCGGTCAGCCTGACCTGC
ATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAGAAGAACGGGAA

GGCAGAGGACAACTACAAGACCACGCCGACCGTGCTGGACAGCGACGGCTCCTACT
TCCTCTACAGCAAGCTCTCAGTGCCCACGAGTGAGTGGCAGCGGGGCGACGTCTTCA
CCTGCTCCGTGATGCACGAGGCCTTGCACAACCACTACACGCAGAAGTCCATCTCCC
GCTCTCCGGGTAAATAG (**SEQ ID NO: 75**)

A11B1_7G12 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGACTCCTACTGCTCTGGCTCCCAGGT
GCCAGATGTGCTGACATTGTGATGACCCAGACTCCAGCCTCCGTGGAGGCAGCTGTG
GGAGGCACAGTCACCATCAAGTGCCAGGCCAGTCAGAGCATTAGTAGTTACTTAGC
CTGGTATCAGCAGAAACCAGGGCAGCGTCCCAAGCTCCTGATCTACAGGGCATCCA
CTCTAAAATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGAGTAC
ACTCTCACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTATTATTGTCAAGCG
TATTATCTTAGTAGTAGTATCAGTTATGGTAATACTTTCGGCGGAGGGACCGAGGTG
GTGGTCAAAGGTGATCCAGTTGCACCTACTGTCCTCATCTTCCCACCAGCTGCTGAT
CAGGTGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGAT
GTCACCGTCACCTGGGAGGTGGATGGCACCACCCAAACAACTGGCATCGAGAACAG
TAAAACACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACT
GACCAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGC
ACGACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (**SEQ ID NO: 76**)

A11B1_6G4 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGCAGCAGCTGGAGGAGTCCGGGGGAGGCCTGGTCAAGCCTGGAGGAACCCTGAC
ACTCACCTGCAAAGCCTCTGGAGTCGCCCTCAATCCCTACTACTATATGTGCTGGGT
CCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCGTGGATGCTGATAGTA
GTGGTAGCACTTACTACGCGAGCTGGGCGAAAGGCCGATTCACCATCTCCAAAACC
TCGTCGACCACGGTGACTCTGAAAATGACCAGTCTGACAGCCGCGGACACGGCCAC
CTATTTCTGTGCGAGAGAATCGGTTGACTATAGTTCTGTTGGTATTGGCTATGTACAT
GGTACGGATGGCTTGTGGGGCCCAGGCACCCTGGTCACCGTCTCCTCAGGGCAACCT
AAGGCTCCATCAGTCTTCCCACTGGCCCCCTGCTGCGGGGACACACCCAGCTCCACG
GTGACCCTGGGCTGCCTGGTCAAAGGCTACCTCCCGGAGCCAGTGACCGTGACCTG
GAACTCGGGCACCCTCACCAATGGGGTACGCACCTTCCCGTCCGTCCGGCAGTCCTC
AGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCAGCCAGCCCGTCA
CCTGCAACGTGGCCCACCCAGCCACCAACACCAAAGTGGACAAGACCGTTGCGCCC
TCGACATGCAGCAAGCCCATGTGCCCACCCCCTGAACTCCCGGGGGGGACCGTCTGTC
TTCATCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCACGCACCCCCGAGGTC
ACATGCGTGGTGGTGGACGTGAGCCAGGATGACCCCGAGGTGCAGTTCACATGGTA
CATAAACAACGAGCAGGTGCGCACCGCCCGGCCGCCGCTACGGGAGCAGCAGTTCA
ACAGCACGATCCGCGTGGTCAGCACCCTCCCCATCGCGCACCAGGACTGGCTGAGG
GGCAAGGAGTTCAAGTGCAAAGTCCACAACAAGGCACTCCCGGCCCCCATCGAGAA
AACCATCTCCAAAGCCAGAGGGCAGCCCCTGGAGCCGAAGGTCTACACCATGGGCC
CTCCCCGGGAGGAGCTGAGCAGCAGGTCGGTCAGCCTGACCTGCATGATCAACGGC
TTCTACCCTTCCGACATCTCGGTGGAGTGGGAGAAGAACGGGAAGGCAGAGGACAA
CTACAAGACCACGCCGACCGTGCTGGACAGCGACGGCTCCTACTTCCTCTACAGCAA
GCTCTCAGTGCCCACGAGTGAGTGGCAGCGGGGCGACGTCTTCACCTGCTCCGTGAT

GCACGAGGCCTTGCACAACCACTACACGCAGAAGTCCATCTCCCGCTCTCCGGGTAA
ATAG (**SEQ ID NO: 77**)

A11B1_6G4 Light Chain
ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCAGATGTGCCGACATCGTGGTGACCCAGACTCCATCCTCCGTGTCTGCAGCTGTG
GGAGGCACAGTCACCATCAAGTGCCAGGCCAGTCAGAGCATTAGCAACTACTTTTCT
TGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTACAGGGCGTCCAC
TCTGGCATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGAGTTCAC
TCTCACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTACTACTGTCAATGCAC
TTACGGTAGAAGTAATAGTAATTTTTTTTATGGTTTCGGCGGAGGGACCGAGGTGGT
GGTCAAAGGTGATCCAGTTGCACCTACTGTCCTCATCTTCCCACCAGCTGCTGATCA
GGTGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGT
CACCGTCACCTGGGAGGTGGATGGCACCACCCAAACAACTGGCATCGAGAACAGTA
AAACACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGA
CCAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACG
ACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (**SEQ ID NO: 78**)

A11B1_6F9 Heavy Chain
ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCCGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCCTCCCTGACACT
CACCTGCACAGCCTCTGGATCCTCCTTCAGTAGTACCTACTGGAACTGCTGGGTCCG
CCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATTAATGCTGGTAGTGGTA
CCACTTACTACGCGAGCTGGGCGAAAGGCCGATTCACCGTCTCCAAAACCTCGTCGA
CCACGGTGACTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATTTCT
GTACGAGAGATAGTGATGGTCGTTTTAGTAGTGGCTACTATTTTAACTTGTGGGGCC
CAGGCACCCTGGTCACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCAC
TGGCCCCCTGCTGCGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCA
AAGGCTACCTCCCGGAGCCAGTGACCGTGACCTGGAACTCGGGCACCCTCACCAAT
GGGGTACGCACCTTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGC
GTGGTGAGCGTGACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGCCCACCCAGC
CACCAACACCAAAGTGGACAAGACCGTTGCGCCCTCGACATGCAGCAAGCCCATGT
GCCCACCCCCTGAACTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCCCAAAACCCA
AGGACACCCTCATGATCTCACGCACCCCCGAGGTCACATGCGTGGTGGTGGACGTG
AGCCAGGATGACCCCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAGGTGCG
CACCGCCCGGCCGCCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTGGTCA
GCACCCTCCCCATCGCGCACCAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAA
GTCCACAACAAGGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAGAGG
GCAGCCCCTGGAGCCGAAGGTCTACACCATGGGCCCTCCCCGGGAGGAGCTGAGCA
GCAGGTCGGTCAGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACATCTCGG
TGGAGTGGGAGAAGAACGGGAAGGCAGAGGACAACTACAAGACCACGCCGACCGT
GCTGGACAGCGACGGCTCCTACTTCCTCTACAGCAAGCTCTCAGTGCCCACGAGTGA
GTGGCAGCGGGGCGACGTCTTCACCTGCTCCGTGATGCACGAGGCCTTGCACAACC
ACTACACGCAGAAGTCCATCTCCCGCTCTCCGGGTAAATAG (**SEQ ID NO: 79**)

A11B1_6F9 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCACATTTGCCCAAGTGCTGACCCAGACTGCATCCCCTGTGTCTGCAGCTGTGGGA
GGCACAGTCACCATCAATTGTCAGTCCAGTCAGAGTGTTTATGATAACAACTGGTTA
GCCTGGTATCAGCAAAAACCAGGGCAGCCTCCCAAACTCTTGATCGACGATGCATC
CAAATTGACATCTGGGGTCTCATCGCGGTTCAAAGGCAGTGGATCTGGGACGCAGTT
CACTCTCACCATCAGCGGCGTGCAGTGTGACGATGCTGCCACTTACTACTGTCAAGG
CGCTTATTATAGTAGTGGTTGGTACTGGGCTTTCGGCGGAGGGACCGAGGTGGTGGT
CAAAGGTGATCCAGTTGCACCTACTGTCCTCATCTTCCCACCAGCTGCTGATCAGGT
GGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCAC
CGTCACCTGGGAGGTGGATGGCACCACCCAAACAACTGGCATCGAGAACAGTAAAA
CACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCA
GCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACC
TCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (**SEQ ID NO: 80**)

A11B1_6C7 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGCAGCAGCTGGAGGAGTCCGGGGGAGGCCTGGTCAAGCCTGGAGGAACCCTGAC
ACTCACCTGCAAAGCCTCTGGAATCGACTTCAGTAGCTACTACTACATGTGTTGGGT
CCGCCAGGCTCCAGGGAAGGGGCTGGAGTTGATCGTATGTATTTATACTAGTAGTGG
TGGCACATGGTACGCGAGCTGGGTGAATGGCCGACTCACCATCTCCAGAAGCACCA
GCCTAAACACGGTGGATCTGAAAATGACCAGTCTGACAGCCGCGGACACGGCCACC
TATTTCTGTGCCAGAGGGGTTTATTCTGGTAGTAGTGATTATCCAACTCGGTTGGATC
TCTGGGGCCAGGGCACCCTGGTCACCGTCTCCTTAGGGCAACCTAAGGCTCCATCAG
TCTTCCCACTGGCCCCCTGCTGCGGGGACACACCCAGCTCCACGGTGACCCTGGGCT
GCCTGGTCAAAGGCTACCTCCCGGAGCCAGTGACCGTGACCTGGAACTCGGGCACC
CTCACCAATGGGGTACGCACCTTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCG
CTGAGCAGCGTGGTGAGCGTGACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGC
CCACCCAGCCACCAACACCAAAGTGGACAAGACCGTTGCGCCCTCGACATGCAGCA
AGCCCATGTGCCCACCCCCTGAACTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCC
CAAAACCCAAGGACACCCTCATGATCTCACGCACCCCCGAGGTCACATGCGTGGTG
GTGGACGTGAGCCAGGATGACCCCGAGGTGCAGTTCACATGGTACATAAACAACGA
GCAGGTGCGCACCGCCCGGCCGCCGCTACGGGAGCAGCAGTTCAACAGCACGATCC
GCGTGGTCAGCACCCTCCCCATCGCGCACCAGGACTGGCTGAGGGGCAAGGAGTTC
AAGTGCAAAGTCCACAACAAGGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAA
AGCCAGAGGGCAGCCCCTGGAGCCGAAGGTCTACACCATGGGCCCTCCCCGGGAGG
AGCTGAGCAGCAGGTCGGTCAGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCG
ACATCTCGGTGGAGTGGGAGAAGAACGGGAAGGCAGAGGACAACTACAAGACCAC
GCCGACCGTGCTGGACAGCGACGGCTCCTACTTCCTCTACAGCAAGCTCTCAGTGCC
CACGAGTGAGTGGCAGCGGGGCGACGTCTTCACCTGCTCCGTGATGCACGAGGCCT
TGCACAACCACTACACGCAGAAGTCCATCTCCCGCTCTCCGGGTAAATAG (**SEQ ID NO: 81**)

A11B1_6C7 Light Chain

ATGGACACGAGCACCTCCACTGCGCTCCTGGGGCTCCTGCTGCTCTGGCTCACAGGT
GCCAGATGTGCCATCGAGATGACCCAGTCTCCACCCTCCCTGTCTGCATCTGTGGGA
GAAACTGTCAGGATTAGGTGCCTGGCCAGTGAGGACATTTACAGTGGTATATCCTGG

TACCAACAGAAGCCAGAGAAACCTCCTACACTCCTGATCTCTGGTGCATCCAATTTA
GAATCTGGGGTCCCACCACGGTTCAGTGGCGGTGGATCCGGGACAGATTACACCCT
CACCATCGGCGGCGTGCAGGCTGAAGATGTTGCCACCTACTACTGTCTAGGCGGTTA
TAGTTTCAGTAGTACCGGTTTGACTTTTGGAGCTGGCACCAAGGTGGAAATCAAACG
TGATCCAGTTGCGCCTTCTGTCCTCCTCTTCCCACCATCTAAGGAGGAGCTGACAAC
TGGAACAGCCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCACCGTCAC
CTGGGAGGTGGATGGCACCACCCAAACAACTGGCATCGAGAACAGTAAAACACCGC
AGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAGCACAC
AGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACCTCAGTC
GTCCAGAGCTTCAATAGGGGTGACTGTTAG (**SEQ ID NO: 82**)

A11B1_6B6 Heavy Chain
ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGCAACATCTGGTGGAGTCCGGGGGAGGCCTGGTCAAGCCTGGGGCATCCCTGAC
ACTCACCTGCACAGCCTCTGGATTCTCCTTCACTACCGGCTATCACATGTGCTGGGTC
CGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGTTTTGGTGTTTATACTAGT
ACCACTACCTACGCGAGCTGGGCGAAAGGTCGATTCACCATCTCCAAAACCTCGTCG
ACCACGGTGACTCTACAAATGACCAGTCTAACAGTCGCGGACACGGCCACCTATTTC
TGTGCGAGAATCAGTGCTGAAGATGGTGGGGACTTGTGGGGCCCAGGCACCCTGGT
CACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCTGCTG
CGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCTCC
CGGAGCCAGTGACCGTGACCTGGAACTCGGGCACCCTCACCAATGGGGTACGCACC
TTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTG
ACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGCCCACCCAGCCACCAACACCAA
AGTGGACAAGACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCCACCCCCTG
AACTCCCGGGGGGGACCGTCTGTCTTCATCTTCCCCCCAAAACCCAAGGACACCCTCA
TGATCTCACGCACCCCCGAGGTCACATGCGTGGTGGTGGACGTGAGCCAGGATGAC
CCCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAGGTGCGCACCGCCCGGCC
GCCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCTCCCCA
TCGCGCACCAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAG
GCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCTGGA
GCCGAAGGTCTACACCATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTCGGTCA
GCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAGA
AGAACGGGAAGGCAGAGGACAACTACAAGACCACGCCGACCGTGCTGGACAGCGA
CGGCTCCTACTTCCTCTACAGCAAGCTCTCAGTGCCCACGAGTGAGTGGCAGCGGGG
CGACGTCTTCACCTGCTCCGTGATGCACGAGGCCTTGCACAACCACTACACGCAGAA
GTCCATCTCCCGCTCTCCGGGTAAATAG (**SEQ ID NO: 83**)

A11B1_6B6 Light Chain
ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCAGATGTGATGTTGTGATGACCCAGACTCCAGCCTCCGTGGAGGCAGCTGTGGG
AGGCACAGTCACCATCACGTGCCAGGCCAGTCAGAGCATTAGCAACTACTTTTCTTG
GTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTACAGGGCGTCCACTCT
GGCATCTGGGGTCCCATCGCGGTTCAGCGGCAGTGGATCTGGGACACAGTTCACTCT
CACCATCAGCGACCTGGAGTGTGCCGATTCTGCCACTTACGCCTGTCAGTGCACTTA
TGGTAGTAGTAGTACTGGTTTTGGTTTCGGCGGAGGGACCGAGGTGGTGGTCAAAG

GTGATCCAGTTGCACCTACTGTCCTCATCTTCCCACCAGCTGCTGATCAGGTGGCAA
CTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCACCGTCA
CCTGGGAGGTGGATGGCACCACCCAAACAACTGGCATCGAGAACAGTAAAACACCG
CAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAGCACA
CAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACCTCAGT
CGTCCAGAGCTTCAATAGGGGTGACTGTTAG (**SEQ ID NO: 84**)

A11B1_5F7 Heavy Chain
ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACT
CACCTGCAAAGCCTCTGGATTCTCCTTCAGTAGTTACTTCTGGATATGCTGGGTCCGC
CAGGCTCCAGGGAAGGGGCTGGAGTGGAGCGCATGCATCTATGGTGATAGTAGTGG
TAGTAGTTACTACGCGAGCTGGGCGAAAGGCCGATTCACCATCTCCAAAACCTCGTC
GACCACGGTGACTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATT
TCTGTGCGAGTTATGGTAGTAGTAGTTATTACTACTCTAATTTATGGGGCCCAGGCA
CCCTGGTCACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCC
CCTGCTGCGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGC
TACCTCCCGGAGCCAGTGACCGTGACCTGGAACTCGGGCACCCTCACCAATGGGGT
ACGCACCTTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGT
GAGCGTGACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGCCCACCCAGCCACCA
ACACCAAAGTGGACAAGACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCCA
CCCCCTGAACTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCCCAAAACCCAAGGAC
ACCCTCATGATCTCACGCACCCCCGAGGTCACATGCGTGGTGGTGGACGTGAGCCA
GGATGACCCCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAGGTGCGCACCG
CCCGGCCGCCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACC
CTCCCCATCGCGCACCAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCA
CAACAAGGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGC
CCCTGGAGCCGAAGGTCTACACCATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGG
TCGGTCAGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAG
TGGGAGAAGAACGGGAAGGCAGAGGACAACTACAAGACCACGCCGACCGTGCTGG
ACAGCGACGGCTCCTACTTCCTCTACAGCAAGCTCTCAGTGCCCACGAGTGAGTGGC
AGCGGGGCGACGTCTTCACCTGCTCCGTGATGCACGAGGCCTTGCACAACCACTACA
CGCAGAAGTCCATCTCCCGCTCTCCGGGTAAATAG (**SEQ ID NO: 85**)

A11B1_5F7 Light Chain
ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCATATGTGACCCTGTGATGACCCAGACTCCATCTTCCACGTCTGCGGCTGTGGGA
GGCACAGTCACCATCAGTTGCCAGTCCAGTCAGAGTGTTTATAATAACAACTACTTA
GCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAACGCCTGATCTACGAATCATC
CAAACTGGCATCTGGGGTCCCATCGCGGTTCAGAGGCAGTGGATCTGGGGCACAGT
TCACTCTCACCATCAGCGACCTGGAGTGTGACGATGCTGCCACTTACTACTGTCTAG
GCGCATATTATACTACTCTTGATTTCGGCGGAGGGACCGAGGTGGTGGTCAGAGGTG
ATCCAGTTGCACCTACTGTCCTCATCTTCCCACCAGCTGCTGATCAGGTGGCAACTG
GAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCACCGTCACCT
GGGAGGTGGATGGCACCACCCAAACAACTGGCATCGAGAACAGTAAAACACCGCA
GAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAGCACACA

GTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACCTCAGTCG
TCCAGAGCTTCAATAGGGGTGACTGTTAG (**SEQ ID NO: 86**)

A11B1_5D7 Heavy Chain
ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGGAGCAGTTGGTGGAGTCCGGGGGAGGCCTGGTCCAGCCTGAGGGATCCCTGAC
ACTCACCTGCAAAGCCTCTGGATTCGACTTCAGTAGCAATGCAATGTGCTGGGTCCG
CCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATTTATAATGGTGATGGCA
GCACATACTACGCGAGCTGGGTGAATGGCCGATTCACCATCTCCAAGACCTCGTCGA
CCACGGTGACTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATTTCT
GTGCGAGAGGTCTCTCTAATTGGAATAGGGATAACTTATGGGGCCCTGGCACCCTGG
TCACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCTGCT
GCGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCTC
CCGGAGCCAGTGACCGTGACCTGGAACTCGGGCACCCTCACCAATGGGGTACGCAC
CTTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGT
GACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGCCCACCCAGCCACCAACACCA
AAGTGGACAAGACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCCACCCCCT
GAACTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCCCAAAACCCAAGGACACCCTC
ATGATCTCACGCACCCCCGAGGTCACATGCGTGGTGGTGGACGTGAGCCAGGATGA
CCCCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAGGTGCGCACCGCCCGGC
CGCCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCTCCCC
ATCGCGCACCAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAA
GGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCTGG
AGCCGAAGGTCTACACCATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTCGGTC
AGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAG
AAGAACGGGAAGGCAGAGGACAACTACAAGACCACGCCGACCGTGCTGGACAGCG
ACGGCTCCTACTTCCTCTACAGCAAGCTCTCAGTGCCCACGAGTGAGTGGCAGCGGG
GCGACGTCTTCACCTGCTCCGTGATGCACGAGGCCTTGCACAACCACTACACGCAGA
AGTCCATCTCCCGCTCTCCGGGTAAATAG (**SEQ ID NO: 87**)

A11B1_5D7 Light Chain
ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCACATTTGCCCAAGTGCTGACCCAGACTCCATCCTCCGTGTCTGCAGCTGTGGGA
GGCACAGCCACCATCAACTGCCAGGCCAGTCAGAGTCTTTATAGTCCCAAGAATTTA
GCCTGGTATCAGCAGACACCAGGGCAGCCTCCCAAGCTCCTGATCTATTCTGCATCG
AAACTGGCATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACACAGTT
CACTCTCACCATCAGCGGCGTGCAGTGTGACGATGCTGCAATTTACTACTGTCAAGG
CGAATTTAGTTGTACTACTGCTGCTTGTTTTGCTTTTGGCGGAGGGACCGAGGTGGT
GGTCAAAGGTGATCCAGTTGCACCTACTGTCCTCATCTTCCCACCAGCTGCTGATCA
GGTGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGT
CACCGTCACCTGGGAGGTGGATGGCACCACCCAAACAACTGGCATCGAGAACAGTA
AAACACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGA
CCAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACG
ACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (**SEQ ID NO: 88**)

A11B1_5A7 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCTTTGGAGGAGTCCGGGGGAGGCCTGGTCCAGCCTGAGGGATCCCTGACACT
CGCCTGCACAGCTTCGGGATTCTCCTTCAGTAGCTACTACTACATCTGCTGGGTCCG
CCAGGCTCCAGGGACGGGGCTGGAGTGGATCGGATGCATTAATACTGGTAGTGATG
ACACTCACTACGCGAGCTGGTTGAAAGGCCGATTCACCTTCTCCAAGGCCTCGTCGA
CCACGTTGACTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATTTCT
GTGCGAGATCATCTGGTAGTAGTGATGATGCTTATGATCTCTGGGGCCCAGGCACCC
TGGTCACTGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCT
GCTGCGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTAC
CTCCCGGAGCCAGTGACCGTGACCTGGAACTCGGGCACCCTCACCAATGGGGTACG
CACCTTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAG
CGTGACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGCCCACCCAGCCACCAACA
CCAAAGTGGACAAGACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCCACCC
CCTGAACTCCCGGGGGGGACCGTCTGTCTTCATCTTCCCCCCAAAACCCAAGGACACC
CTCATGATCTCACGCACCCCCGAGGTCACATGCGTGGTGGTGGACGTGAGCCAGGA
TGACCCCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAGGTGCGCACCGCCC
GGCCGCCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCTC
CCCATCGCGCACCAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAA
CAAGGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCC
TGGAGCCGAAGGTCTACACCATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTCG
GTCAGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGG
GAGAAGAACGGGAAGGCAGAGGACAACTACAAGACCACGCCGACCGTGCTGGACA
GCGACGGCTCCTACTTCCTCTACAGCAAGCTCTCAGTGCCCACGAGTGAGTGGCAGC
GGGGCGACGTCTTCACCTGCTCCGTGATGCACGAGGCCTTGCACAACCACTACACGC
AGAAGTCCATCTCCCGCTCTCCGGGTAAATAG (**SEQ ID NO: 89**)

A11B1_5A7 Light Chain
ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCAGATGTGATGTTGTGATGACCCAGACTCCAGCCTCCGTGTCTGAACCTGTGGGA
GGCGCAGTCACCATCAAGTGCCAGGCCAGTCAGAGCATTGGTAGTAATTTAGCCTG
GTATCAGCACAAACCAGGGCAGCCTCCCAAGCTCCTGATCTATTTTGCATCCAGCCT
GGCATCTGGGGTCTCGTCGCGGTTCAAGGGCGGTAGATCTGGGACACAGTTCACTCT
CACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTACTACTGTCACTGTACTTA
TTATCCTCTTAGTTATGTTACTTTCGGCGGAGGGACCGAGGTGGTGGTCAAAGGTGA
TCCAGTTGCACCTACTGTCCTCATCTTCCCACCAGCTGCTGATCAGGTGGCAACTGG
AACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCACCGTCACCTG
GGAGGTGGATGGCACCACCCAAACAACTGGCATCGAGAACAGTAAAACACCGCAG
AATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAGCACACAG
TACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACCTCAGTCGT
CCAGAGCTTCAATAGGGGTGACTGTTAG (**SEQ ID NO: 90**)

A11B1_4E1 Heavy Chain
ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGACATCCCTGACACT
CTCCTGCACAGCCTCTGGATTCTCCTTCGGTAGCTATTATTATATGTGCTGGGTCCGC
CAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATTGATGTTGGTAGTAGTGG

TGACACATACTACGCGAGCTGGGTGAATGGCCGATTCACCATCTCCAAAACCTCGTC
GACCACGGTGACTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATT
TCTGTGCGAGAGATGATACTGCTGCTGGTGGTTTTGGTAATTTGGAATTGTGGGGCC
CAGGCACCCTGGTCACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCAC
TGGCCCCCTGCTGCGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCA
AAGGCTACCTCCCGGAGCCAGTGACCGTGACCTGGAACTCGGGCACCCTCACCAAT
GGGGTACGCACCTTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGC
GTGGTGAGCGTGACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGCCCACCCAGC
CACCAACACCAAAGTGGACAAGACCGTTGCGCCCTCGACATGCAGCAAGCCCATGT
GCCCACCCCCTGAACTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCCCAAAACCCA
AGGACACCCTCATGATCTCACGCACCCCCGAGGTCACATGCGTGGTGGTGGACGTG
AGCCAGGATGACCCCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAGGTGCG
CACCGCCCGGCCGCCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTGGTCA
GCACCCTCCCCATCGCGCACCAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAA
GTCCACAACAAGGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAGAGG
GCAGCCCCTGGAGCCGAAGGTCTACACCATGGGCCCTCCCCGGGAGGAGCTGAGCA
GCAGGTCGGTCAGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACATCTCGG
TGGAGTGGGAGAAGAACGGGAAGGCAGAGGACAACTACAAGACCACGCCGACCGT
GCTGGACAGCGACGGCTCCTACTTCCTCTACAGCAAGCTCTCAGTGCCCACGAGTGA
GTGGCAGCGGGGCGACGTCTTCACCTGCTCCGTGATGCACGAGGCCTTGCACAACC
ACTACACGCAGAAGTCCATCTCCCGCTCTCCGGGTAAATAG (**SEQ ID NO: 91**)

A11B1_4E1 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCAGATGTGCATTCGAATTGACCCAGACTCCATCCTCCGTGTCTGAACCTGTGGGA
GGCACAGTCACCATCAAGTGCCAGGCCAGTCAGAGCATTTACAGCTACTTTTCCTGG
TATCAGCAGAAACCAGGGCAGCCTCCCAAGCGCCTGATTTACCAGGCATCCACTCTG
GCTTCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGATTTCACTCTC
ACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTACTACTGTCAAAACAATTAT
GGTAGGGGTAGTGGTAGTTATTTTTTTGGTTTCGGCGGAGGGACCGAGGTGGTGGTC
AAAGGTGATCCAGTTGCACCTACTGTCCTCATCTTCCCACCAGCTGCTGATCAGGTG
GCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCACC
GTCACCTGGGAGGTGGATGGCACCACCCAAACAACTGGCATCGAGAACAGTAAAAC
ACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAG
CACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACCT
CAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (**SEQ ID NO: 92**)

A11B1_3H9 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACT
CACCTGCAAAGCCTCTGGAATCGACTTCAGTAGCGGCTACGGCATGTGGTGGGTCCG
CCAGGCTCCAGGGAAGGGACTGGAGTATATCGGATACATTGATACTGGTAGTGGTA
GCACTTACTACGCGAACTGGGCGAAAGGCCGATTCACCATCTCCAAAACCTCGTCG
ACCATGGTGACTCTGCAAATGACCAGTCTGACAGTCGCGGACACGGCCACCTATTTC
TGTGCGAAAGGGGGCGCCATAGACCTCTGGGGCCCAGGGACCCTCGTCACCGTCTC
TTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCTGCTGCGGGGACAC

ACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCTCCCGGAGCCAGT
GACCGTGACCTGGAACTCGGGCACCCTCACCAATGGGGTACGCACCTTCCCGTCCGT
CCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCA
GCCAGCCCGTCACCTGCAACGTGGCCCACCCAGCCACCAACACCAAAGTGGACAAG
ACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCCACCCCCTGAACTCCCGGGG
GGACCGTCTGTCTTCATCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCACGC
ACCCCCGAGGTCACATGCGTGGTGGTGGACGTGAGCCAGGATGACCCCGAGGTGCA
GTTCACATGGTACATAAACAACGAGCAGGTGCGCACCGCCCGGCCGCCGCTACGGG
AGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCTCCCCATCGCGCACCAG
GACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAGGCACTCCCGGC
CCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCTGGAGCCGAAGGTCT
ACACCATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTCGGTCAGCCTGACCTGC
ATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAGAAGAACGGGAA
GGCAGAGGACAACTACAAGACCACGCCGACCGTGCTGGACAGCGACGGCTCCTACT
TCCTCTACAGCAAGCTCTCAGTGCCCACGAGTGAGTGGCAGCGGGGCGACGTCTTCA
CCTGCTCCGTGATGCACGAGGCCTTGCACAACCACTACACGCAGAAGTCCATCTCCC
GCTCTCCGGGTAAATAG (**SEQ ID NO: 93**)

A11B1_3H9 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGACTCCTACTGCTCTGGCTCCCAGGT
GCCAGATGTGCTGACATTGTGATGACCCAGACTCCAGCCTCCGTGGAGGCAGCTGTG
GGAGGCACAGTCACCATCAAGTGCCAGGCCAGTCAGAGCATTAGTAGTTACTTAGC
CTGGTATCAGCAGAAACCAGGGCAGCGTCCCAAGCTCCTGATCTACAGGGCATCCA
CTCTGGCATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGACTACA
CTCTCACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTATTATTGTCATACCTA
TTATCTTAGTAGTAGTATCAGTTATGGTAATACTTTCGGCGGAGGGACCGAGGTGGT
GGTCAAAGGTGATCCAGTTGCACCTACTGTCCTCATCTTCCCACCAGCTGCTGATCA
GGTGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGT
CACCGTCACCTGGGAGGTGGATGGCACCACCCAAACAACTGGCATCGAGAACAGTA
AAACACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGA
CCAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACG
ACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (**SEQ ID NO: 94**)

A11B1_3G2 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGGAGCAGCTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGAGGGATCCCTGAC
ACTCACCTGCAAAGCCTCTGGATTCTCCTTCAGTAGCATCTACTGGATTTGCTGGGTC
CGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCACTACTGTTGTCAAAAG
TGGTAGAACTTACTACGCGAACTGGGCGAAAGGCCGATTCACCATCTCCAAAACCT
CGTCGACCACGGTGACTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACC
TATTTCTGTGCGAGAGAATTTGTTGATGGTGGTGGTAGTAGTGGTAGGGACTTGTGG
GGCCCAGGCACCCTGGTCACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTTC
CCACTGGCCCCCTGCTGCGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTG
GTCAAAGGCTACCTCCCGGAGCCAGTGACCGTGACCTGGAACTCGGGCACCCTCAC
CAATGGGGTACGCACCTTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGAG
CAGCGTGGTGAGCGTGACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGCCCACC

CAGCCACCAACACCAAAGTGGACAAGACCGTTGCGCCCTCGACATGCAGCAAGCCC
ATGTGCCCACCCCCTGAACTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCCCAAAA
CCCAAGGACACCCTCATGATCTCACGCACCCCCGAGGTCACATGCGTGGTGGTGGA
CGTGAGCCAGGATGACCCCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAGG
TGCGCACCGCCCGGCCGCCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTG
GTCAGCACCCTCCCCATCGCGCACCAGGACTGGCTGAGGGGCAAGGAGTTCAAGTG
CAAAGTCCACAACAAGGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCA
GAGGGCAGCCCCTGGAGCCGAAGGTCTACACCATGGGCCCTCCCCGGGAGGAGCTG
AGCAGCAGGTCGGTCAGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACATC
TCGGTGGAGTGGGAGAAGAACGGGAAGGCAGAGGACAACTACAAGACCACGCCGA
CCGTGCTGGACAGCGACGGCTCCTACTTCCTCTACAGCAAGCTCTCAGTGCCCACGA
GTGAGTGGCAGCGGGGCGACGTCTTCACCTGCTCCGTGATGCACGAGGCCTTGCAC
AACCACTACACGCAGAAGTCCATCTCCCGCTCTCCGGGTAAATAG (**SEQ ID NO: 95**)

A11B1_3G2 Light Chain

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCAGATGTGCCTATGATATGACCCAGACTCCAGCCTCCGTGGAGGCAGCTGTGGG
AGGCACAGTCACCATCAAGTGCCAGGCCAGTCAGAGCATTAGTAGGGACTTATCCT
GGTATCAGCAGAAACCTGGACAGCCTCCCAAGCGCCTAATCTACAAGGCATCCACT
CTGGCATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGATTTCACT
CTCACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTACTACTGTCAACAGGGT
TATAGTAGTATTGATGTTGATAATGATTTCGGCGGAGGGACCGAGGTGGTGGTCAAA
GGTGATCCAGTTGCACCTACTGTCCTCATCTTCCCACCAGCTGCTGATCAGGTGGCA
ACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCACCGTC
ACCTGGGAGGTGGATGGCACCACCCAAACAACTGGCATCGAGAACAGTAAAACACC
GCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAGCAC
ACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACCTCAG
TCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (**SEQ ID NO: 96**)

A11B1_3B1 Heavy Chain

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGGAGCAGCTGGAGGAGTCCGGGGGAGGCCTGGTCAAGCCTGAGGGATCCCTGAC
ACTCACCTGCAAAGCCTCTGGATTCGACCTCAGTAGCGGCTATGACATGTGCTGGGT
CCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATTTATGCTGATTATA
GTGGTAGCACATACTACGCGAGCTGGGTGAATGGCCGATTCACCATCTCCAGCAGC
ACCAGCCTAAACACGGTGGATCTGAAAATGACCAGTCTGACAGCCGCGGACACGGC
CACCTATTTCTGTGCCAGAGGGGCTACTGGTAATGGTGGTTATGGATACTACTTTAA
CTTGTGGGGCCCAGGCACCCTGGTCACCGTCTCCTCAGGGCAACCTAAGGCTCCATC
AGTCTTCCCACTGGCCCCCTGCTGCGGGGACACACCCAGCTCCACGGTGACCCTGGG
CTGCCTGGTCAAAGGCTACCTCCCGGAGCCAGTGACCGTGACCTGGAACTCGGGCA
CCCTCACCAATGGGGTACGCACCTTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACT
CGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCAGCCAGCCCGTCACCTGCAACGTG
GCCCACCCAGCCACCAACACCAAAGTGGACAAGACCGTTGCGCCCTCGACATGCAG
CAAGCCCATGTGCCCACCCCCTGAACTCCCGGGGGGACCGTCTGTCTTCATCTTCCC
CCCAAAACCCAAGGACACCCTCATGATCTCACGCACCCCCGAGGTCACATGCGTGG
TGGTGGACGTGAGCCAGGATGACCCCGAGGTGCAGTTCACATGGTACATAAACAAC

GAGCAGGTGCGCACCGCCCGGCCGCCGCTACGGGAGCAGCAGTTCAACAGCACGAT
CCGCGTGGTCAGCACCCTCCCCATCGCGCACCAGGACTGGCTGAGGGGCAAGGAGT
TCAAGTGCAAAGTCCACAACAAGGCACTCCCGGCCCCCATCGAGAAAACCATCTCC
AAAGCCAGAGGGCAGCCCCTGGAGCCGAAGGTCTACACCATGGGCCCTCCCCGGGA
GGAGCTGAGCAGCAGGTCGGTCAGCCTGACCTGCATGATCAACGGCTTCTACCCTTC
CGACATCTCGGTGGAGTGGGAGAAGAACGGGAAGGCAGAGGACAACTACAAGACC
ACGCCGACCGTGCTGGACAGCGACGGCTCCTACTTCCTCTACAGCAAGCTCTCAGTG
CCCACGAGTGAGTGGCAGCGGGGCGACGTCTTCACCTGCTCCGTGATGCACGAGGC
CTTGCACAACCACTACACGCAGAAGTCCATCTCCCGCTCTCCGGGTAAATAG (**SEQ ID NO: 97**)

A11B1_3B1 Light Chain
ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTACTGCTCTGGCTCCCAGGT
GCCAGATGTGCTGACATTGTGATGACCCAGACTCCAGCCTCCGTGTCTGAACCTGTG
GGAGGCACAGTCACCATCAAGTGTCAGGCCAGTCAGAACATTAATAGCGGCTTAGC
CTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTACAAGGCATCCA
CTCTGGCATCTGGGGTCTCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGAATTCA
CTCTCACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTACTACTGTCAAACCT
ATTATTATAGTAGTAGTAGTAGTGATAATGCTTTCGGCGGAGGGACCGAGGTGGTGG
TCAAAGGTGATCCAGTTGCACCTACTGTCCTCATCTTCCCACCAGCTGCTGATCAGG
TGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCA
CCGTCACCTGGGAGGTGGATGGCACCACCCAAACAACTGGCATCGAGAACAGTAAA
ACACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACC
AGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGA
CCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (**SEQ ID NO: 98**)

A11B1_2D3 Heavy Chain
ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACT
CACCTGCACAGCTTCTGGATTCTCCTTCAGTAGCAGTTATTGGATATGCTGGGTCCGC
CAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGTATTTATGGTGGTAGTAGTGG
TAACATTGCCTACGCGAGCTGGGCGAAAGGCCGATTCACCATCTCCAAAACCTCGTC
GACCACGGTGACTCTACAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATT
TCTGTGCGAGAGATATTCCTAGTGATGCTTTCACCTTAGACTTGTGGGGCCCAGGCA
CCCTGGTCACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCC
CCTGCTGCGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGC
TACCTCCCGGAGCCAGTGACCGTGACCTGGAACTCGGGCACCCTCACCAATGGGGT
ACGCACCTTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGT
GAGCGTGACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGCCCACCCAGCCACCA
ACACCAAAGTGGACAAGACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCCA
CCCCCTGAACTCCCGGGGGGACCGTCTGTCTTCATCTTCCCCCCAAAACCCAAGGAC
ACCCTCATGATCTCACGCACCCCCGAGGTCACATGCGTGGTGGTGGACGTGAGCCA
GGATGACCCCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAGGTGCGCACCG
CCCGGCCGCCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACC
CTCCCCATCGCGCACCAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCA
CAACAAGGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGC

CCCTGGAGCCGAAGGTCTACACCATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGG
TCGGTCAGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAG
TGGGAGAAGAACGGGAAGGCAGAGGACAACTACAAGACCACGCCGACCGTGCTGG
ACAGCGACGGCTCCTACTTCCTCTACAGCAAGCTCTCAGTGCCCACGAGTGAGTGGC
AGCGGGGCGACGTCTTCACCTGCTCCGTGATGCACGAGGCCTTGCACAACCACTACA
CGCAGAAGTCCATCTCCCGCTCTCCGGGTAAATAG (**SEQ ID NO: 99**)

A11B1_2D3 Light Chain
ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCACATTTGCCCAAGTGCTGACCCAGACTCCATCCTCCGTGTCTGCAGCTGTGGGA
AGCACAGTCACCATCAATTGCCAGGCCAGTCAGAGTGTTTATAAAGACAACAATTTA
GCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTACAAGGCTTCC
ACTCTGGCATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACACAGTTC
ACTCTCACCATCAGCGGCGTGCAGTGTGAAGATGCTGCCACTTACTACTGTCAAGGC
GAATTCAGTTGTGGTAGTGCTGATTGTATTGCTTTCGGCGGAGGGACCGAGGTGGTG
GTCAAAGGTGATCCAGTTGCACCTACTGTCCTCATCTTCCCACCAGCTGCTGATCAG
GTGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTC
ACCGTCACCTGGGAGGTGGATGGCACCACCCAAACAACTGGCATCGAGAACAGTAA
AACACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGAC
CAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACG
ACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (**SEQ ID NO: 100**)

A11B1_2A7 Heavy Chain
ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGT
CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACT
CACCTGCAAAGGCTCTGGAATCGACTTCAGTAGCGGCTACGGCATGTGGTGGGTCCG
CCAGGCTCCAGGGAAGGGACTGGAGTATATCGGATACATTGATACTGGTTATGGTA
GCACTTACTACGCGAGCTGGGCGAAAGGCCGATTCACCATCTCCAAGACCTCGTCG
ACCACGGTGACTCTGCAAATGACCAGTCTGACAGTCGCGGACACGGCCACCTATTTC
TGTGCGAAAGGGGGCGCCATAGACCTCTGGGGCCCAGGGACCCTCGTCACCGTCTC
TTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCTGCTGCGGGGACAC
ACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGCTACCTCCCGGAGCCAGT
GACCGTGACCTGGAACTCGGGCACCCTCACCAATGGGGTACGCACCTTCCCGTCCGT
CCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCA
GCCAGCCCGTCACCTGCAACGTGGCCCACCCAGCCACCAACACCAAAGTGGACAAG
ACCGTTGCGCCCTCGACATGCAGCAAGCCCATGTGCCCACCCCCTGAACTCCCGGGG
GGACCGTCTGTCTTCATCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCACGC
ACCCCCGAGGTCACATGCGTGGTGGTGGACGTGAGCCAGGATGACCCCGAGGTGCA
GTTCACATGGTACATAAACAACGAGCAGGTGCGCACCGCCCGGCCGCCGCTACGGG
AGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCTCCCCATCGCGCACCAG
GACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAGGCACTCCCGGC
CCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCTGGAGCCGAAGGTCT
ACACCATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTCGGTCAGCCTGACCTGC
ATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAGAAGAACGGGAA
GGCAGAGGACAACTACAAGACCACGCCGACCGTGCTGGACAGCGACGGCTCCTACT
TCCTCTACAGCAAGCTCTCAGTGCCCACGAGTGAGTGGCAGCGGGGCGACGTCTTCA

CCTGCTCCGTGATGCACGAGGCCTTGCACAACCACTACACGCAGAAGTCCATCTCCC
GCTCTCCGGGTAAATAG (**SEQ ID NO: 101**)

A11B1_2A7 Light Chain
ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGT
GCCACATTTGCAGCCGTGCTGACCCAGACTCCGGCTTCCACGTCTGCAGCTGTGGGA
GGCACAGTCACCATCAATTGTCAGTCCAGTCAGAGCGTGTATCGTAGCAACTGGTTA
GCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTATGATGTATTT
AATTTGGCATCTGGGGTCCCATCCCGGTTCAAGGGCAGTGGATCTGGGACACAGTTC
ACTCTCACCATCAGCGGCGTGCAGTGTGCCGATGCTGCCACTTACTACTGTCAAGGC
AGTTATTATAGTGGTAATTGGTACAGTGCTTTCGGCGGAGGGACCGAGGTGGTGGTC
AAAGGTGATCCAGTTGCACCTACTGTCCTCATCTTCCCACCAGCTGCTGATCAGGTG
GCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAAATACTTTCCCGATGTCACC
GTCACCTGGGAGGTGGATGGCACCACCCAAACAACTGGCATCGAGAACAGTAAAAC
ACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGACACTGACCAG
CACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCACGACCT
CAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG (**SEQ ID NO: 102**)

Protein sequences of anti-α11β1 monoclonal antibodies

Rat mAb sequences
Signal peptide-FR1-**CDR1**-FR2-**CDR2**-FR3-**CDR3**-FR4

79E3E3 Heavy Chain Variable Region
*MDWLWNLLFLMVVAQSAQA*QIQLVQSGPEVKKPGESVKISCKASGYTFT**DYAMN**WVKQ
APGNGLKWMG**WINTQTGKPTYADDFKQ**RFVFSLETSARTTYLQINNLNIEDTATYFCT
R**LGTGNTKGFAY**WGQGTLVTVSS (**SEQ ID NO: 145**)

79E3E3 Light Chain Variable Region
*MESQTHVLISLLLCVSGTCG*DILINQSPASLTVSAGERVTMSC**KSSQSLLYSENNQDYLA**
WYQQKPGQFPKLLIY**GASNRHT**GVPDRFTGSGSGTDFTLTISSVQAEDLADYYC**EQTY**
RYPFTFGSGTKLEIK (**SEQ ID NO: 146**)

24E4G6 Heavy Chain Variable Region
*MELELSLIFIFSLLKDVQC*EVQLVESGGSLVQPGGSLKLSCVASGYTFS**NYWMD**WVRQSP
GKSLEWIG**EINTDGRRTNYAPSIKD**RFTISRDNAKSTLYLQMSNVKSDDTAIYYCTI**LR**
VYPHYFDYWGQGVMVTVSS (**SEQ ID NO: 147**)

24E4G6 Light Chain Variable Region
*MMSPAQFLFLLMLWIQEARG*DVVMTQTPPSLSVAIGQSVSISC**KSSQSLVYSDGETYLH**
WFLQSPGRSPKRLIY**HVSNLGS**GVPDRFSGTGSLTDFTLRISRVEAEDLGVYYC**AQTTH**
FPPTFGAGTKLELK (**SEQ ID NO: 148**)

8H8E9 Heavy Chain Variable Region

*MAVLVLLLCLVTFPSCALS*QVQLKESGPGLVQPSQTLSLTCTVSGFSLT**SNSVS**WVRQAPG KGLEWMG**AIWSGGSTDYNSALKS**RLSISRDTSKSQVFLKMNSLQTEDTAIYFCTR**SHW EPFDY**WGQGVMVTVSS (**SEQ ID NO: 149**)

8H8E9 Light Chain Variable Region

*MESQTQALISLLLWVYGTCG*DIVMTQSPFSLAVSEGEMVTINC**KSSQGLLSSGNQKNYLA** WYQQRPGQSPKLLIY**YASTRQS**GVPDRFIGGGSGTDFTLTISDVQAEDLADYYC**LQHYS YPPT**FGSGTKLEIK (**SEQ ID NO: 150**)

6E5C11 Heavy Chain Variable Region

*MAVLVLLLCLVTFPSCALS*QVQLRESGPGLVQPSQTLSLTCTVSGFSLT**SNSVT**WVRQPPG KGLEWMG**AIWSDGSTDYNSTLKS**RLSISRDTSKSQVFLKMSSLQTEDTAIYFCTR**SHW EPFDY**WGQGVMVTVSS (**SEQ ID NO: 151**)

6E5C11 Light Chain Variable Region

*MESQTQALISLLLWVYGTCG*DIVMTQSPLSLAVSEGETVTMNC**KSSQSLFSSGNQKNYLA** WYQQKPGQSPKLLIY**YASTRQS**GVPDRFIGSGSGTDFTLTISDVQTEDLADYYC**LQHYN YPPT**FGSGTKLEIK (**SEQ ID NO: 152**)

7D8B10 Heavy Chain Variable Region

*MDLRLTYVFIVAILKGVLC*EVKLEESGGGLVQPGMSVKLSCATSGFIFS**DYWME**WVRQAP GKGLEWVA**EIRNKANNYATYYGKSMKG**RFTISRDDSKSIVYLQVNSIRSEDTAIYYCA P**NFDY**WGQGVMVTVSS (**SEQ ID NO: 153**)

7D8B10 Light Chain Variable Region

*MSPVQSLFLLLLWILGTHG*DVVLTQTPPTLSATIGQSVSISC**RSSQSLLHSTGNTYLN**WLL QRPGQPPQLLIY**LVSRLES**GVPNRFSASGSGTDFTLKISGIEAEDLGVYYC**VQSSHTPYT** FGTGTKLELK (**SEQ ID NO: 154**)

18E10F10 Heavy Chain Variable Region

*MDIRLSLVFLVLFMKGVQC*EVQLVESGGGLVQPGRSLKLSCAASRFTFS**DYNMA**WVRQA PKKGLEWVA**TIYHDDSGSYYRDSVKG**RFTISRNNAKSTLYLQMDSLRSEDMATYYCA R**HNNGFDY**WGQGVMVTVAS (**SEQ ID NO: 155**)

18E10F10 Light Chain Variable Region

*MKWPVRLLVLFFWIPASGG*DVVMTQTPVSLPVRLGGQASISC**RSSQSLVHSNGNTYLH**W YLQKPGQSPQLLIN**RVSNRFS**GVPDRFSGSGSGTDFTLKINRVEPEDLGDYYC**LQSTHFP LT**FGSGTKLETK (**SEQ ID NO: 156**)

40G10H11 Heavy Chain Variable Region

*MDIRLSLGFLVLFIKGDQC*AVQLVESGGGLVQPGRSLKLSCAASRITFT**DYYMA**WVRQA PTKGLEWVA**TISSDGGDTFYRDSVKG**RFTISRDNAKSTLYLQMVSLRSEDTATYYCST **DRGAQFGY**WGQGTLVTVSS (**SEQ ID NO: 157**)

40G10H11 Light Chain Variable Region

*MAPVQLLGLLLIWLPAMRC*DIQMTQSPSFLSASVGDRVSINC**KASQNVHENLN**WYQQKL GEAPKRLIY**NTNNLQT**GIPSRFSGSGSGADYTLTISSLQPEDFATYFC**LQHNAFPYT**FGP GTKLELK (**SEQ ID NO: 158**)

Mouse mAb sequences
FR1-**CDR1**-FR2-**CDR2**-FR3-**CDR3**-FR4

9-G05 Heavy Chain Variable Region
EVQLQQSGPELVKPGASVKIPCKAS**GYTFPDY**NMDWVKQSHGKSLEWIGYI**NPDNGG**T IYNQKFKGKATLTVDKSSSTAYMELRSLTSEDTAVYYCAR**LDSSGYGYYAMDY**WGQG TSVTVSS (**SEQ ID NO: 103**)

9-G05 Light Chain Variable Region
DIVLTQSPASLAVSLGQRATISC**RASESVDNYGISFMH**WYQQKPGQPPKLLIY**RASNLD SE**IPARFSGSGSRTDFTLTIDPVETDDVATYYC**QQSYKDPRT**FGGGTKLEIK (**SEQ ID NO: 104**)

8-P20 Heavy Chain Variable Region
KVMLVESGGALVKPGGSLKLSCVAS**GFTFSNY**AMSWVRQTPEKRLEWVATI**SSGGYY** TYYPDSVKGRFTISRDNARNTLFLQMSSLRSEDTAMFYCAR**EDDYGRYSYTMDY**WGQ GTSVTVSS (**SEQ ID NO: 105**)

8-P20 Light Chain Variable Region
DVVMTQTPLSLPVSLGDQVSISC**RCSQSLVHSNGNTYLH**WYLQKPGQSPQLLIY**KISNR FS**GVPDRFSGSGSGTDFTLKISRVEAEDLGVYFC**SQSTHVPYT**FGGGTELEIK (**SEQ ID NO: 106**)

8-G15 Heavy Chain Variable Region
EVQLQQSGPELVKPGASVRISCKAS**GYTFTDY**YIHWVKQKPGQGLECIGEI**YPGTDN**TY YSKKFRGKATLTADKSSDTAYMQLSSLTSEDSAVYFCAR**GDYYRGYFDV**WGAGTTVT VSS (**SEQ ID NO: 107**)

8-G15 Light Chain Variable Region
DVVMTQTSLTLSVTIGQPASISC**KSSQSLLHSNGKTYLN**WLLQRPGQSPKFLIY**LVSKL ES**GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYC**LQSTHFPWT**FGGGTKLEIK (**SEQ ID NO: 108**)

8-I14 Heavy Chain Variable Region
EVQLQQSGPELVKPGASVKKSCKAS**GYTFTDY**YMHWVKQKPGQGLEWIGKI**YPGSGN** THYNEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCAT**NYYGYRAMNY**WGQGSS VTVSS (**SEQ ID NO: 109**)

8-I14 Light Chain Variable Region

DIHLTQSPSSLSASLGERISLTC**RASQDIYISLN**WFQQKPDGTIKLLIY**GTSSLDS**GVPKRF SGSRSGSDYSLTISSLESEDFADYYC**LQYASSPYT**FGGGTKLEIK (**SEQ ID NO: 110**)

9-E16 Heavy Chain Variable Region

EVQLQQSGPELVKPGASVKISCKAS**GYTFTDY**YMHWVKQKPGQGLEWIGEI**YPGSGN**P YYNEKFKGKATLTADKSSSSAYMQLSSLTSEDSAVYFCAR**TSYGRVGTGFAY**WGQGT LVTVSA (**SEQ ID NO: 111**)

9-E16 Light Chain Variable Region

NFVMTQTPLSLPVSLGDQASISC**RSSQSLLHSNGNTYLH**WYLQKPGQSPKLLIY**KVSNR FS**GVPDRFSGSGSGTDFTLKINRVETEDLGIYFC**SQSSHVPT**FGAGTKLELK (**SEQ ID NO: 112**)

8-J17 Heavy Chain Variable Region

QVQLQQSGAELAKPGASVKMSCKAS**GYTFTNYW**MHWVKQRPGQGLEWIGY**INPNNG YT**EYNQRFKDKATLTADRSSTTAYMQLSSLTSEDSAVYYC**ARSDIITTDY**WGQGTTLT VSS (**SEQ ID NO: 113**)

8-J17 Light Chain Variable Region

DVVMTQTPLSLPVSLGDQASISCRSS**QSLVYSNGNTY**LHWYLQKPGQSPKLLIY**KVS**NR FSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFC**SQSTHVPWT**FGGGTKLEIK (**SEQ ID NO: 114**)

9-B11 Heavy Chain Variable Region

QVQLQQPGAELVRPGTSVKLSCKAS**GYTFTSYW**MHWVQQRPGQGLEWIGV**IDPSDSY T**NYNQKFKGKATLTVDTSSSSAYMQLSSLTSEDSAVYYC**ARDDVAMDY**WGQGTSVTV SS (**SEQ ID NO: 115**)

9-B11 Light Chain Variable Region

DIVVTQSPASLAVSLGQRATISCRAS**ESVDSYGNSF**IHWYQQKPGQPPKLLIY**RAS**NLKS GIPARFSGSGSRTDFTLTINPVEADDVATYYC**QQSNEDPYT**FGGGTKLEIK (**SEQ ID NO: 116**)

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

6-O12 Heavy Chain Variable Region

EVKLEESGGGLVQPGGSMKLSCAASGFTFSDAWMDWVRQSPEAGLEWVAEIRNKAHN PATYYAESVKGRFTISRDDSKSSVYLQMNSLRAEDTGIYY**<u>CTLVAPDAMDYW</u>**GQGTS VTVSS (**SEQ ID NO: 117**)

6-O12 Light Chain Variable Region

DIVMSLSPSSLAVSVGEKVTMSCKSSQSLLYSRNQKNYLAWYQQKPGQSPKLLIYWAST RASGVPDRFTGSGSGTDFTLTISSVKAEDLAVYY**<u>CQQYYSYPYTF</u>**GGGTKLEIK (**SEQ ID NO: 118**)

10-L15 Heavy Chain Variable Region
QVQLQQSGPELVRPGASVKMSCKASGYTFTSYWMHWVKQRPGQGLEWIGMIDPSNSE TWLNQKFKDKATLNVDKSSNTAYMQLSSLTSEDSAVYY**CARYDGYYDYW**GQGTTLT VSS (**SEQ ID NO: 119**)

10-L15 Light Chain Variable Region
NIVLTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQQKPGQPPKLLIYLASNVES GVPARFSGSGSRTDFTLTIDPVEADDAATYY**CQQNNEDPWTF**GGGTKLEIK (**SEQ ID NO: 120**)

7-H14 Heavy Chain Variable Region
QVQLQQPGAELVRPGASVKLSCKPSGYTFTSYWMNWVKQRPGQGLEWIGMIDPSDSET HYNQMFKDKATLTVDKSSNTAYMQLSSLTSEDSAVYY**CAQIYYAYDKAYW**GQGTLV TVSA (**SEQ ID NO: 121**)

7-H14 Light Chain Variable Region
DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSSHQKNYLAWYQQKPGQSPKLLIYWAST RESGVPDRFTGSGSGTDFSLTISSVKAEDLAVYY**CQEYYSWTF**GGGTKLEIK (**SEQ ID NO: 122**)

6-B21 Heavy Chain Variable Region
EVQLQQSGPELVKPGASVKISCKASGYTFTDYYMNWVKQSHGKSLEWIGDINPHNGGT SFIQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYY**CAPLGRKEGFAYW**GQGTLVTV SA (**SEQ ID NO: 123**)

6-B21 Light Chain Variable Region
DTVLTQSPASLVVSLGQRATISCRASKSVSTSGYSYMHWYQQKPGQPPKLLIYLASNLES GVPARFSGSGSGTAFTLNIHPVEEEDAATYY**CQHSRELPYTF**GGGTKLEIK (**SEQ ID NO: 124**)

10-F23 Heavy Chain Variable Region
QVTLKESGPGILQPSQTLSLTCSFSGFSLSTFAMGVGWIRQPSGKGLEWLAHIWWDDDK YYNPALKSRLTISKDTSKNHVFLKIANVDTADTATYY**CARMPLTFYFDYW**GQGTTLTV SS (**SEQ ID NO: 125**)

10-F23 Light Chain Variable Region
DVLLTQTPLSLPVSLGDQASISCRSSQSIVHSNGHTYLEWYLQKPGQSPKLLIYKVSNRFS GVPDRFSGSGSGTDFTLKISRVEAEDLGVYY**CFQGSHVPFTF**GGGTKLEIK (**SEQ ID NO: 126**)

6-A12 Heavy Chain Variable Region
QVTLKESGPGILQPSQTLSLTCSFSGFSLRTFAMGVGWIRQPSGKGLEWLAHIWWDDDK YYNPALKSRLTISKDTSKNQVFLKIANVDTADTATYY**CARMPLTFYFDYW**GQGTTLTV SS (**SEQ ID NO: 127**)

6-A12 Light Chain Variable Region
DVLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSTRF SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYY**CFQGSHVPFTF**GGGTKLEIK (**SEQ ID NO: 128**)

6-M8 Heavy Chain Variable Region
QVQLQQPGAELVMPGASVKLSCKASGYTFTNYWMHWVKQRPGQGLEWIGEIDPSDSY TNYNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYY**CTRQGSTYAW**GQGTSVTVS S (**SEQ ID NO: 129**)

6-M8 Light Chain Variable Region
DIVMTQAAFSNPVTLGTSASISCRSSKSLLHSNGITYLYWYLQKPGQSPQLLIYQMSNLA SGVPDRFSSSGSGTDFTLRISRVEAEDVGVYY**CAQNLELPPTF**GGGTKLEIK (**SEQ ID NO: 130**)

2-A3 Heavy Chain Variable Region
EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMMWVKQSHGKSLEWIGDINPYNGG SSYNPKFKGRATLTVDKSSSTAYMQLNSLTSEDSAVYY**CARGTYW**GQGTLVTVSA (**SEQ ID NO: 131**)

2-A3 Light Chain Variable Region
DVVMTQTPLTLSVTIGQPASISCKSSQSLLDSAGKTYLNWLLQRPGQSPKRLMYLVSKL DSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYY**CWQGTHFPYTF**GGGTKLEIK (**SEQ ID NO: 132**)

6-O17 Heavy Chain Variable Region
QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWIKQRPGQGLEWIGEINPSNGGS NYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYH**CKSRGYW**GQGTTLTVSS (**SEQ ID NO: 133**)

6-O17 Light Chain Variable Region
DVVMTQTPLTLSVTIGQPASISCKSSQSLLDSYGKTYLNWLLQRPGQSPKRLIYLVSKLD SGVPDRFTGSGSGTDFTLKISRVEAEDLGIYY**CWQGTHFPHTF**GSGTKLEIK (**SEQ ID NO: 134**)

3-G5 Heavy Chain Variable Region
QVQLQQSGAELARPGASVKLSCKASGYTFTSYGISWVKQRTGQGLEWIGEIFPRSSNTY YNEKFKGKATLTADKSSSTVYMEFRSLTSEDSAVYF**CAREGGLAWFAYW**GQGTLVTV SA (**SEQ ID NO: 135**)

3-G5 Light Chain Variable Region
DVVMTQTPLTLSVTIGQPASISCKSSQSLLYTNGNTYLNWLLQRPGQSPKRLIYLVSKLD SGIPDRFSGSGSGTDFTLRISRVEAEDLGVYY**CLQSTHFPFTF**GSGTKLEIK (**SEQ ID NO: 136**)

6-A15 Heavy Chain Variable Region
EVQLQQSGPELVKPGASVKMSCKASGYTITDYYMMWLKQSHGKSLEWIGDINPYTGGT SYNQKFKGKATLTVDKSSSTAYLQLHSLTSEDSAVYY**CARGAYW**GQGTTLTVSS (**SEQ ID NO: 137**)

6-A15 Light Chain Variable Region
DVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSKLD SGVPDRFTGSGSGTDFTLKISRVEAEDLGVYY**CWQGTHFPYTF**GGGTKLEIK (**SEQ ID NO: 138**)

10-K10 Heavy Chain Variable Region
EVQLQQSGPELVKPGASVKMSCKASGYTITDYYMMWLKQSHGKSLEWIGDINPYTGGT SYNQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYY**CARGAYW**GQGTTLTVSS **(SEQ ID NO: 139**)

10-K10 Light Chain Variable Region
DVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSKLD SGVPDRFTGSGSGTDFTLKISRVEAEDLGVYY**CWQGTHFPYTF**GGGTKLEIK (**SEQ ID NO: 140**)

6-P20 Heavy Chain Variable Region
EVQLQQSGPELVKPGASVKISCKASGYTFTDYYMNWVKQSHGRSLELIGDINPNNGGSN FNQKFRGKATLTVDKSSSTAYMELRSLTSEDSAIYY**CARMGYW**GQGTLVTVSA (**SEQ ID NO: 141**)

6-P20 Light Chain Variable Region
DVVMTQTPLTLSVTIGQPASISCKSSQSLLHSDGKTYLNWMFQRPGQSPKRLIYLVSKLD SGVPYRFTGGGSGTDFTLQISRVETEDLGVYY**CWQGTHFPRTF**GGGTKLEIK (**SEQ ID NO: 142**)

7-O8 Heavy Chain Variable Region
EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYIHWVKQKPGQGLEYIGEIYPGSGNT YYNGKFRGKATLTADKSSSTAYMQLSSLTSEDSAVYF**CGSGYFDYW**GQGTTLTVSS **(SEQ ID NO: 143**)

7-O8 Light Chain Variable Region
DVVMTQTPLTLSVTIGQPASISCKSSQSLLYSNGKTYLNWLLQSPGQSPKLLIYLVSKLES GVPDRFSGSGSGTDFTLKLSRVEAEDLGVYY**CVQGTHFPFTF**GSGTKLEIK (**SEQ ID NO: 144**)

Rabbit mAb sequences

A11B1_16G7 Heavy Chain

METGLRWLLLVAVFKGVQCQEQLVESGGDLVKPGASLTLTCTASGFSFNKNYWMCWV
RQAPGKGLEWIGCIYNGDGNTYYASWVNGRFTISKTSSTTVTLQMTSLTVADTAIYFCA
RLLNMWGPGTLVTVSSGQPKAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVTVTWNS
GTLTNGVRTFPSVRQSSGLYSLSSVVSVTSSSQPVTCNVAHPATNTKVDKTVAPSTCSKP
MCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRTA
RPPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEPK
VYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSDGSYFL
YSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (**SEQ ID NO: 159**)

A11B1_16G7 Light Chain

MDTRAPTQLLGLLLLWLPGARCADIVMTQTPASVEAAVGGTVTIKCQASESIGNALAW
YQQKPGQPPKLLIYTAATLASGVPSRFSGSGSGTEFTLTISGVQCDDAATYYCQSYYFTS
VSSYGNAFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWE
VDGTTQTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNSHKEYTCKVTQGTTSVVQSFNR
GDC* (**SEQ ID NO: 160**)

A11B1_16E10 Heavy Chain

METGLRWLLLVAVLKGVQCQSLEESGGDLVKPGASLTLTCRVSGFSFSSSYYMCWVRQ
APGKGLEWIACIGTTRGSTYYATWAKGRFTISKISSTTVTLQMTSLTDADTATYFCARDA
TGYRINTIGLYFNLWGPGTLVTVSSGQPKAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPE
PVTVTWNSGTLTNGVRTFPSVRQSSGLYSLSSVVSVTSSSQPVTCNVAHPATNTKVDKT
VAPSTCSKPMCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYI
NNEQVRTARPPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKA
RGQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVL
DSDGSYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (**SEQ ID NO: 161**)

A11B1_16E10 Light Chain

MDTRAPTQLLGLLLLWLPGARCAFELTQTPSSVEAAVGGTPTIKCQASQTIYSYLSWYQ
QKPGQPPKLLIYEASKLASGVPSRFSGSGSGTDYTLTISDLECADAATYYCQSYHGTAST
EYNTFGGGTEVVVRGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVDG
TTQTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNSHKEYTCKVTQGTTSVVQSFNRGDC
* (**SEQ ID NO: 162**)

A11B1_15G10 Heavy Chain

METGLRWLLLVAVLKGVQCQQQLVESGGGLVKPGAALTFTCTASGFSFSGNYWICWV
RQAPGKGLEWIACIGTITSRTYYASWAKGRFTISKTSSTTVTLQMTSLTAADTATYFCAR
GAVVSSGNAPYYFTLWGPGTLVTVSSGQPKAPSVFPLAPCCGDTPSSTVTLGCLVKGYL
PEPVTVTWNSGTLTNGVRTFPSVRQSSGLYSLSSVVSVTSSSQPVTCNVAHPATNTKVD
KTVAPSTCSKPMCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFT
WYINNEQVRTARPPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTI
SKARGQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTP
TVLDSDGSYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (**SEQ ID NO: 163**)

A11B1_15G10 Light Chain

MDTRAPTQLLGLLLLWLPGARCAFELTQTPSSVEAAVGGTVTIKCQASQSISSYLSWYQ
QKPGQPPKLLIYRASTLESGVPSRFKGSGSGTEFTLTISDLECADAATYFCQSYYGVTFSG
FAFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVDGTT
QTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNSHKEYTCKVTQGTTSVVQSFNRGDC*
(**SEQ ID NO: 164**)

A11B1_14H1 Heavy Chain
METGLRWLLLVAVLKGVQCQSLEESGGDLVKPGASLTLTCKASGIDFNNYWITWVRQA
PGKGLEWIACIYVGITGRTWYANWAKGRFTISKASSTVDLKMTSLTAADTATYFCARN
GDGGIYALNLWGPGTLVTVSSGQPKAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVT
VTWNSGTLTNGVRTFPSVRQSSGLYSLSSVVSVTSSSQPVTCNVAHPATNTKVDKTVAP
STCSKPMCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNE
QVRTARPPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQ
PLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSDG
SYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (**SEQ ID NO: 165**)

A11B1_14H1 Light Chain
MDTRAPTQLLGLLLLWLPGATFAQVLTQTASSVSAAVGGTVTISCQSSQSVYNNNWLA
WYQQKPGQPPKLLIYRASTLTSGVPSRFKGSGSGTQFTLTISDLECDDAATYYCAGGYS
GNIYVNDFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWE
VDGTTQTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNSHKEYTCKVTQGTTSVVQSFNR
GDC* (**SEQ ID NO: 166**)

A11B1_13G4 Heavy Chain
METGLRWLLLVAVLKGVQCQEQLEESGGDLVKPGGSLTLTCKASGFSFSNTYWACWV
RQAPGKGLEWIACMNPASSGSSYYASWAKGRFTISKTSSTTVTLHMPSLTAADTATYFC
AKWDTAFDVWGPGTLVTVSSGQPKAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVTV
TWNSGTLTNGVRTFPSVRQSSGLYSLSSVVSVTSSSQPVTCNVAHPATNTKVDKTVAPS
TCSKPMCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNE
QVRTARPPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQ
PLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSDG
SYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (**SEQ ID NO: 167**)

A11B1_13G4 Light Chain
MDTRAPTQLLGLLLLWLPGARCADVVMTQTPSSVEAAVGGTVTIKCQASQSISSYLAW
YQQKPGQPPKLLIYGASNLESGVPSRFKGSGSGTEYTLTISGVQCDDAATYYCQNYYAI
DTYGHAFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEV
DGTTQTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNSHKEYTCKVTQGTTSVVQSFNRG
DC* (**SEQ ID NO: 168**)

A11B1_13C3 Heavy Chain
METGLRWLLLVAVLKGVQCQEQLEESGGDLVKPGASLTLTCTASGFSFSSNYHICWVR
QAPGKGLELIACIYVGDGSTYYASWAKGRFTISKSSSTTVALQMTSLTAADTATYFCGR
MFNLWGPGTLVTVSSGQPKAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVTVTWNSG
TLTNGVRTFPSVRQSSGLYSLSSVVSVTSSSQPVTCNVAHPATNTKVDKTVAPSTCSKPM
CPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRTARP

PLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEPKVY
TMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSDGSYFLYSK
LSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (**SEQ ID NO: 169**)

A11B1_13C3 Light Chain

MDTRAPTQLLGLLLLWLPGAICDPVLTQTPSSVSAAVGVTVTINCQSSPSVYSNYLSWY
QQKPGQPPKLLIYLASTLASGVPSRFKGSGSGTQFTLTISDVQCDDAATYYCAGTYSGNI
WSFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVDGTT
QTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNSHKEYTCKVTQGTTSVVQSFNRGDC*
(**SEQ ID NO: 170**)

A11B1_12F2 Heavy Chain

METGLRWLLLVAVLKGVQCQQQLVESGGGLVKPGASLTLTCTASGFSFSSGYHMCWV
RQAPGKGLEWIACFGVYTGTTTYASWAKGRFTISKTSSTTVTLQMTSLTVADTATYFCA
RISAENGGDLWGPGTLVTVSSGQPKAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVTV
TWNSGTLTNGVRTFPSVRQSSGLYSLSSVVSVTSSSQPVTCNVAHPATNTKVDKTVAPS
TCSKPMCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNE
QVRTARPPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQ
PLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSDG
SYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (**SEQ ID NO: 171**)

A11B1_12F2 Light Chain

MDTRAPTQLLGLLLLWLPGARCDVVMTQTPASVEAAVGGTVTIKCQASQSISNYFSWY
QQKPGQPPKLLIYRASTLASGVPSRFSGSGSGTEFTLTISDLECADSATYYCQCTYGSSST
GFGFGGGTEVVVKGDPVAPTVPIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVDGT
TQTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNSHKEYTCKVTQGTTSVVQSFNRGDC*
(**SEQ ID NO: 172**)

A11B1_11D10 Heavy Chain

METGLRWLLLVAVLKGVQCQSLEESGGDLVKPGASLTLTCMASGIDFSSGYGMWWVR
QAPGKGLEYIGYIDTGDDNTYYANWAKGRFTISKTSSTTVTLQMTSLTVADTATYFCAK
GGAIDLWGPGTLVTVSSGQPKAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVTVTWN
SGTLTNGVRTFPSVRQSSGLYSLSSVVSVTSSSQPVTCNVAHPATNTKVDKTVAPSTCSK
PMCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRT
ARPPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEP
KVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSDGSYF
LYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (**SEQ ID NO: 173**)

A11B1_11D10 Light Chain

MDTRAPTQLLGLLLLWLPGARCADIVMTQTPASVEAAVGGTVTIKCQASQSISSYLAWY
QQKPGQRPKLLIYRASTLKSGVPSRFKGSGSGTEYTLTISDLECADAATYYCQAYYLSSS
ISYGNTFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVD
GTTQTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNSHKEYTCKVTQGTTSVVQSFNRGD
C* (**SEQ ID NO: 174**)

A11B1_10F9 Heavy Chain

METGLRWLLLVAVLKGVQCQSLEESGGDLVKPGASLTLTCTASGFSLSSGYGMCWVR
QAPGKGLEWIGYTDTATGTIHYASWAKGRFTISKTSSTTVTLQMTSLTAADTATYFCAK
GGAMDLWGPGTLVTVSSGQPKAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVTVTW
NSGTLTNGVRTFPSVRQSSGLYSLSSVVSVTSSSQPVTCNVAHPATNTKVDKTVAPSTCS
KPMCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVR
TARPPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEP
KVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSDGSYF
LYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (**SEQ ID NO: 175**)

A11B1_10F9 Light Chain

MDTRAPTQLLGLLLLWLPGARCADIVMTQTPASVEAAVGGTVTIKCQASQSISSYLAWY
QQKPGQPPKLLIYRTSTLASGVPSRFKGSGSGTEYTLTISDLECADAATYYCQSYAYSSSS
SYGNAFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVD
GTTQTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNSHKEYTCKVTQGTTSVVQSFNRGD
C* (**SEQ ID NO: 176**)

A11B1_7H12 Heavy Chain

METGLRWLLLVAVLKGVQCQSLEESGGDLVKPGASLTLTCTGSGIDFSSSYWICWVRQ
APGKGLEWIACIDGSDGNTYYASWARGRFTISKTSSTTVTLQMASLTAADTATYFCTRD
LRLWGPGTLVTVSSGQPKAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVTVTWNSGT
LTNGVRTFPSVRQSSGLYSLSSVVSVTSSSQPVTCNVAHPATNTKVDKTVAPSTCSKPM
CPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRTARP
PLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEPKVY
TMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSDGSYFLYSK
LSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (**SEQ ID NO: 177**)

A11B1_7H12 Light Chain

MDTRAPTQLLGLLLLWLPGARCADIVLTQTPASVSAAVGGTVTINCQASQNVYSNNAL
AWHQQKPGQRPNLLIYKASTLASGVPSRFKGSGSGTQFTLTISDVQCDDAATYYCLGEF
SCSSGDCFVFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTW
EVDGTTQTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNSHKEYTCKVTQGTTSVVQSFN
RGDC* (**SEQ ID NO: 178**)

A11B1_7G12 Heavy Chain

METGLRWLLLVAVLKGVQCQSLEESGGDLVKPGASLTLTCMASGIDFSSGYGMWWVR
QAPGKGLEYIGYIDTGDDNTYYANWAKGRFTISKTSSTTVTLQMTSLTVADTATYFCAK
GGAIDLWGPGTLVTVSSGQPKAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVTVTWN
SGTLTNGVRTFPSVRQSSGLYSLSSVVSVTSSSQPVTCNVAHPATNTKVDKTVAPSTCSK
PMCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRT
ARPPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEP
KVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSDGSYF
LYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (**SEQ ID NO: 179**)

A11B1_7G12 Light Chain

MDTRAPTQLLGLLLLWLPGARCADIVMTQTPASVEAAVGGTVTIKCQASQSISSYLAWY
QQKPGQRPKLLIYRASTLKSGVPSRFKGSGSGTEYTLTISDLECADAATYYCQAYYLSSS

ISYGNTFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVD
GTTQTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNSHKEYTCKVTQGTTSVVQSFNRGD
C* (**SEQ ID NO: 180**)

A11B1_6G4 Heavy Chain

METGLRWLLLVAVLKGVQCQQQLEESGGGLVKPGGTLTLTCKASGVALNPYYYMCW
VRQAPGKGLEWIACVDADSSGSTYYASWAKGRFTISKTSSTTVTLKMTSLTAADTATYF
CARESVDYSSVGIGYVHGTDGLWGPGTLVTVSSGQPKAPSVFPLAPCCGDTPSSTVTLG
CLVKGYLPEPVTVTWNSGTLTNGVRTFPSVRQSSGLYSLSSVVSVTSSSQPVTCNVAHP
ATNTKVDKTVAPSTCSKPMCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQD
DPEVQFTWYINNEQVRTARPPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKAL
PAPIEKTISKARGQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAED
NYKTTPTVLDSDGSYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK*
(**SEQ ID NO: 181**)

A11B1_6G4 Light Chain

MDTRAPTQLLGLLLLWLPGARCADIVVTQTPSSVSAAVGGTVTIKCQASQSISNYFSWY
QQKPGQPPKLLIYRASTLASGVPSRFKGSGSGTEFTLTISDLECADAATYYCQCTYGRSN
SNFFYGFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEV
DGTTQTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNSHKEYTCKVTQGTTSVVQSFNRG
DC* (**SEQ ID NO: 182**)

A11B1_6F9 Heavy Chain

METGLRWLLLVAVLKGVQCQSLEESGGDLVKPGASLTLTCTASGSSFSSTYWNCWVRQ
APGKGLEWIACINAGSGTTYYASWAKGRFTVSKTSSTTVTLQMTSLTAADTATYFCTRD
SDGRFSSGYYFNLWGPGTLVTVSSGQPKAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEP
VTVTWNSGTLTNGVRTFPSVRQSSGLYSLSSVVSVTSSSQPVTCNVAHPATNTKVDKTV
APSTCSKPMCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYIN
NEQVRTARPPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKAR
GQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDS
DGSYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (**SEQ ID NO:
183**)

A11B1_6F9 Light Chain

MDTRAPTQLLGLLLLWLPGATFAQVLTQTASPVSAAVGGTVTINCQSSQSVYDNNWLA
WYQQKPGQPPKLLIDDASKLTSGVSSRFKGSGSGTQFTLTISGVQCDDAATYYCQGAYY
SSGWYWAFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWE
VDGTTQTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNSHKEYTCKVTQGTTSVVQSFNR
GDC* (**SEQ ID NO: 184**)

A11B1_6C7 Heavy Chain

METGLRWLLLVAVLKGVQCQQQLEESGGGLVKPGGTLTLTCKASGIDFSSYYYMCWV
RQAPGKGLELIVCIYTSSGGTWYASWVNGRLTISRSTSLNTVDLKMTSLTAADTATYFC
ARGVYSGSSDYPTRLDLWGQGTLVTVSLGQPKAPSVFPLAPCCGDTPSSTVTLGCLVKG
YLPEPVTVTWNSGTLTNGVRTFPSVRQSSGLYSLSSVVSVTSSSQPVTCNVAHPATNTK
VDKTVAPSTCSKPMCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQF

TWYINNEQVRTARPPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKT
ISKARGQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTP
TVLDSDGSYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (**SEQ ID NO: 185**)

A11B1_6C7 Light Chain

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

A11B1_6B6 Heavy Chain

METGLRWLLLVAVLKGVQCQQHLVESGGGLVKPGASLTLTCTASGFSFTTGYHMCWV
RQAPGKGLEWIACFGVYTSTTTYASWAKGRFTISKTSSTTVTLQMTSLTVADTATYFCA
RISAEDGGDLWGPGTLVTVSSGQPKAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVTV
TWNSGTLTNGVRTFPSVRQSSGLYSLSSVVSVTSSSQPVTCNVAHPATNTKVDKTVAPS
TCSKPMCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNE
QVRTARPPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQ
PLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSDG
SYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (**SEQ ID NO: 187**)

A11B1_6B6 Light Chain

MDTRAPTQLLGLLLLWLPGARCDVVMTQTPASVEAAVGGTVTITCQASQSISNYFSWY
QQKPGQPPKLLIYRASTLASGVPSRFSGSGSGTQFTLTISDLECADSATYACQCTYGSSST
GFGFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVDGT
TQTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNSHKEYTCKVTQGTTSVVQSFNRGDC*
(**SEQ ID NO: 188**)

A11B1_5F7 Heavy Chain

METGLRWLLLVAVLKGVQCQSLEESGGDLVKPGASLTLTCKASGFSFSSYFWICWVRQ
APGKGLEWSACIYGDSSGSSYYASWAKGRFTISKTSSTTVTLQMTSLTAADTATYFCAS
YGSSSYYYSNLWGPGTLVTVSSGQPKAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVT
VTWNSGTLTNGVRTFPSVRQSSGLYSLSSVVSVTSSSQPVTCNVAHPATNTKVDKTVAP
STCSKPMCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNE
QVRTARPPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQ
PLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSDG
SYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (**SEQ ID NO: 189**)

A11B1_5F7 Light Chain

MDTRAPTQLLGLLLLWLPGAICDPVMTQTPSSTSAAVGGTVTISCQSSQSVYNNNNYLAW
YQQKPGQPPKRLIYESSKLASGVPSRFRGSGSGAQFTLTISDLECDDAATYYCLGAYYTT
LDFGGGTEVVVRGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVDGTT
QTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNSHKEYTCKVTQGTTSVVQSFNRGDC*
(**SEQ ID NO: 190**)

A11B1_5D7 Heavy Chain
METGLRWLLLVAVLKGVQCQEQLVESGGGLVQPEGSLTLTCKASGFDFSSNAMCWVR
QAPGKGLEWIACIYNGDGSTYYASWVNGRFTISKTSSTTVTLQMTSLTAADTATYFCAR
GLSNWNRDNLWGPGTLVTVSSGQPKAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVT
VTWNSGTLTNGVRTFPSVRQSSGLYSLSSVVSVTSSSQPVTCNVAHPATNTKVDKTVAP
STCSKPMCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNE
QVRTARPPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQ
PLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSDG
SYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (**SEQ ID NO: 191**)

A11B1_5D7 Light Chain
MDTRAPTQLLGLLLLWLPGATFAQVLTQTPSSVSAAVGGTATINCQASQSLYSPKNLAW
YQQTPGQPPKLLIYSASKLASGVPSRFKGSGSGTQFTLTISGVQCDDAAIYYCQGEFSCTT
AACFAFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVD
GTTQTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNSHKEYTCKVTQGTTSVVQSFNRGD
C* (**SEQ ID NO: 192**)

A11B1_5A7 Heavy Chain
METGLRWLLLVAVLKGVQCQSLEESGGGLVQPEGSLTLACTASGFSFSSYYYICWVRQ
APGTGLEWIGCINTGSDDTHYASWLKGRFTFSKASSTTLTLQMTSLTAADTATYFCARS
SGSSDDAYDLWGPGTLVTVSSGQPKAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVT
VTWNSGTLTNGVRTFPSVRQSSGLYSLSSVVSVTSSSQPVTCNVAHPATNTKVDKTVAP
STCSKPMCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNE
QVRTARPPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQ
PLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSDG
SYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (**SEQ ID NO: 193**)

A11B1_5A7 Light Chain
MDTRAPTQLLGLLLLWLPGARCDVVMTQTPASVSEPVGGAVTIKCQASQSIGSNLAWY
QHKPGQPPKLLIYFASSLASGVSSRFKGGRSGTQFTLTISDLECADAATYYCHCTYYPLS
YVTFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVDGT
TQTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNSHKEYTCKVTQGTTSVVQSFNRGDC*
(**SEQ ID NO: 194**)

A11B1_4E1 Heavy Chain
METGLRWLLLVAVLKGVQCQSLEESGGDLVKPGTSLTLSCTASGFSFGSYYYMCWVRQ
APGKGLEWIACIDVGSSGDTYYASWVNGRFTISKTSSTTVTLQMTSLTAADTATYFCAR
DDTAAGGFGNLELWGPGTLVTVSSGQPKAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPE
PVTVTWNSGTLTNGVRTFPSVRQSSGLYSLSSVVSVTSSSQPVTCNVAHPATNTKVDKT
VAPSTCSKPMCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYI
NNEQVRTARPPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKA
RGQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVL
DSDGSYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (**SEQ ID NO: 195**)

A11B1_4E1 Light Chain

MDTRAPTQLLGLLLLWLPGARCAFELTQTPSSVSEPVGGTVTIKCQASQSIYSYFSWYQ
QKPGQPPKRLIYQASTLASGVPSRFKGSGSGTDFTLTISDLECADAATYYCQNNYGRGS
GSYFFGFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEV
DGTTQTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNSHKEYTCKVTQGTTSVVQSFNRG
DC* (**SEQ ID NO: 196**)

A11B1_3H9 Heavy Chain
METGLRWLLLVAVLKGVQCQSLEESGGDLVKPGASLTLTCKASGIDFSSGYGMWWVR
QAPGKGLEYIGYIDTGSGSTYYANWAKGRFTISKTSSTMVTLQMTSLTVADTATYFCAK
GGAIDLWGPGTLVTVSSGQPKAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVTVTWN
SGTLTNGVRTFPSVRQSSGLYSLSSVVSVTSSSQPVTCNVAHPATNTKVDKTVAPSTCSK
PMCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRT
ARPPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEP
KVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSDGSYF
LYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (**SEQ ID NO: 197**)

A11B1_3H9 Light Chain
MDTRAPTQLLGLLLLWLPGARCADIVMTQTPASVEAAVGGTVTIKCQASQSISSYLAWY
QQKPGQRPKLLIYRASTLASGVPSRFKGSGSGTDYTLTISDLECADAATYYCHTYYLSSS
ISYGNTFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVD
GTTQTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNSHKEYTCKVTQGTTSVVQSFNRGD
C* (**SEQ ID NO: 198**)

A11B1_3G2 Heavy Chain
METGLRWLLLVAVLKGVQCQEQLEESGGDLVKPEGSLTLTCKASGFSFSSIYWICWVRQ
APGKGLEWIACTTVVKSGRTYYANWAKGRFTISKTSSTTVTLQMTSLTAADTATYFCA
REFVDGGGSSGRDLWGPGTLVTVSSGQPKAPSVFPLAPCCGDTPSSTVTLGCLVKGYLP
EPVTVTWNSGTLTNGVRTFPSVRQSSGLYSLSSVVSVTSSSQPVTCNVAHPATNTKVDK
TVAPSTCSKPMCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTW
YINNEQVRTARPPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTIS
KARGQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPT
VLDSDGSYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (**SEQ ID NO: 199**)

A11B1_3G2 Light Chain
MDTRAPTQLLGLLLLWLPGARCAYDMTQTPASVEAAVGGTVTIKCQASQSISRDLSWY
QQKPGQPPKRLIYKASTLASGVPSRFKGSGSGTDFTLTISDLECADAATYYCQQGYSSID
VDNDFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVDG
TTQTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNSHKEYTCKVTQGTTSVVQSFNRGDC
* (**SEQ ID NO: 200**)

A11B1_3B1 Heavy Chain
METGLRWLLLVAVLKGVQCQEQLEESGGGLVKPEGSLTLTCKASGFDLSSGYDMCWV
RQAPGKGLEWIACIYADYSGSTYYASWVNGRFTISSSTSLNTVDLKMTSLTAADTATYF
CARGATGNGGYGYYFNLWGPGTLVTVSSGQPKAPSVFPLAPCCGDTPSSTVTLGCLVK
GYLPEPVTVTWNSGTLTNGVRTFPSVRQSSGLYSLSSVVSVTSSSQPVTCNVAHPATNT

KVDKTVAPSTCSKPMCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEV QFTWYINNEQVRTARPPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIE KTISKARGQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKT TPTVLDSDGSYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (**SEQ ID NO: 201**)

A11B1_3B1 Light Chain
MDTRAPTQLLGLLLLWLPGARCADIVMTQTPASVSEPVGGTVTIKCQASQNINSGLAWY QQKPGQPPKLLIYKASTLASGVSSRFKGSGSGTEFTLTISDLECADAATYYCQTYYYSSS SSDNAFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVD GTTQTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNSHKEYTCKVTQGTTSVVQSFNRGD C* (**SEQ ID NO: 202**)

A11B1_2D3 Heavy Chain
METGLRWLLLVAVLKGVQCQSLEESGGDLVKPGASLTLTCTASGFSFSSSYWICWVRQ APGKGLEWIACIYGGSSGNIAYASWAKGRFTISKTSSTTVTLQMTSLTAADTATYFCAR DIPSDAFTLDLWGPGTLVTVSSGQPKAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVT VTWNSGTLTNGVRTFPSVRQSSGLYSLSSVVSVTSSSQPVTCNVAHPATNTKVDKTVAP STCSKPMCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNE QVRTARPPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQ PLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSDG SYFLYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (**SEQ ID NO: 203**)

A11B1_2D3 Light Chain
MDTRAPTQLLGLLLLWLPGATFAQVLTQTPSSVSAAVGSTVTINCQASQSVYKDNNLA WYQQKPGQPPKLLIYKASTLASGVPSRFKGSGSGTQFTLTISGVQCEDAATYYCQGEFS CGSADCIAFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWE VDGTTQTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNSHKEYTCKVTQGTTSVVQSFNR GDC* (**SEQ ID NO: 204**)

A11B1_2A7 Heavy Chain
METGLRWLLLVAVLKGVQCQSLEESGGDLVKPGASLTLTCKGSGIDFSSGYGMWWVR QAPGKGLEYIGYIDTGYGSTYYASWAKGRFTISKTSSTTVTLQMTSLTVADTATYFCAK GGAIDLWGPGTLVTVSSGQPKAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVTVTWN SGTLTNGVRTFPSVRQSSGLYSLSSVVSVTSSSQPVTCNVAHPATNTKVDKTVAPSTCSK PMCPPPELPGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRT ARPPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEP KVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPTVLDSDGSYF LYSKLSVPTSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK* (**SEQ ID NO: 205**)

A11B1_2A7 Light Chain
MDTRAPTQLLGLLLLWLPGATFAAVLTQTPASTSAAVGGTVTINCQSSQSVYRSNWLA WYQQKPGQPPKLLIYDVFNLASGVPSRFKGSGSGTQFTLTISGVQCADAATYYCQGSYY SGNWYSAFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWE VDGTTQTTGIENSKTPQNSADCTYNLSSTLTLTSTQYNSHKEYTCKVTQGTTSVVQSFNR 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	WGQGTLVTVSS (**SEQ ID NO: 214**)
Heavy Chain V Gene Segment	IGHV3-48
Light Chain FR1	DIEMTQSPSSPSASVGDRVTITCRAS (**SEQ ID NO: 215**)
Light Chain CDR1	QSISSY (**SEQ ID NO: 216**)
Light Chain FR2	LNWYQQKPGKAPKLLIY (**SEQ ID NO: 217**)
Light Chain CDR2	AAS (**SEQ ID NO: 218**)
Light Chain FR3	SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC (**SEQ ID NO: 219**)
Light Chain CDR3	QQSYSTPLT (**SEQ ID NO: 220**)
Light Chain FR4	FGGGTKVEIK (**SEQ ID NO: 221**)
Light Chain V Gene Segment	IGKV1-39;IGKV1D-39
Light Chain Locus	kappa

2004_05_A06

Heavy Chain FR1	EVQLLESGGGVVQSGRSLRVSCAAS (**SEQ ID NO: 222**)
Heavy Chain CDR1	GFSFSSYG (**SEQ ID NO: 223**)
Heavy Chain FR2	MHWVRQAPGKGLEWVSY (**SEQ ID NO: 224**)
Heavy Chain CDR2	ISSSGSTI (**SEQ ID NO: 225**)
Heavy Chain FR3	YYADSVKGRFTISRDNAENSLYLQMNSLRAEDTAVYYCAR (**SEQ ID NO: 226**)
Heavy Chain CDR3	DLGHFDSGSSYFDY (**SEQ ID NO: 442**)
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	QGISNY (**SEQ ID NO: 228**)
Light Chain FR2	LAWYQQKPGKVPKLLIY (**SEQ ID NO: 229**)
Light Chain CDR2	AAS (**SEQ ID NO: 218**)
Light Chain FR3	TLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC (**SEQ ID NO: 230**)

Light Chain CDR3	QQSYSTPLT (**SEQ ID NO: 220**)
Light Chain FR4	FGGGTKVEVK (**SEQ ID NO: 231**)
Light Chain V Gene Segment	IGKV1-27
Light Chain Locus	kappa

2004_04_C12

Heavy Chain FR1	EVQLLESGGGVVQPGRSLRLSCAAS (**SEQ ID NO: 232**)
Heavy Chain CDR1	GFTFSNYG (**SEQ ID NO: 209**)
Heavy Chain FR2	MNWVRQAPGKGLEWVSY (**SEQ ID NO: 210**)
Heavy Chain CDR2	ISSSSSTI (**SEQ ID NO: 233**)
Heavy Chain FR3	YYADSVKGRFTISRDNAKNSLYLQMNSLRDEDTAVYYCAS (**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	SLQSGVPSRFSGSGSGTDFTLTISSLQPEDXATYYC (**SEQ ID NO: 237**)
Light Chain CDR3	QQSYSTPLT (**SEQ ID NO: 220**)
Light Chain FR4	FGGGXKXEIK (**SEQ ID NO: 238**)
Light Chain V Gene Segment	IGKV1-39; IGKV1D-39
Light Chain Locus	kappa

2002_02_B07

Heavy Chain FR1	EVQLLESGGGVVQPGRSLRLSCAAS (**SEQ ID NO: 232**)
Heavy Chain CDR1	GFTFSTYG (**SEQ ID NO: 436**)
Heavy Chain FR2	MHWVRQAPGKGLEWVSY (**SEQ ID NO: 224**)
Heavy Chain CDR2	ISSSGSTI (**SEQ ID NO: 225**)
Heavy Chain FR3	YYADSVKGRFAISRDNAKNTLYLQMNSLRAEDTALYYCAK (**SEQ ID NO: 239**)
Heavy Chain CDR3	ATRYDILTGYSDGVDYFDY (**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	SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC

	(SEQ ID NO: 219)
Light Chain CDR3	HQSYSTPYT (**SEQ ID NO: 241**)
Light Chain FR4	FGQGTKLEIK (**SEQ ID NO: 242**)
Light Chain V Gene Segment	IGKV1-39; IGKV1D-39
Light Chain Locus	kappa

2004_05_B04

Heavy Chain FR1	QVQLVESGGGLVQPGGSLRLSCAAS (**SEQ ID NO: 243**)
Heavy Chain CDR1	GFTFSSYW (**SEQ ID NO: 437**)
Heavy Chain FR2	MSWVRQAPGKGLEWVAN (**SEQ ID NO: 244**)
Heavy Chain CDR2	IKQDGSEK (**SEQ ID NO: 245**)
Heavy Chain FR3	YYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR (**SEQ ID NO: 246**)
Heavy Chain CDR3	VTSPHAFDI (**SEQ ID NO: 247**)
Heavy Chain FR4	WGRGTLVTVSS (**SEQ ID NO: 248**)
Heavy Chain V Gene Segment	IGHV3-7
Light Chain FR1	DIQMTQSPSAMSASVGDRVTITCRAS (**SEQ ID NO: 249**)
Light Chain CDR1	QGISNY (**SEQ ID NO: 228**)
Light Chain FR2	LAWFQQKPGKVPKRLIY (**SEQ ID NO: 250**)
Light Chain CDR2	AAS (**SEQ ID NO: 218**)
Light Chain FR3	SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC (**SEQ ID NO: 219**)
Light Chain CDR3	QQSYSTPLT (**SEQ ID NO: 220**)
Light Chain FR4	FGGGTKVEVK (**SEQ ID NO: 231**)
Light Chain V Gene Segment	IGKV1-39; IGKV1D-17; IGKV1D-39
Light Chain Locus	kappa

2003_03_E12

Heavy Chain FR1	QVQLVESGGGVVRPGGSLRLSCAAS (**SEQ ID NO: 251**)
Heavy Chain CDR1	GFTFDDYG (**SEQ ID NO: 438**)
Heavy Chain FR2	MSWVRQAPGKGLEWVSG (**SEQ ID NO: 252**)
Heavy Chain CDR2	INWNGGST (**SEQ ID NO: 253**)
Heavy Chain FR3	GYADSVKGRFTISRDNSKNTLYLQMNSLRGEDTAVYYCVT (**SEQ ID NO: 254**)
Heavy Chain CDR3	QGSAFDI (**SEQ ID NO: 255**)
Heavy Chain FR4	WGRGTLVTVSS (**SEQ ID NO: 248**)
Heavy Chain V Gene Segment	IGHV3-20
Light Chain FR1	SYELTQPPSLSVSPGQTARITCSGD (**SEQ ID NO: 256**)
Light Chain CDR1	ALAKQY (**SEQ ID NO: 257**)
Light Chain FR2	AYWYQQTPGQAPVLVIY (**SEQ ID NO: 258**)
Light Chain CDR2	KDT (**SEQ ID NO: 259**)

Light Chain FR3	ERPSGIPERFSGSSSGTTVTLTISGVQAEDEVDYYC (**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	QVQLVQSGAEVKKPGASVKVSCKAS (**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	WGQGTMVTVSS (**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	SLESGVPSRFSGSGSGTEFTLTISSLQPDDFAVYYC (**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	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR (**SEQ ID NO: 276**)
Heavy Chain CDR3	DYGGYDGVYFDY (**SEQ ID NO: 277**)
Heavy Chain FR4	WGRGTLVTVSS (**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	EVQLLESGGGLVKPGGSLRLSCAAS (**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	YYADSVKGRFAISRDNSKNTLYLQMNSLRAEDTAVYYCAR (**SEQ ID NO: 288**)
Heavy Chain CDR3	DRDVGPTYYYYGMDV (**SEQ ID NO: 289**)
Heavy Chain FR4	WGQGTMVTVSS (**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	EVQLLESGGGVVQPGRSLRLSCAAS (**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	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK (**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	DIQMTQSPSSLSASVGDTISITCRAS (**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	SLQSGVPSRFSGSGSRTDFTLTISSVQPEDFATYYC (**SEQ ID NO: 299**)
Light Chain CDR3	QQSYSTPFT (**SEQ ID NO: 300**)
Light Chain FR4	FGPGTKVEIK (**SEQ ID NO: 301**)
Light Chain V Gene Segment	IGKV1-39; IGKV1D-39
Light Chain Locus	kappa

2002_02_B05

Heavy Chain FR1	EVQLLESGGGVVQPGRSLRLSCAAS (**SEQ ID NO: 232**)
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	YYADSVKGRFAISRDNAKNTLYLQMNSLRAEDTALYYCAK (**SEQ ID NO: 239**)
Heavy Chain CDR3	ATRYDILTGYSDGVDYFDY (**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	SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC (**SEQ ID NO: 219**)
Light Chain CDR3	QQSYSTPFT (**SEQ ID NO: 300**)
Light Chain FR4	FGPGTKVEIK (**SEQ ID NO: 301**)
Light Chain V Gene Segment	IGKV1-39; IGKV1D-39
Light Chain Locus	kappa

2003_03_F05

Heavy Chain FR1	EVQLVESGAEVKKPGASVKVSCKAS (**SEQ ID NO: 302**)
Heavy Chain CDR1	GYTFTRYY (**SEQ ID NO: 441**)
Heavy Chain FR2	MHWVRQAPGQGLEWMGI (**SEQ ID NO: 303**)
Heavy Chain CDR2	INPSGGST (**SEQ ID NO: 304**)
Heavy Chain FR3	IYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR (**SEQ ID NO: 305**)
Heavy Chain CDR3	SLRDGYNYIGSLGY (**SEQ ID NO: 306**)
Heavy Chain FR4	WGQGTLVTVSS (**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	QRPSGVPDRFSGSKSGTSASLAIRGLQSEDEAGYYC (**SEQ ID NO: 311**)
Light Chain CDR3	AAWDDSLNGLNWV (**SEQ ID NO: 207**)
Light Chain FR4	FGGGTQLTVL (**SEQ ID NO: 294**)
Light Chain V Gene Segment	IGLV1-44; IGLV1-47
Light Chain Locus	lambda

1994_01_A07

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

1994_01_A09

Heavy Chain FR1	QMQLVQSGAEVKKPGSSVKVSCKAS (**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	NYAQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCAR (**SEQ ID NO: 323**)
Heavy Chain CDR3	DINRYNWNFRAFDI (**SEQ ID NO: 324**)
Heavy Chain FR4	WGQGTLVTVSS (**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	QVQLVQSGAEVKKPGSSVKVSCKAS (**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	WGQGTLVTVSS (**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	SLQSGVPSRFSGSGSGTDFTLTISSLQPEDAATYYC (**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	YYADSVKGRFTISRDNSKSTLYLQMNSLRVDDTAVYYCAK (**SEQ ID NO: 337**)
Heavy Chain CDR3	DLGWQNDY (**SEQ ID NO: 338**)
Heavy Chain FR4	WGQGTLVTVSS (**SEQ ID NO: 214**)
Light Chain FR1	QSVLTQPASVSGSPGQSITISCTGT DLGWQNDY (**SEQ ID NO: 339**)
Light Chain CDR1	SSDVGGHNY (**SEQ ID NO: 340**)
Light Chain FR2	VSWYQQHPGKAPKLMIY (**SEQ ID NO: 341**)
Light Chain CDR2	DVS (**SEQ ID NO: 342**)
Light Chain FR3	NRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYC (**SEQ ID NO: 343**)
Light Chain CDR3	SSYTSSSPWV (**SEQ ID NO: 344**)
Light Chain FR4	FGGGTKLTVLG (**SEQ ID NO: 345**)
Light Chain Locus	lambda

1995_01_F09

Heavy Chain FR1	EVQLVESGGGLVQPGGSLRLSCAAS (**SEQ ID NO: 346**)

Heavy Chain CDR1	GFTFSSYA (**SEQ ID NO: 440**)
Heavy Chain FR2	MSWVRQAPGKGLEWVSA (**SEQ ID NO: 274**)
Heavy Chain CDR2	ISGSGGST (**SEQ ID NO: 275**)
Heavy Chain FR3	YYADSVKGRFTISRDNSKNALYLQMNSLRAEDTAVYYCRG (**SEQ ID NO: 347**)
Heavy Chain CDR3	YCSSTSCYGRRGAFDI (**SEQ ID NO: 348**)
Heavy Chain FR4	SGQGTLVTVSS (**SEQ ID NO: 349**)
Light Chain FR1	QAVLTQPPSASGTPGQRVTISCSGR (**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	QVQLVESGGGLVQPGGSLRLSCAAS (**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	SYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR (**SEQ ID NO: 359**)
Heavy Chain CDR3	DFWSGRPYYYYMDV (**SEQ ID NO: 360**)
Heavy Chain FR4	WGQGTTVTVSS (**SEQ ID NO: 297**)
Light Chain FR1	DIQMTQSPSSLSASVGDRVTITCRAS (**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	TLQGGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC (**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	YYADSVKGRFTISRDNSKNTLYLQMNSRRAEDTAVYYCAR (**SEQ ID NO: 365**)
Heavy Chain CDR3	WGIVAARPNYYYGMDV (**SEQ ID NO: 366**)
Heavy Chain FR4	WGQGTLVTVSS (**SEQ ID NO: 214**)

Light Chain FR1	QSALTQPRSVSGSPGQSVTISCTGT (**SEQ ID NO: 367**)
Light Chain CDR1	SSDVGGYNY (**SEQ ID NO: 368**)
Light Chain FR2	VSWYQQHPGKAPKLMIY (**SEQ ID NO: 341**)
Light Chain CDR2	DVS (**SEQ ID NO: 342**)
Light Chain FR3	KRPSGVPDRFSGSKSGNTASLTISGLQAEDEADYHC (**SEQ ID NO: 443**)
Light Chain CDR3	SSYANNSPWV (**SEQ ID NO: 369**)
Light Chain FR4	FGGGTKVTVLG (**SEQ ID NO: 370**)
Light Chain Locus	lambda

2002_02_E01

Heavy Chain FR1	QVQLVQSGAEVRKPGASVKVSCKAS (**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	WGQGTLVTVSS (**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	NLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYC (**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	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR (**SEQ ID NO: 276**)
Heavy Chain CDR3	GGLTGDDAFDI (**SEQ ID NO: 380**)
Heavy Chain FR4	WGQGTLVTVSS (**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	SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC (**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	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR (**SEQ ID NO: 276**)
Heavy Chain CDR3	DKELSY (**SEQ ID NO: 385**)
Heavy Chain FR4	WGQGTLVTVSS (**SEQ ID NO: 214**)
Light Chain FR1	QSGLTQPASVSGSPGQSITISCTGT (**SEQ ID NO: 386**)
Light Chain CDR1	SSDVGGYNY (**SEQ ID NO: 368**)
Light Chain FR2	VSWYQQHPGKAPKLMIY (**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	YYADSVKGRFTISRDNAKNSLYLQMNSLRDEDTAVYYCAS (**SEQ ID NO: 212**)
Heavy Chain CDR3	GQLDTSDAFDI (**SEQ ID NO: 213**)
Heavy Chain FR4	WGQGTTVTVSS (**SEQ ID NO: 297**)
Light Chain FR1	DIQMTQSPSSLSASVGDRVTITCRAS (**SEQ ID NO: 227**)
Light Chain CDR1	QSISSY (**SEQ ID NO: 216**)
Light Chain FR2	LNWYQQKPGKAPKLLIY (**SEQ ID NO: 217**)
Light Chain CDR2	KTS (**SEQ ID NO: 389**)
Light Chain FR3	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	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK (**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	QQSYSTPLT (**SEQ ID NO: 220**)
Light Chain FR4	FGGGTKLEIK (**SEQ ID NO: 394**)
Light Chain Locus	kappa

2005_05_E05

Heavy Chain FR1	EVQLVQSGAEVKKPGASVKVSCKAS (**SEQ ID NO: 395**)
Heavy Chain CDR1	GYTFTSYY (**SEQ ID NO: 396**)
Heavy Chain FR2	MHWVRQAPGQGLEWMGI (**SEQ ID NO: 303**)
Heavy Chain CDR2	INPSGGST (**SEQ ID NO: 304**)
Heavy Chain FR3	SYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR (**SEQ ID NO: 397**)
Heavy Chain CDR3	SPWLITFGGVIAMGY (**SEQ ID NO: 402**)
Heavy Chain FR4	WGQGTLVTVSS (**SEQ ID NO: 214**)
Light Chain FR1	QSVLTQPPSASGTPGQRVTISCSGS (**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	QVQLVQSGAEVRKPGASVKVSCKAS (**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	WGQGTLVTVSS (**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	NLETGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC (**SEQ ID NO: 317**)
Light Chain CDR3	QQFNNYPLT (**SEQ ID NO: 408**)
Light Chain FR4	FGGGTKLEIK (**SEQ ID NO: 394**)
Light Chain Locus	kappa

1997_02_B03

Heavy Chain FR1	QVQLVESGAEVKKPGASVKVSCKAS (**SEQ ID NO: 409**)
Heavy Chain CDR1	GYTFTSYY (**SEQ ID NO: 396**)
Heavy Chain FR2	MHWVRQAPGQGLEWMGI (**SEQ ID NO: 303**)
Heavy Chain CDR2	INPSGGST (**SEQ ID NO: 304**)
Heavy Chain FR3	SYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR (**SEQ ID NO: 397**)
Heavy Chain CDR3	AGGYYYYYMDV (**SEQ ID NO: 398**)
Heavy Chain FR4	WGQGTLVTVSS (**SEQ ID NO: 214**)
Light Chain FR1	QSGLTQPPSASGTPGQRVTISCSGS (**SEQ ID NO: 399**)
Light Chain CDR1	GPNIGNNY (**SEQ ID NO: 400**)
Light Chain FR2	VYWYQQLPGTAPKLLMY (**SEQ ID NO: 401**)
Light Chain CDR2	RNN (**SEQ ID NO: 310**)
Light Chain FR3	QRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYC (**SEQ ID NO: 410**)
Light Chain CDR3	AAWDDSLNGYV (**SEQ ID NO: 411**)
Light Chain FR4	FGTGTKLTVLG (**SEQ ID NO: 412**)
Light Chain Locus	lambda

Humanized mAb sequences

Humanized 79E3E3 Heavy Chain Variable Region
QIQLVQSGAEVKKPGESLKISCKASGYTFTDYAIGWVRQMPGKGLEWMGIINTQTGKPK
YSPSFQGQFIFSLDTSINTTYLQWSSLKASDTAIYFCTRLGTGNTKGFAYWGQGTTVTVS
S (**SEQ ID NO: 413**)

Humanized 79E3E3 Light Chain Variable Region
DIQITQSPSSLSASLGDKVTITCRSSQSLLYSENNQDYLAWYQQKPGKAPKLLIYGASNL
QSGVPSRFSGRGSGTDFTLTISSLQPEDFATYYCEQTYRYPFTFGPGTKVDIKR (**SEQ ID NO: 414**)

Humanized 9-G05 Heavy Chain VH_1
Leader sequence-VH-**hIgG1CH-Stop codon***
MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFPDYNMDWVR
QAPGQRLEWMGYINPDNGGTIYNQKFKGRVTLTVDTSASTAYMELSSLRSEDTAVYYC
ARLDSSGYGYYAMDYWGQGTSVTVSS**ASTKGPSVFPLAPSSKSTSGGTAALGCLVKD**

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

Humanized 9-G05 Heavy Chain VH_2

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

MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFPDYNMDWVR QAPGQRLEWIGYINPDNGGTIYNQKFKGRVTLTVDTSASTAYMELSSLRSEDTAVYYCA RLDSSGYGYYAMDYWGQGTSVTVSS**ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK* (SEQ ID NO: 416)**

Humanized 9-G05 Heavy Chain VH_3

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

MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFPDYNMDWVR QAPGQRLEWMGYINPDNGGTIYNQKFKGRATLTVDTSASTAYMELSSLRSEDTAVYYC ARLDSSGYGYYAMDYWGQGTSVTVSS**ASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPGK* (SEQ ID NO: 417)**

Humanized 9-G05 Heavy Chain VH_4

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

MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFPDYNMDWVR QAPGQSLEWIGYINPDNGGTIYNQKFKGRATLTVDTSASTAYMELSSLRSEDTAVYYCA RLDSSGYGYYAMDYWGQGTSVTVSS**ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK* (SEQ ID NO: 418)**

Humanized 9-G05 Light Chain VL_1

Leader sequence-VL-**hIgKCL-Stop codon***
MGWSCIILFLVATATGVHSDIVMTQSPDSLAVSLGERATINCRASESVDNYGISFMHWY
QQKPGQPPKLLIYRASNLDSGVPDRFSGSGSGTDFTLTISSLQAEDVATYYCQQSYKDPR
TFGGGTKLEIK**RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN
RGEC* (SEQ ID NO: 419)**

Humanized 9-G05 Light Chain VL_2

Leader sequence-VL-**hIgKCL-Stop codon***
MGWSCIILFLVATATGVHSDIVLTQSPASLAVSPGQRATITCRASESVDNYGISFMHWYQ
QKPGQPPKLLIYRASNLDSEVPARFSGSGSRTDFTLTINPVEANDTATYYCQQSYKDPRT
FGGGTKLEIK**RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR
GEC* (SEQ ID NO: 420)**

16E10 Heavy Chain Variable Region
QSLEESGGDLVKPGASLTLTCRVSGFSFSSSYYMCWVRQAPGKGLEWIACIGTTRGSTY
YATWAKGRFTISKISSTTVTLQMTSLTDADTATYFCARDATGYRINTIGLYFNLWGPGTL
VTVSS (**SEQ ID NO: 421**)

Humanized 16E10 Heavy Chain Variable Region VH_1
QSLLESGGGLVKPGGSLRLSCAVSGFSFSSSYYMCWVRQAPGKGLEWVSCIGTTRGSTY
YADSAKGRFTISKISKNTVYLQMTSLRAEDTAVYFCARDATGYRINTIGLYFNLWGPGT
LVTVSS (**SEQ ID NO: 422**)

Humanized 16E10 Heavy Chain Variable Region VH_2
EVQLLESGGGLVKPGGSLRLSCAVSGFSFSSSYYMCWVRQAPGKGLEWVSCIGTTRGST
YYADSAKGRFTISKDNSKNTVYLQMTSLRAEDTAVYFCARDATGYRINTIGLYFNLWG
QGTLVTVSS (**SEQ ID NO: 423**)

Humanized 16E10 Heavy Chain Variable Region VH_3
QSLLESGGGLVKPGGSLRLSCAVSGFSFSSSYYMCWVRQAPGKGLEWVSCIGTTRGSTY
YADSAKGRFTISKESKNTVYLQMSSLRAEDTAVYFCARDATGYRINTIGLYFNLWGPGT
LVTVSS (**SEQ ID NO: 424**)

Humanized 16E10 Heavy Chain Variable Region VH_4
EVQLLESGGGLVKPGGSLRLSCAVSGFSFSSSYYMCWVRQAPGKGLEWVSCIGTTRGST
YYADSAKGRFTISKDNSKNTVYLQMSSLRAEDTAVYFCARDATGYRINTIGLYFNLWG
QGTLVTVSS (**SEQ ID NO: 425**)

Humanized 16E10 Heavy Chain Variable Region VH_5
QSLLESGGGLVKPGGSLRLSCAVSGFSFSSSYYMCWVRQAPGKGLEWVSCIGTTRGSTY
YADSAKGRFTISKESKNTVYLQMSSLRAEDTAVYFCARDATGYRIQTIGLYFNLWGPGT
LVTVSS (**SEQ ID NO: 426**)

Humanized 16E10 Heavy Chain Variable Region VH_6
EVQLLESGGGLVKPGGSLRLSCAVSGFSFSSSYYMCWVRQAPGKGLEWVSCIGTTRGST YYADSAKGRFTISKDNSKNTVYLQMSSLRAEDTAVYFCARDATGYRIQTIGLYFNLWG QGTLVTVSS (**SEQ ID NO: 427**)

16E10 Light Chain Variable Region
ELTQTPSSVEAAVGGTPTIKCQASQTIYSYLSWYQQKPGQPPKLLIYEASKLASGVPSRFS GSGSGTDYTLTISDLECADAATYYCQSYHGTASTEYNTFGGGTEVVVK (**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 (α11β1) 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-α11β1 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-α11β1 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-α11β1 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-α11β1 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-α11β1 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-α11β1 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-α11β1 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-α11β1 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-α11β1 antibody, or antigen-binding fragment thereof, of any one of claims 1-9, wherein the antibody, or antigen-binding fragment thereof, reduces interaction of α11β1 with collagen in human α11β1-expressing cells.

11. An anti-α11β1 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, TGFβ, CTGF, PDGF, MMP9, or a combination thereof.

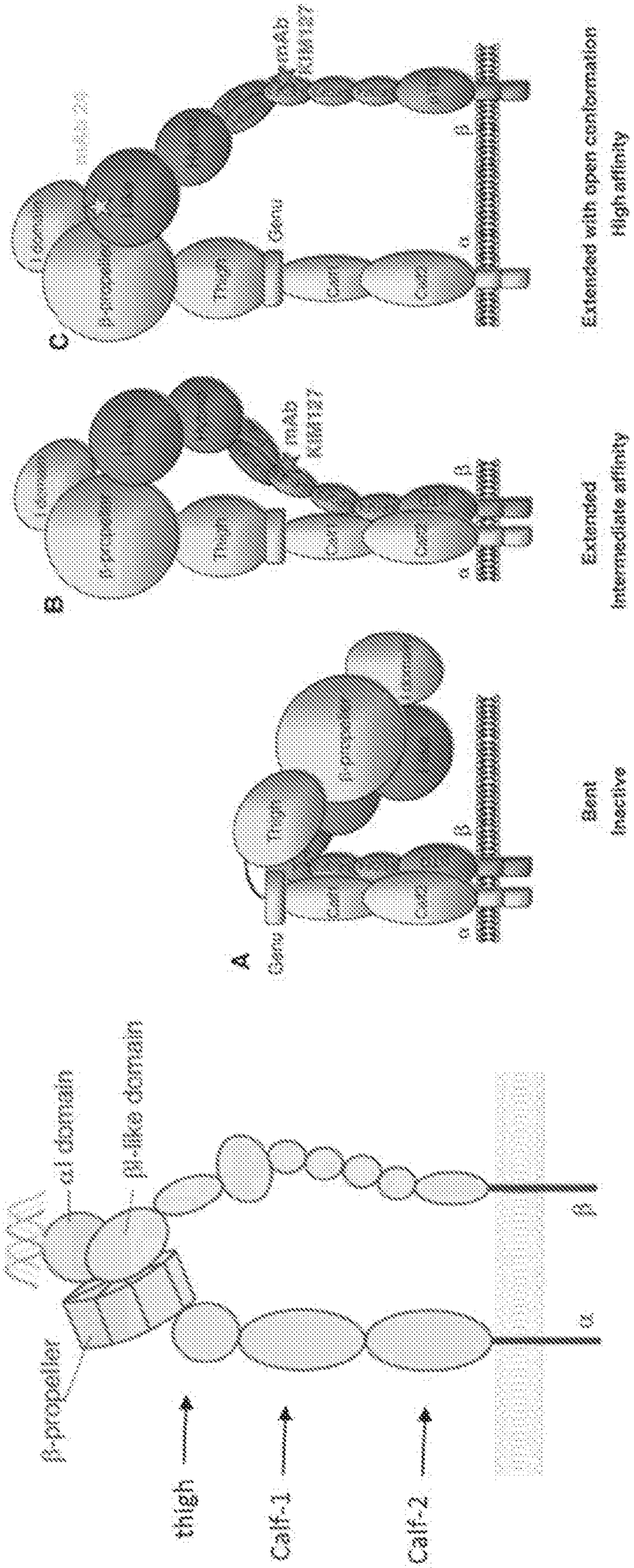

Extended with open conformation
High affinity
Extended
Intermediate affinity
Bent
Inactive
thigh
Calf-1
Calf-2

FIGURE 1

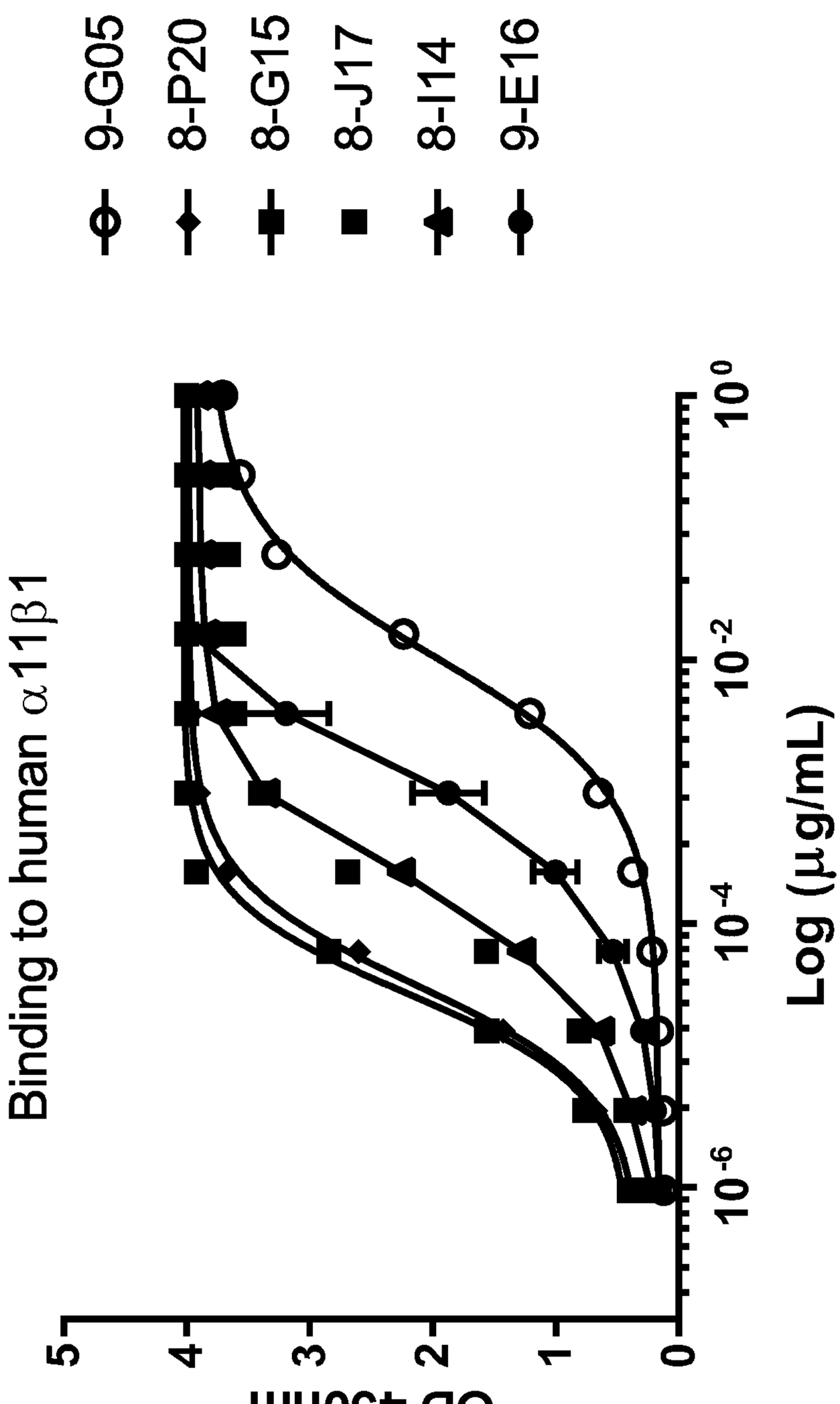

G05
P20
G15
J17
I14
E16
Binding to human α11β1
10^0
10^-2
10^-4
10^-6
Log (µg/mL)
OD 450nm
5
4
3
2
1
0

FIGURE 2A

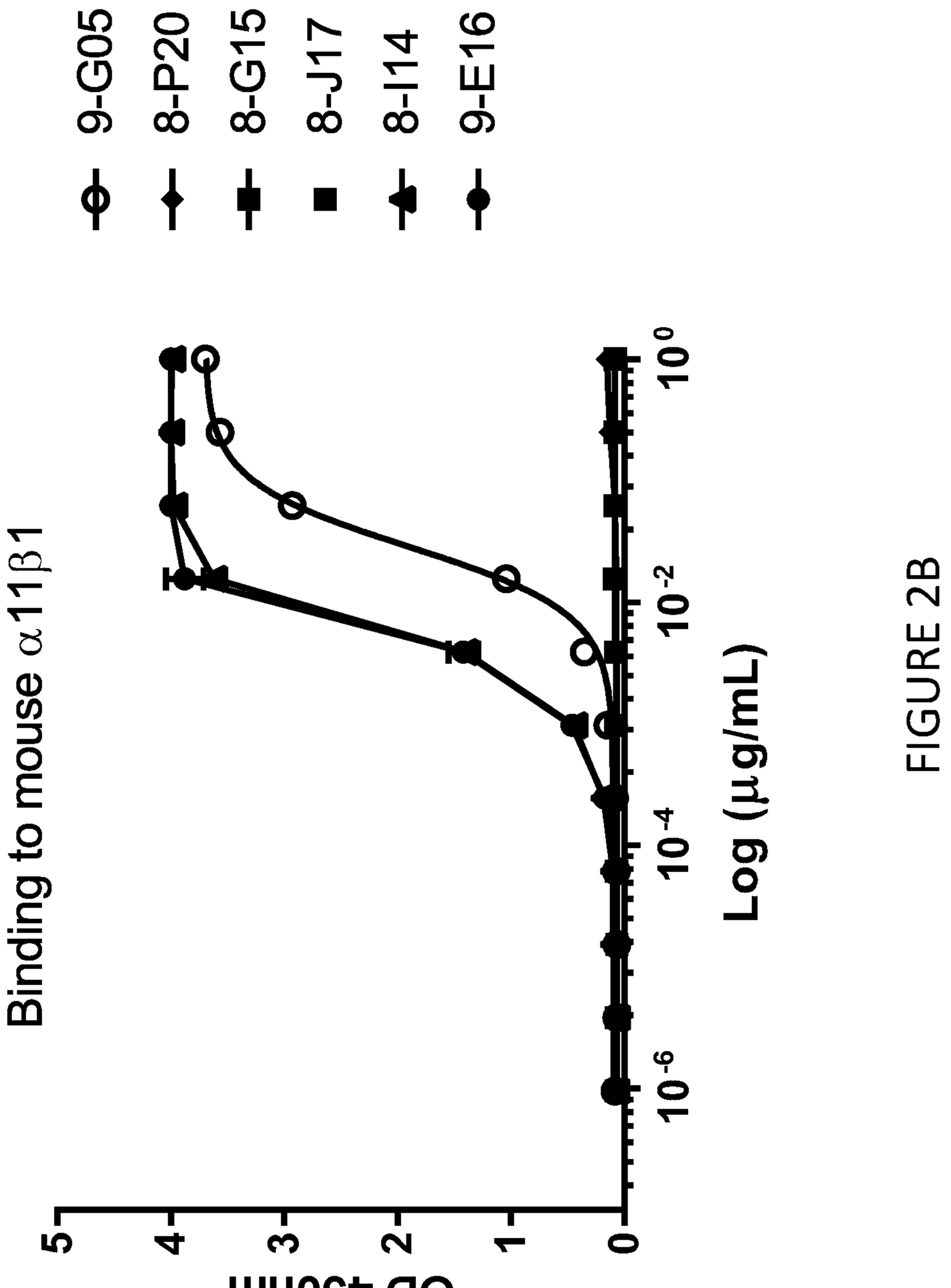

G05
P20
G15
J17
I14
E16
9-
8-
8-
8-
8-
9-
Binding to mouse α11β1
10^{0}
10^{-2}
10^{-4}
10^{-6}
Log (µg/mL)
OD 450nm
5
4
3
2
1
0

FIGURE 2B

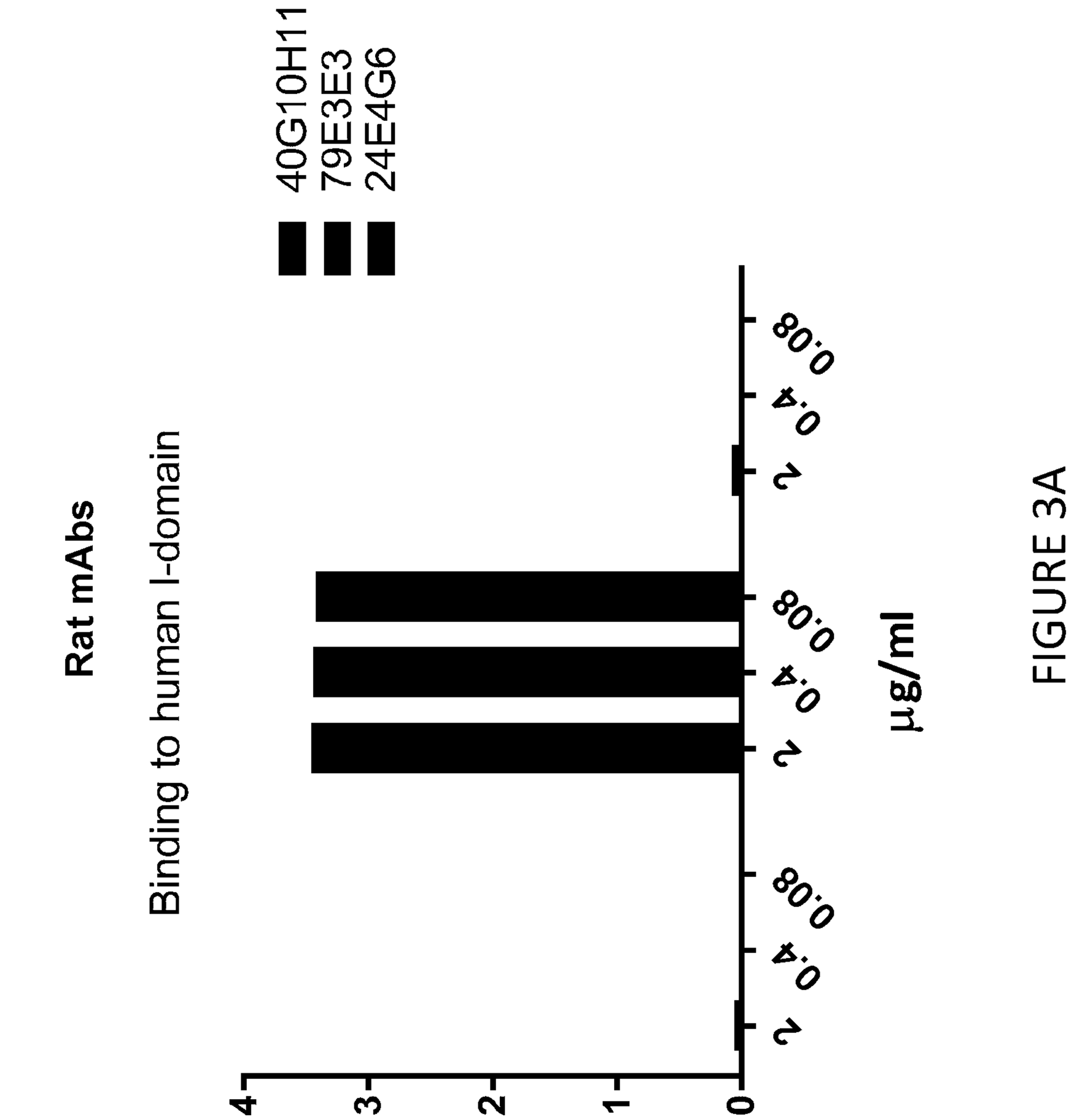

Rat mAbs
Binding to human I-domain
40G10H1
79E3E3
24E4G6
0
1
2
3
4
2
4.0
8.0
2
4.0
8.0
2
4.0
8.0
µg/ml
OD 450nm

FIGURE 3A

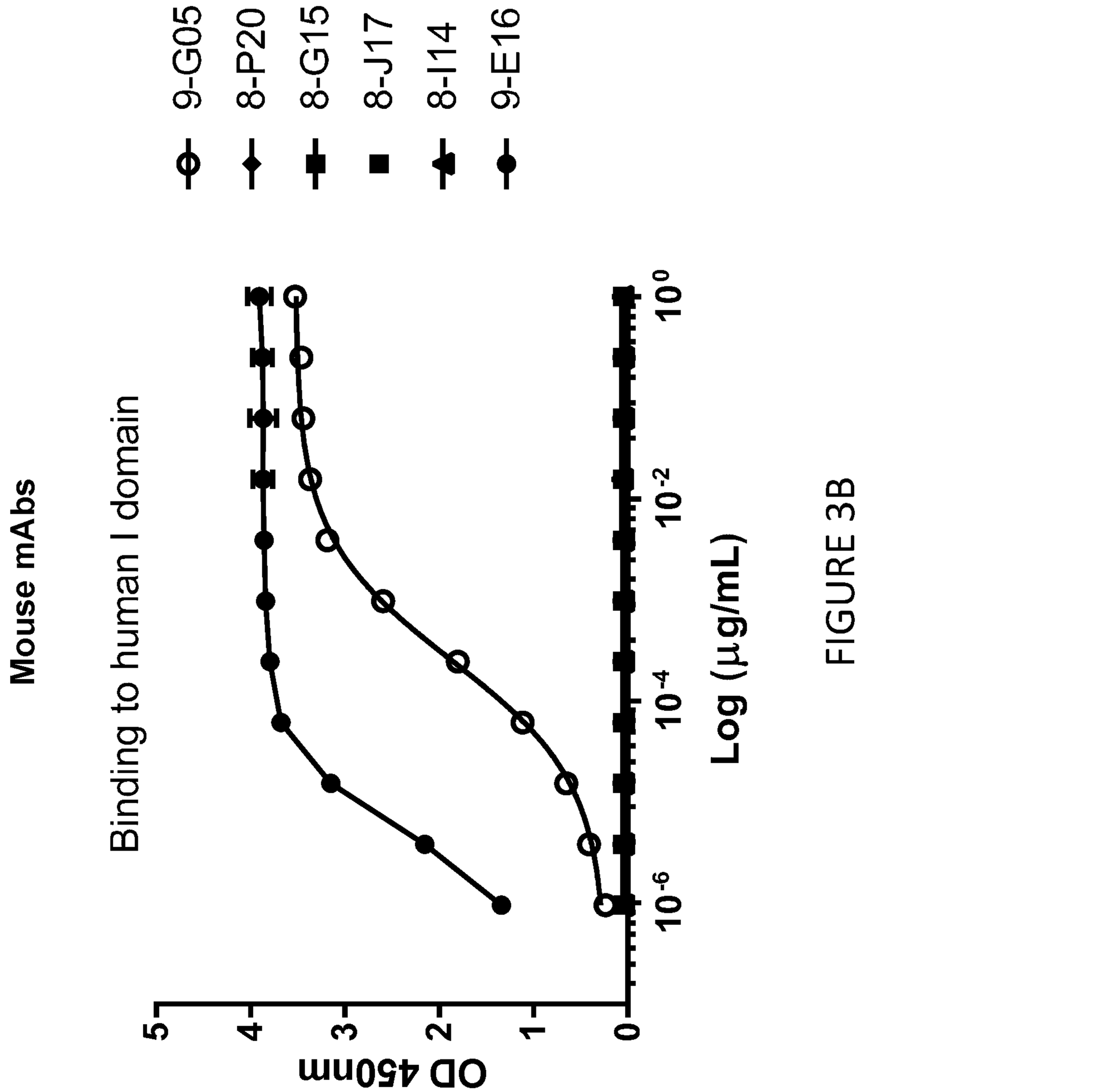

OD 450nm
Mouse mAbs
Binding to human I domain
0
1
2
3
4
5
10^{-6}
10^{-4}
10^{-2}
10^{0}
Log (µg/mL)
-G05
-P20
-G15
-J17
-I14
-E16
96
88
88
88
88
96

FIGURE 3B

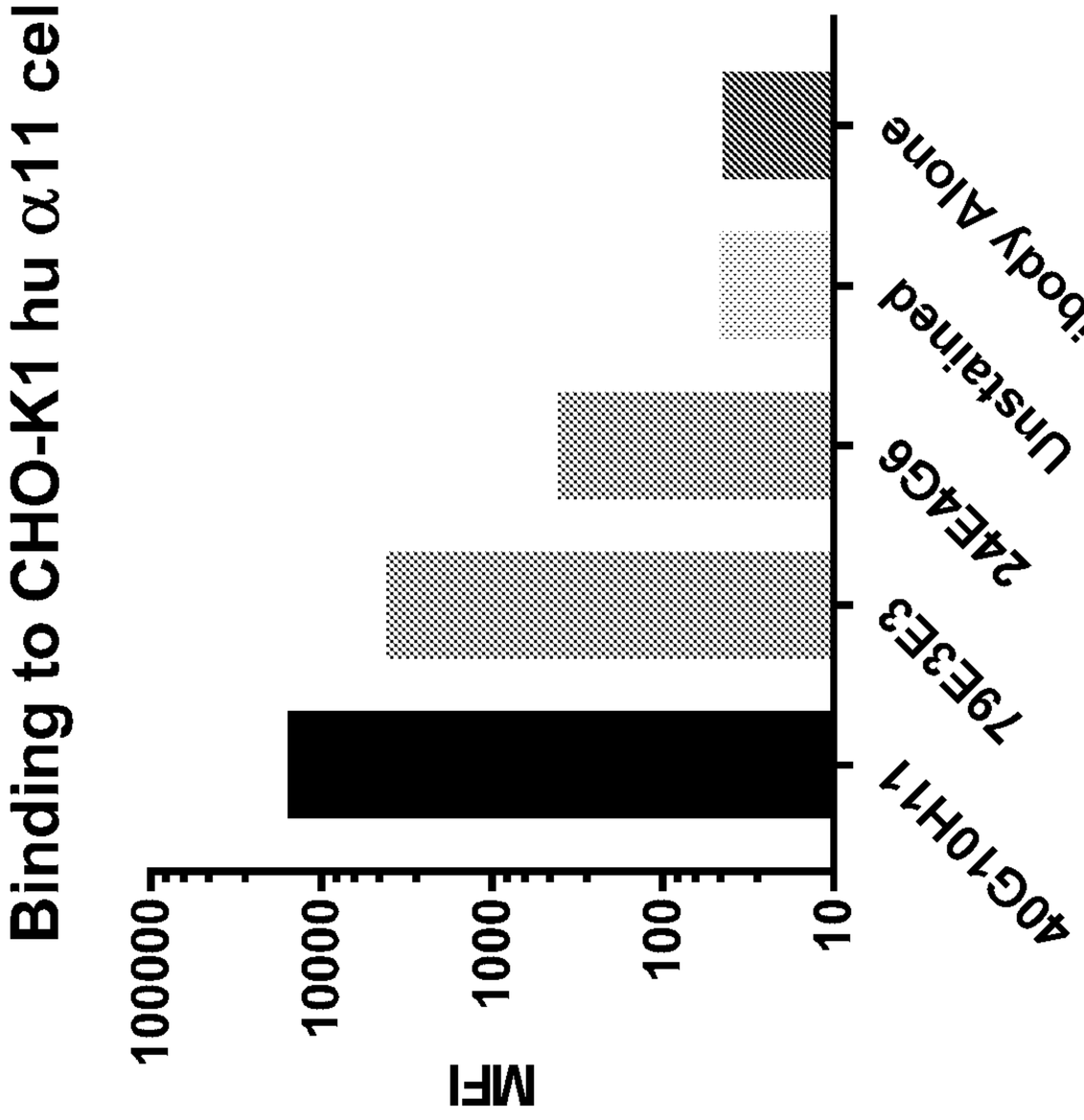

Rat mAbs
Binding to CHO-K1 hu α11 cells
MFI
100000
10000
1000
100
10
40G10H11
79E3E3
24E4G6
Unstained
Detection Antibody Alone

FIGURE 4A

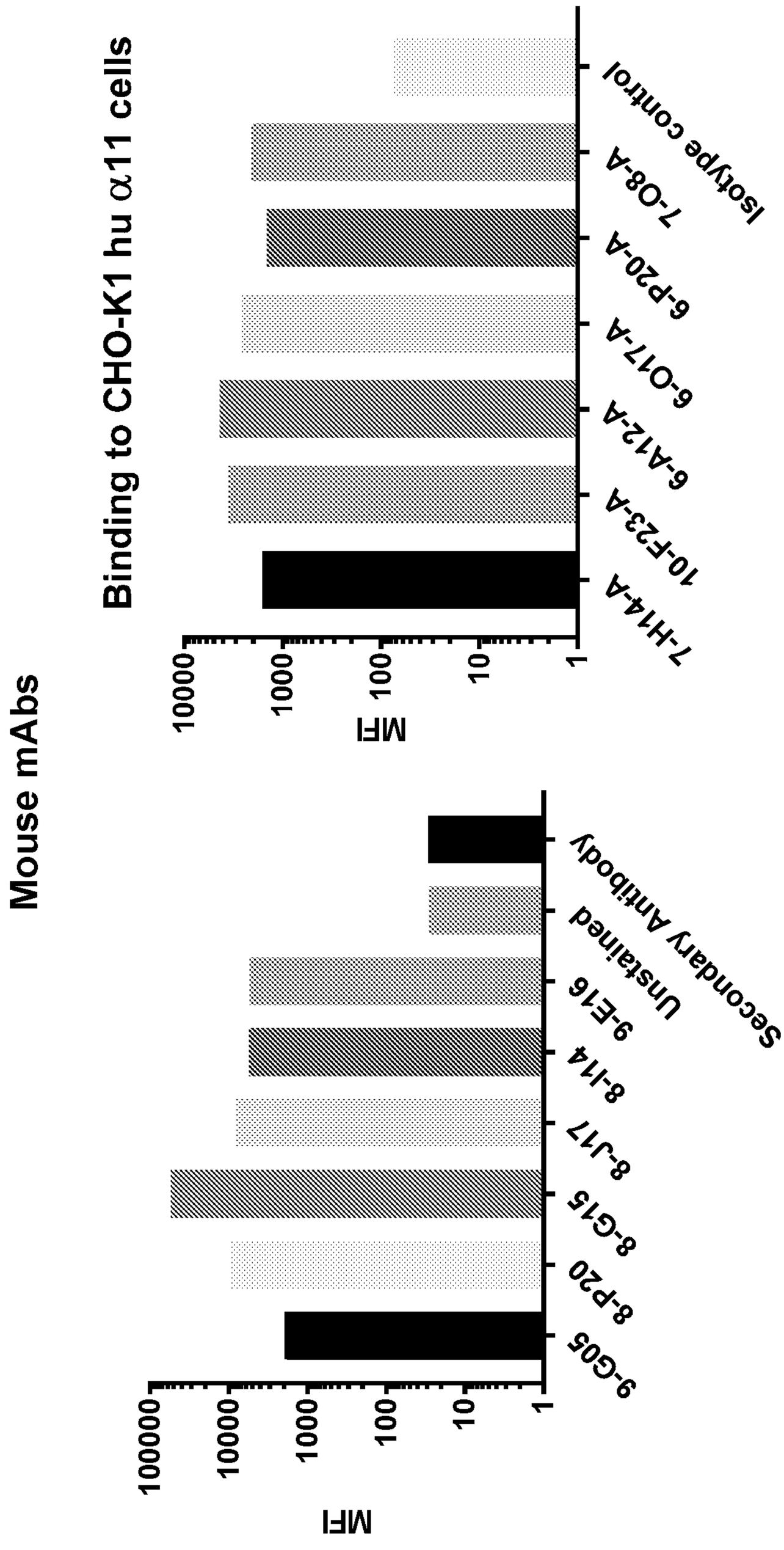

Binding to CHO-K1 hu α11 cells
MFI
10000
1000
100
10
1
7-H14-A
10-F23-A
6-A12-A
6-O17-A
6-P20-A
7-O8-A
Isotype control
Mouse mAbs
MFI
100000
10000
1000
100
10
1
9-G05
8-P20
8-G15
8-J17
8-I14
9-E16
Unstained
Secondary Antibody

FIGURE 4B

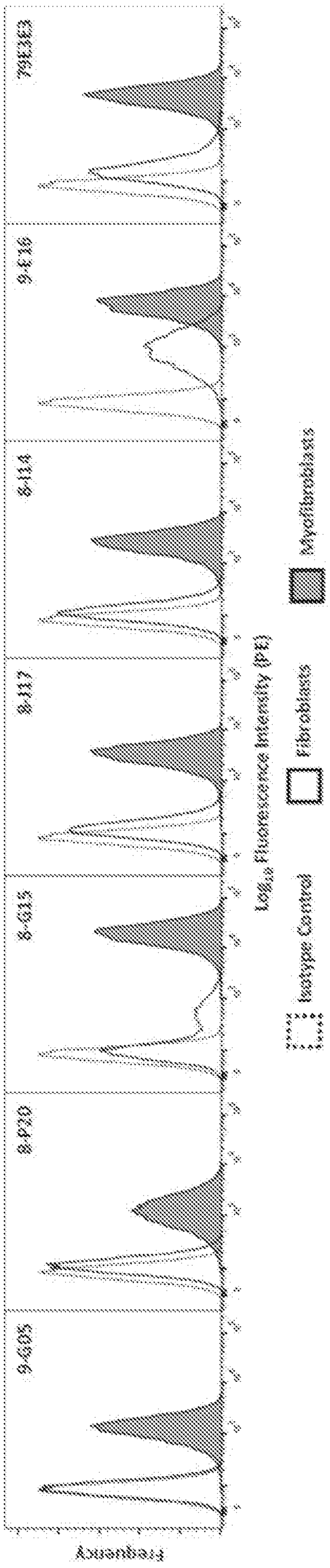
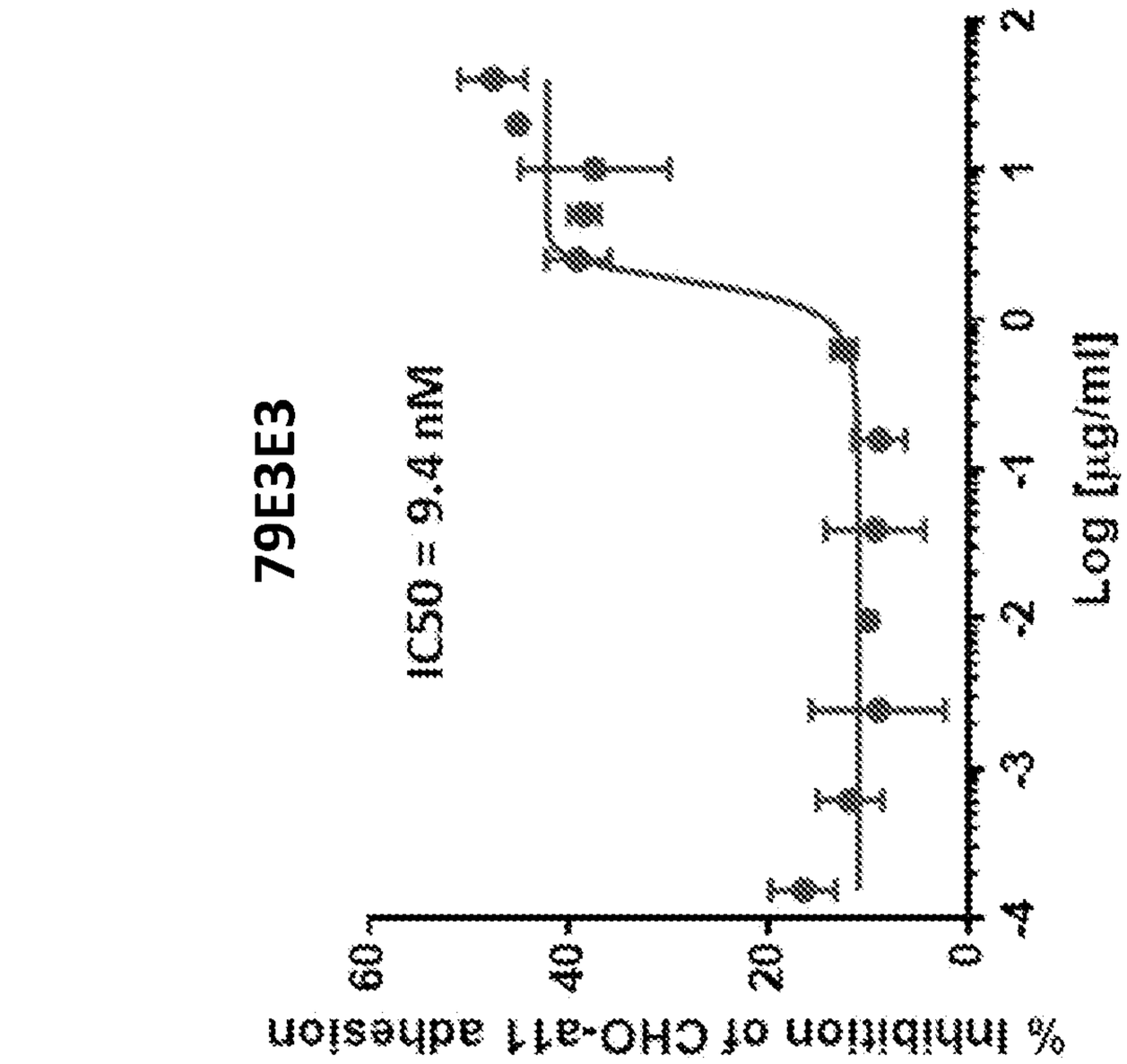

7913E3
9-E10
8-114
8-117
8-G11
8-P20
9-G05
Frequency
Log10 Fluorescence Intensity (RFI)
Fibroblasts
Myofibroblasts
Isotype Control

FIGURE 5


79E3E3
IC50 = 9.4 nM
% inhibition of CHO-a11 adhesion
60
40
20
0
-4
-3
-2
-1
0
Log [µg/ml]

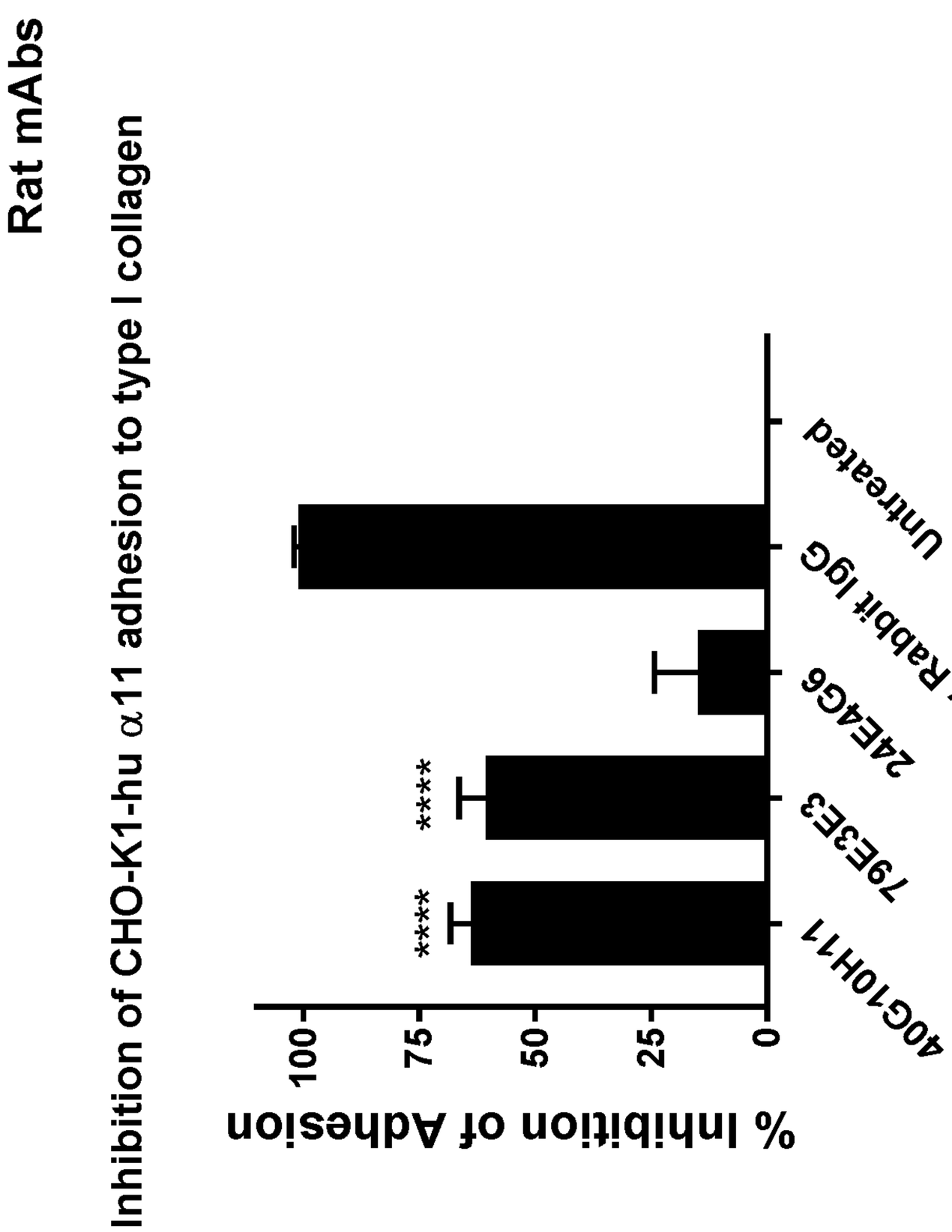
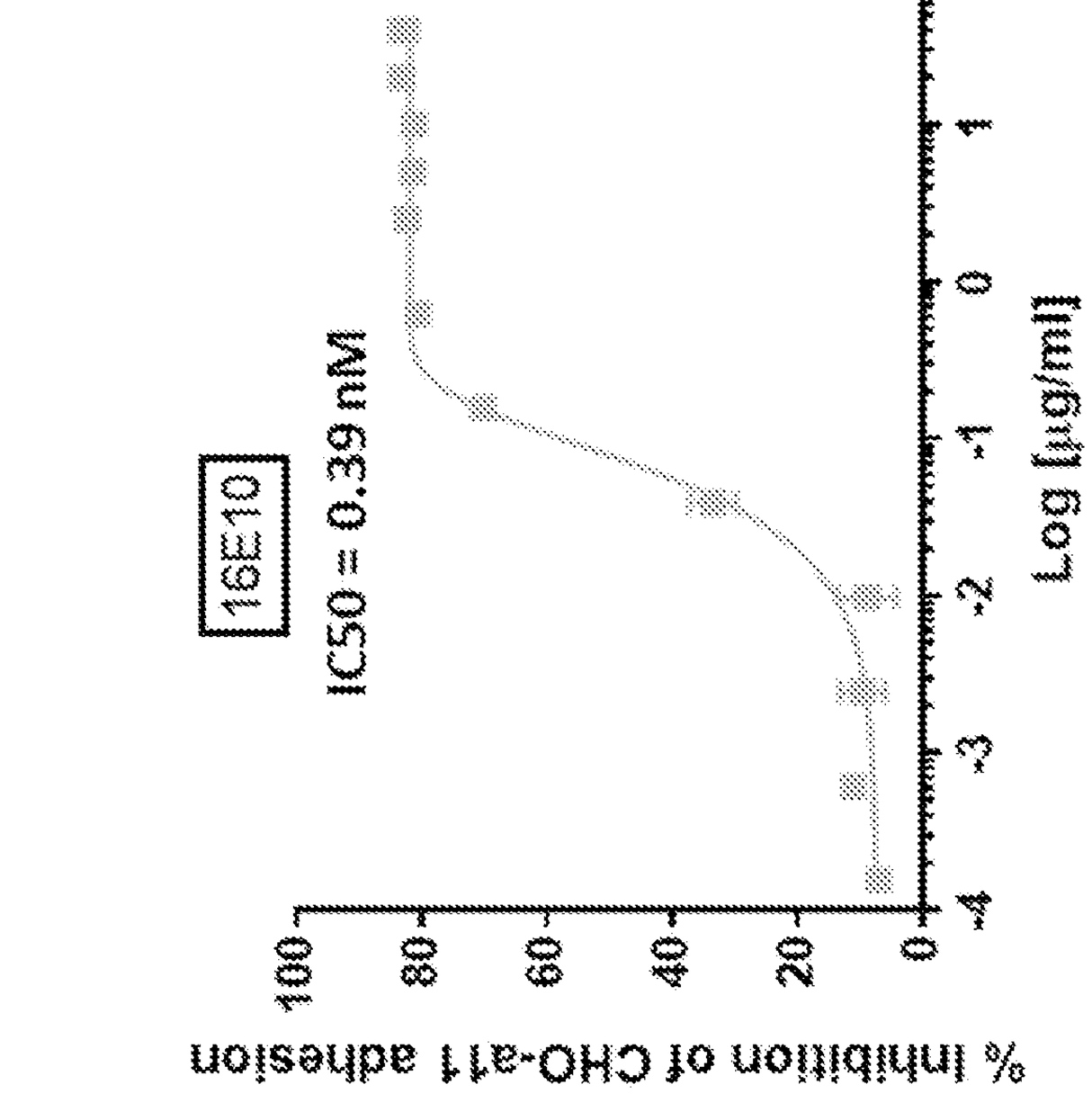

Rat mAbs
Inhibition of CHO-K1-hu α11 adhesion to type I collagen
% Inhibition of Adhesion
100
75
50
25
0
****
****
40G10H11
79E3E3
24E4G6
Poly Rabbit IgG
Untreated

FIGURE 6A


16E10
IC50 = 0.39 nM
% Inhibition of CHO-a11 adhesion
100
80
60
40
20
0
-4
-3
-2
-1
0
1
2
Log (µg/ml)

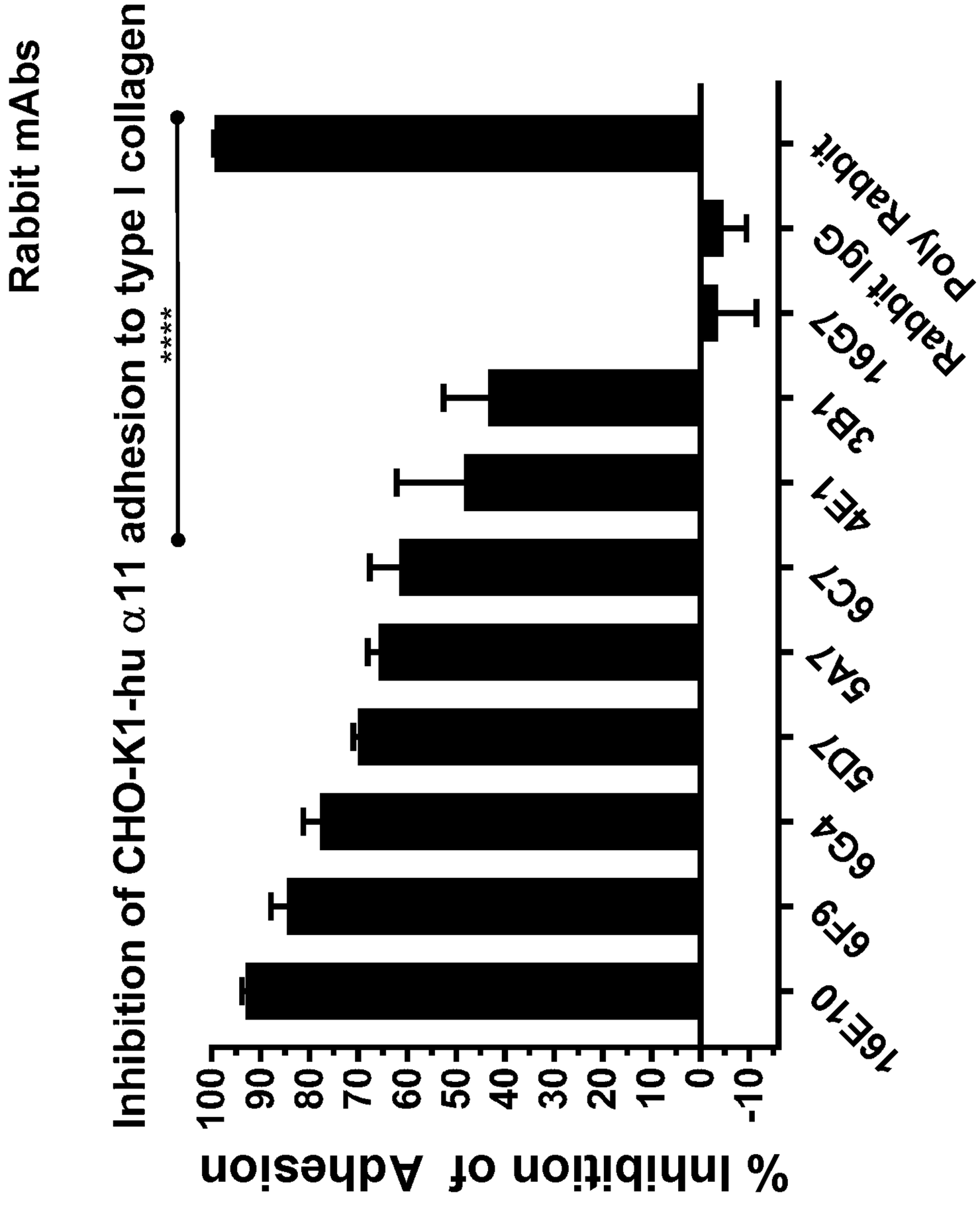
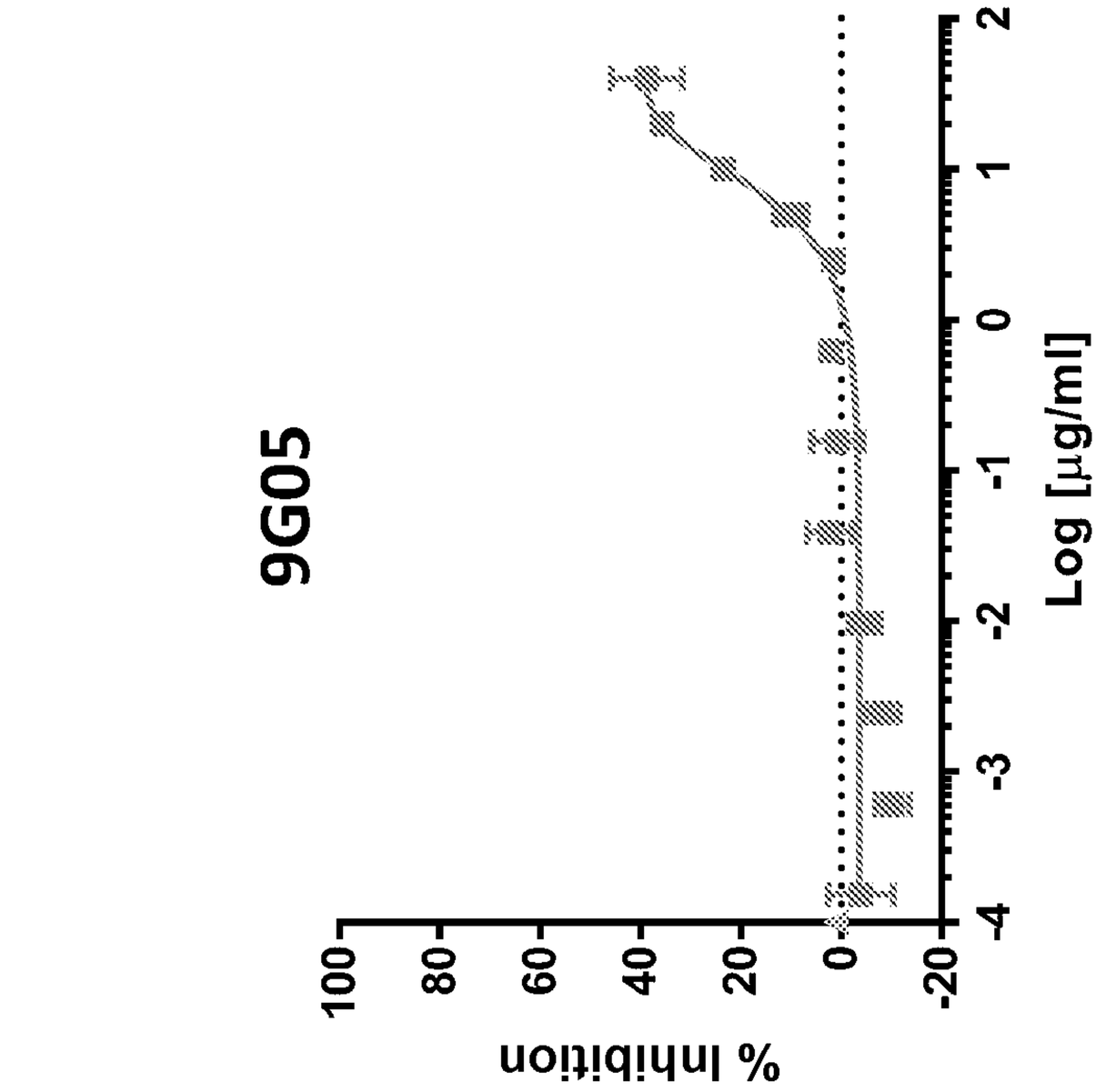

Rabbit mAbs
CHO-K1-hu α11 adhesion to type I collagen
****
5A7
6C7
4E1
3B1
16G7
Rabbit IgG
Poly Rabbit
Inhibition of CHO-K1-hu α11 adhesion to type I collagen
% Inhibition of Adhesion
100
90
80
70
60
50
40
30
20
10
0
-10
16E10
6F9
6G4
5D7
5A7

FIGURE 6B


9G05
% Inhibition
100
80
60
40
20
0
-20
-4
-3
-2
-1
0
1
2
Log [µg/ml]

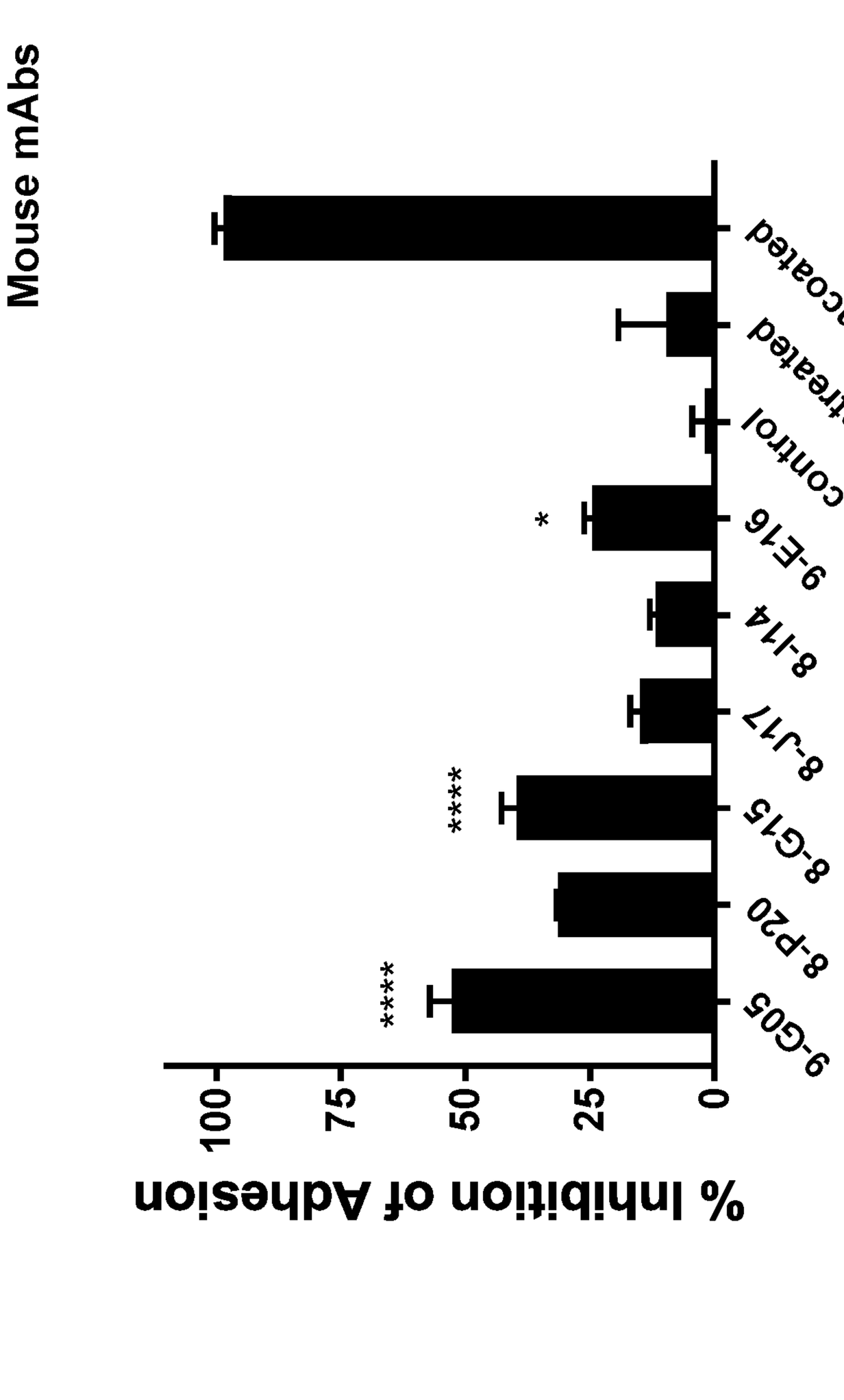

Mouse mAbs
% Inhibition of Adhesion
100
75
50
25
0
9-G05
8-P20
8-G15
8-J17
8-I14
9-E16
Isotype control
Untreated
Uncoated
*****
*****
*

FIGURE 6C

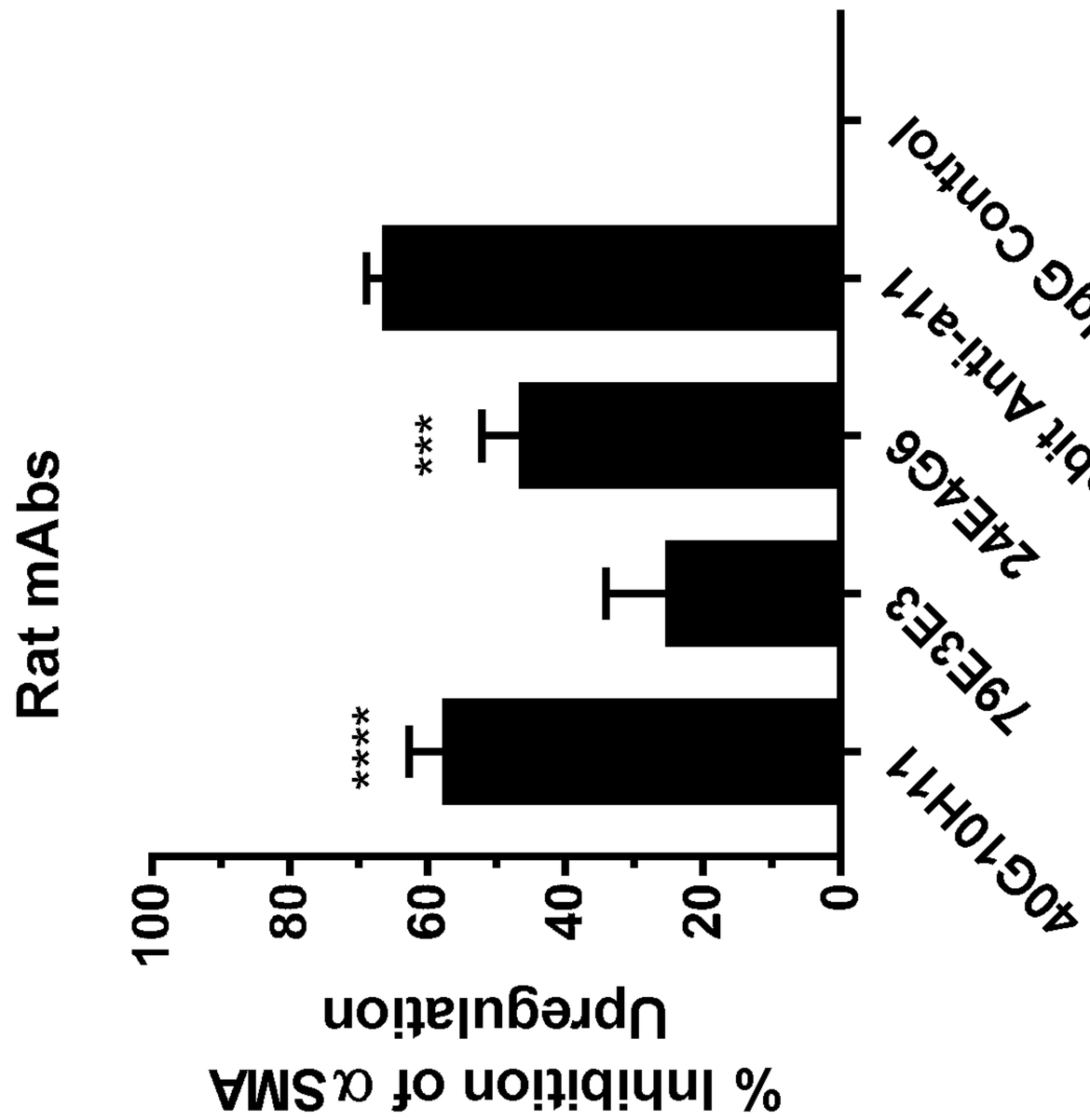

% Inhibition of αSMA Upregulation
Rat mAbs
100
80
60
40
20
0
****
***
4OG10H11
79E3E3
24EAG6
Poly Rabbit Anti-a11
Rabbit IgG Control

FIGURE 7A

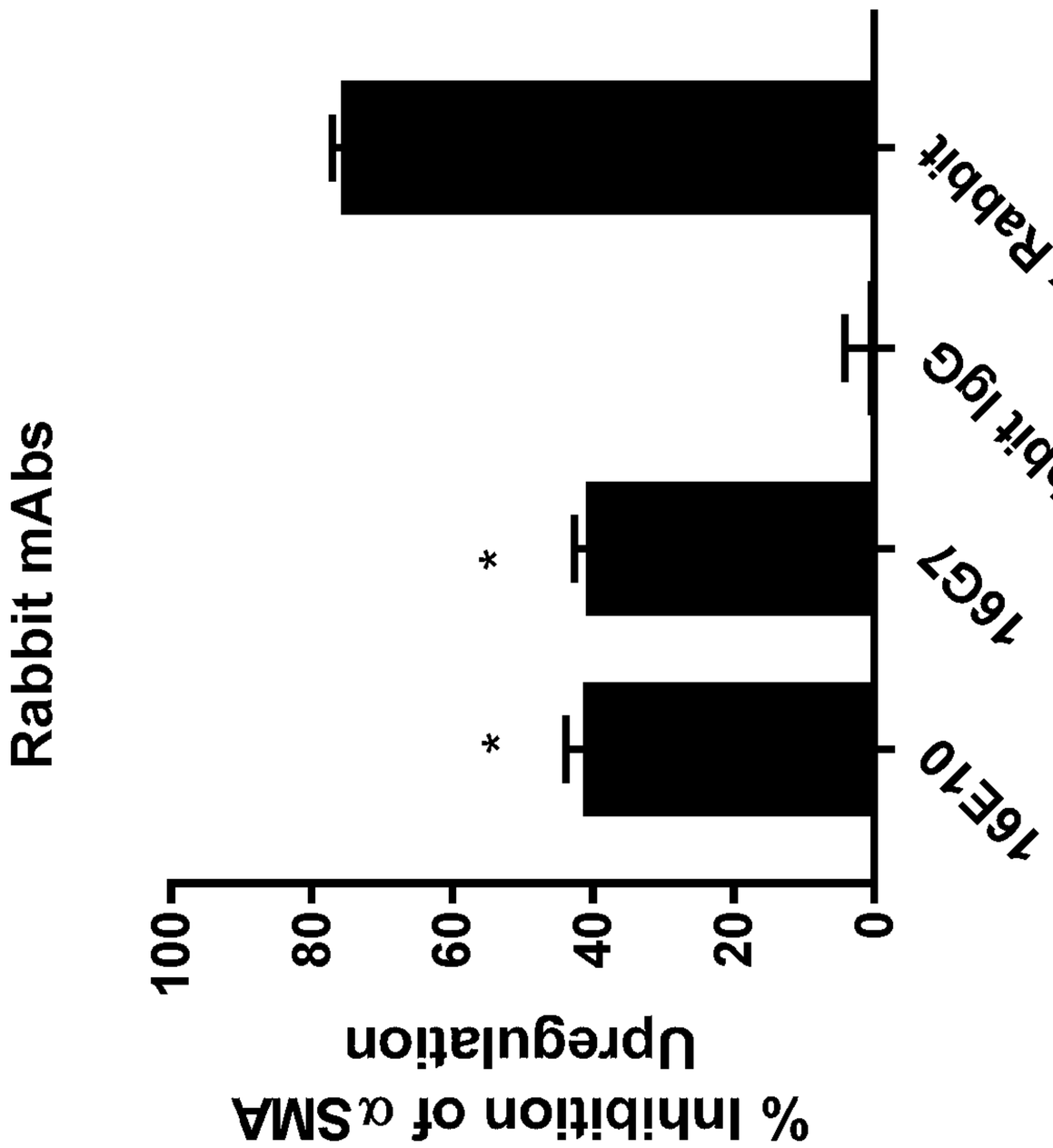

% Inhibition of αSMA Upregulation
100
80
60
40
20
0
16E10
16G7
Rabbit IgG
Poly Rabbit
*
*
Rabbit mAbs

FIGURE 7B

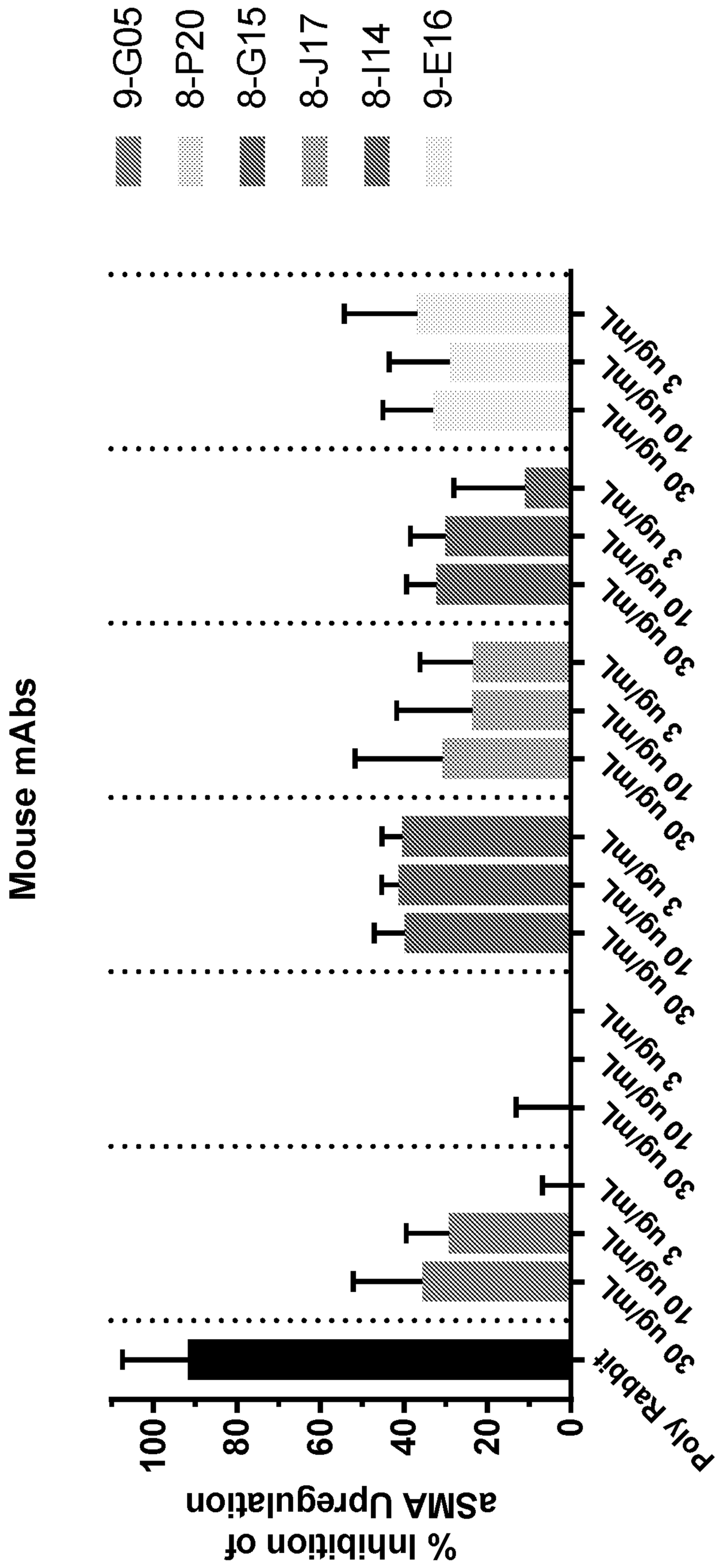

9-G05
8-P20
8-G15
8-J17
8-I14
9-E16
% Inhibition of aSMA Upregulation
Mouse mAbs
Poly Rabbit
30 ug/mL
10 ug/mL
3 ug/mL
0
20
40
60
80
100

FIGURE 7C

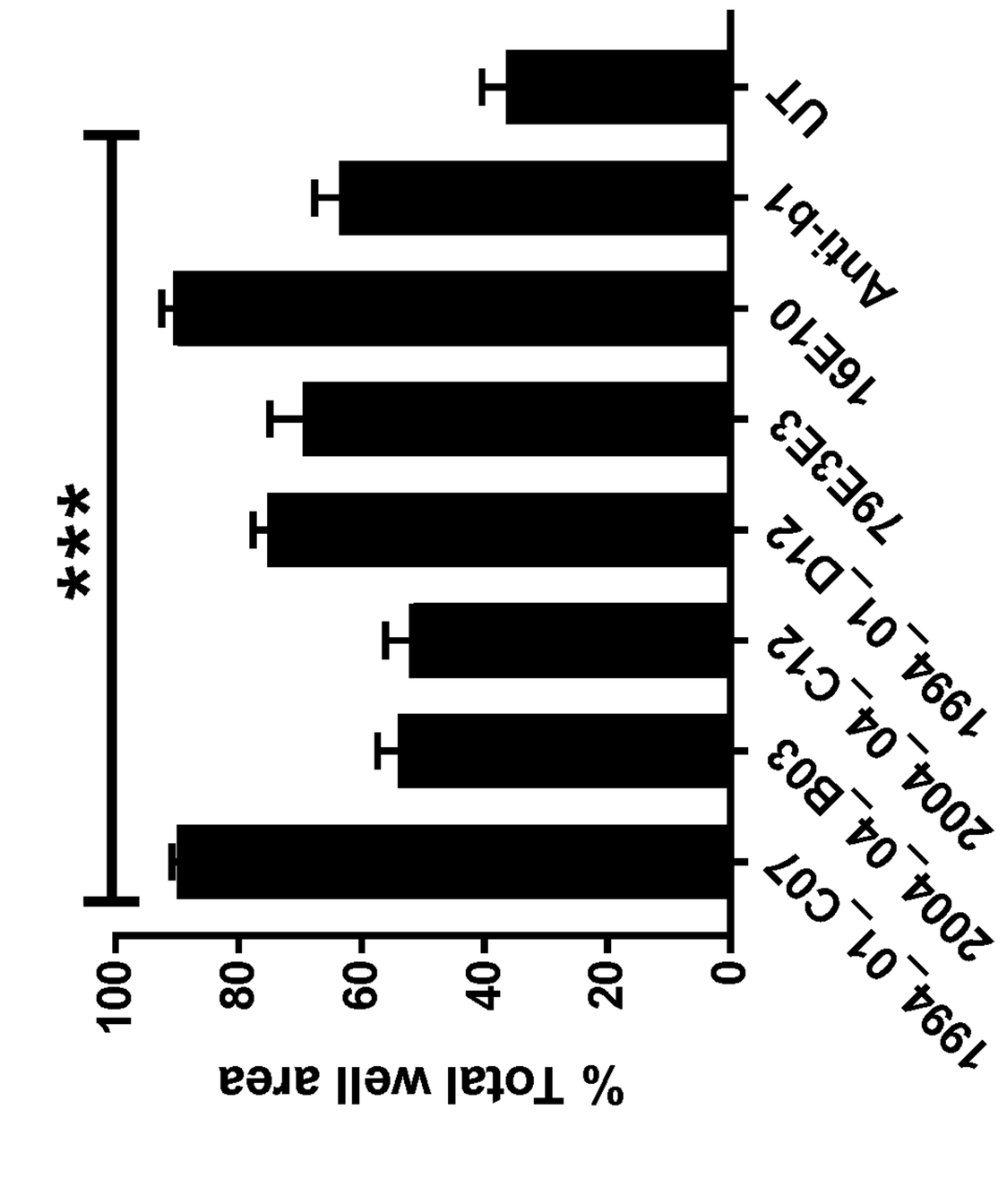
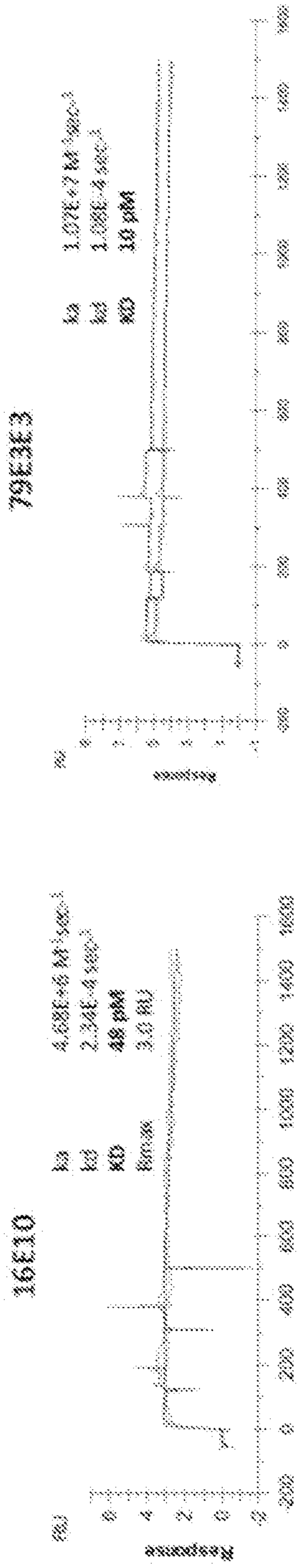
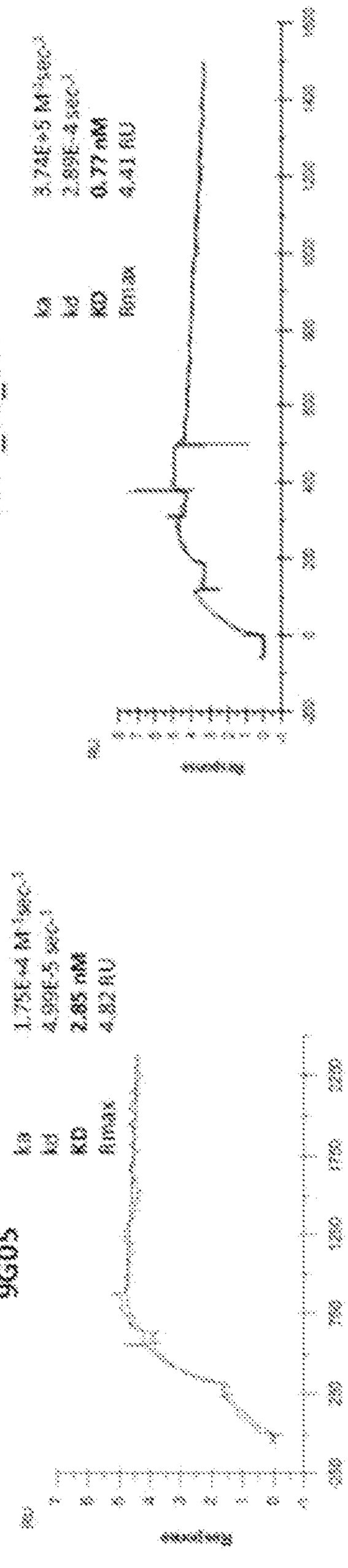

% Total well area
0
20
40
60
80
100
****
1994_01_C07
2004_04_B03
2004_04_C12
1994_01_D12
79E3E3
16E10
9B11
UT
b7
16E10
9B11
24EAG6
81I4
9G05
9E16
79E3E3
UT
% of initial gel area
0
50
100
*****
ns
**
*****

FIGURE 8


79E343
ka 1.57E+7 M-1sec-1
kd 1.00E-4 sec-1
KD 10 pM
Rmax 30 RU
Response
Time


1994_01_C07
ka 3.73E+5 M-1sec-1
kd 2.89E-4 sec-1
KD 0.77 nM
Rmax 6.41 RU
Response
Time

16E10
ka 4.08E+6 M-1sec-1
kd 2.33E-4 sec-1
KD 49 pM
Rmax 3.0 RU
Response
Time

9G05
ka 1.75E+6 M-1sec-1
kd 4.99E-3 sec-1
KD 2.85 nM
Rmax 4.22 RU
Response

FIG 6

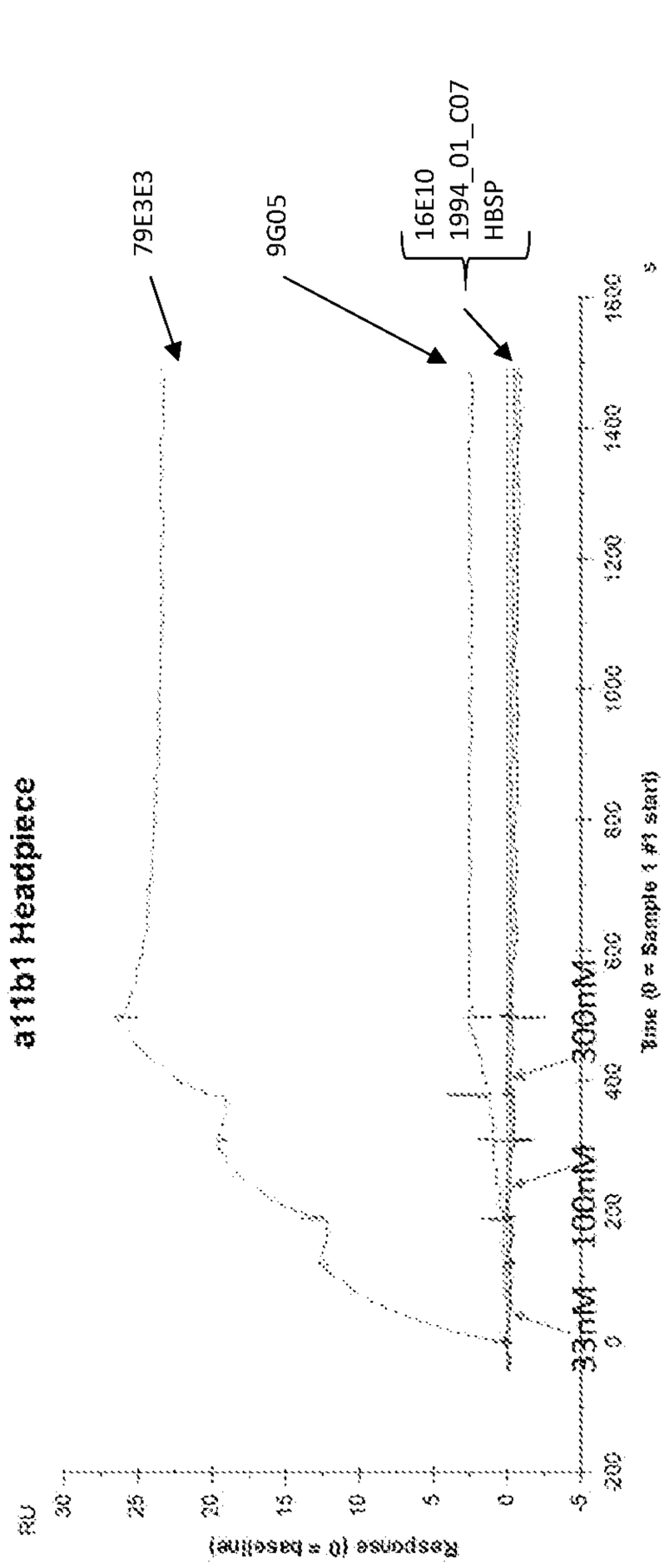

79E3E3
9G05
16E10
1994_01_C07
HBSP
a11b1 Headpiece
33nM
100nM
300nM
Time (0 = Sample 1 #1 start)
Response (0 = baseline)
RU
30
25
20
15
10
5
0
-5
200
400
600
800
1000
1200
1400
1600
s

FIGURE 10A

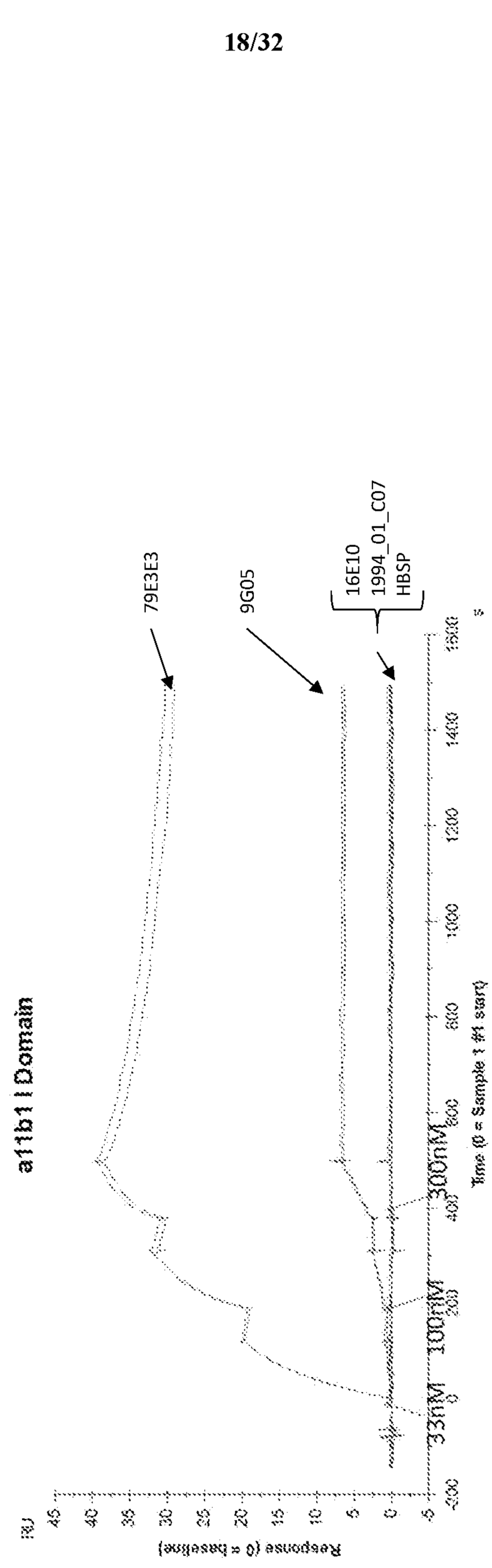

a11b1 I Domain
79E3E3
9G05
16E10
1994_01_C07
HBSP
33nM
100nM
300nM
Time (0 = Sample 1 #1 start)
Response (0 = baseline)

FIGURE 10B

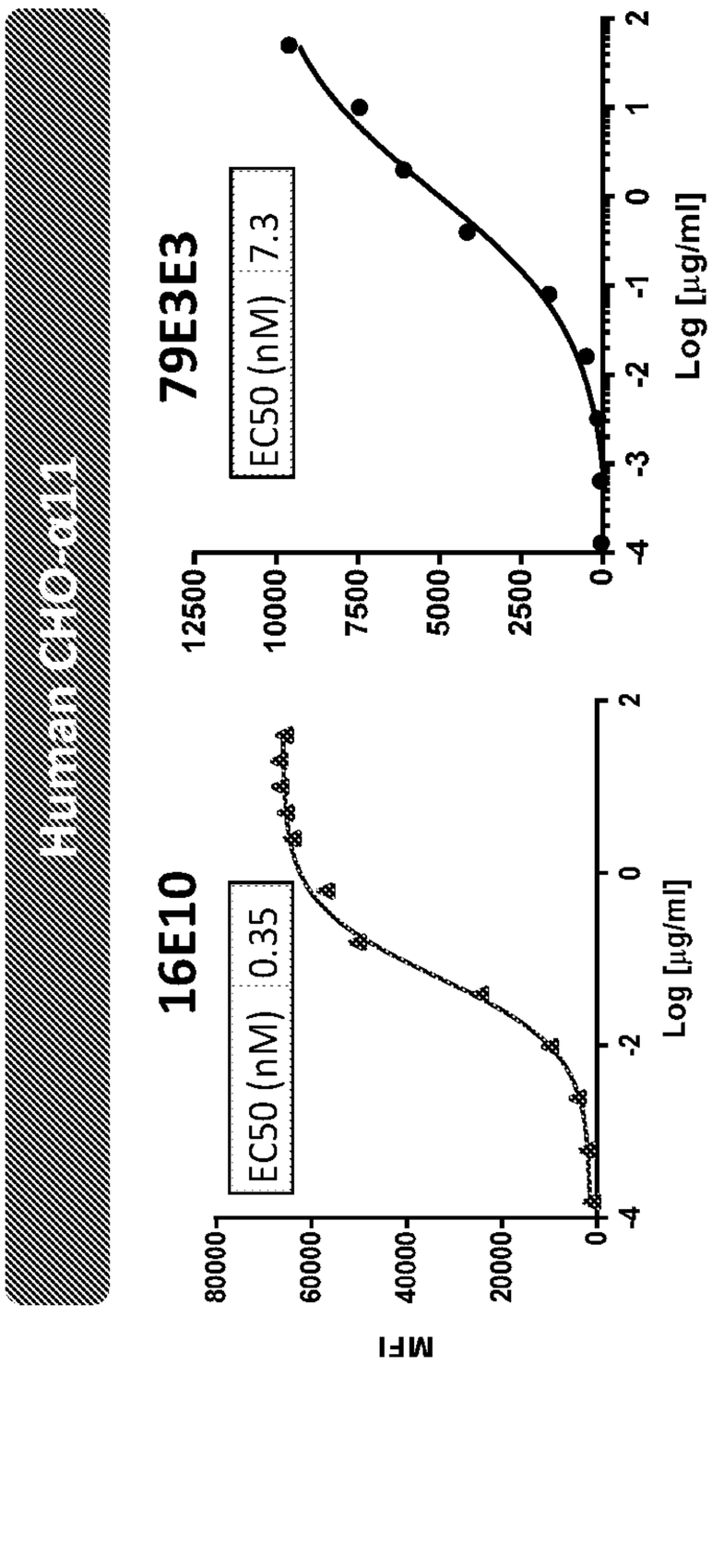

Human CHO-c11
79E3E3
EC50 (nM) 7.3
1994_01_C07
EC50 (nM) 7.75
16E10
EC50 (nM) 0.35
9G05
EC50 (nM) 187
MFI
Log [µg/ml]

FIGURE 11A

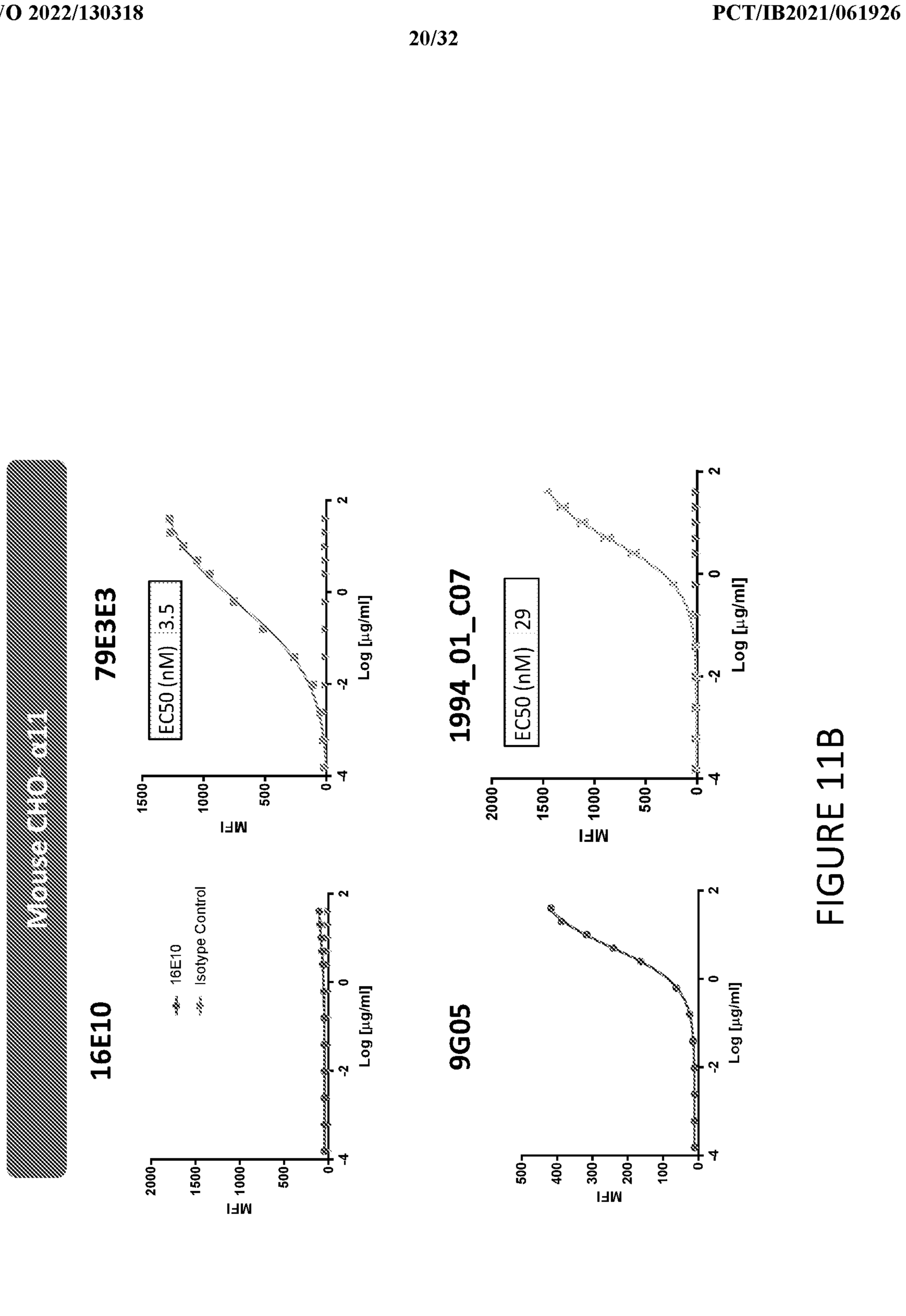

Mouse cHO_e11
16E10
16E10
Isotype Control
MFI
Log [µg/ml]
79E3E3
EC50 (nM) 3.5
1994_01_C07
EC50 (nM) 29
9G05

FIGURE 11B

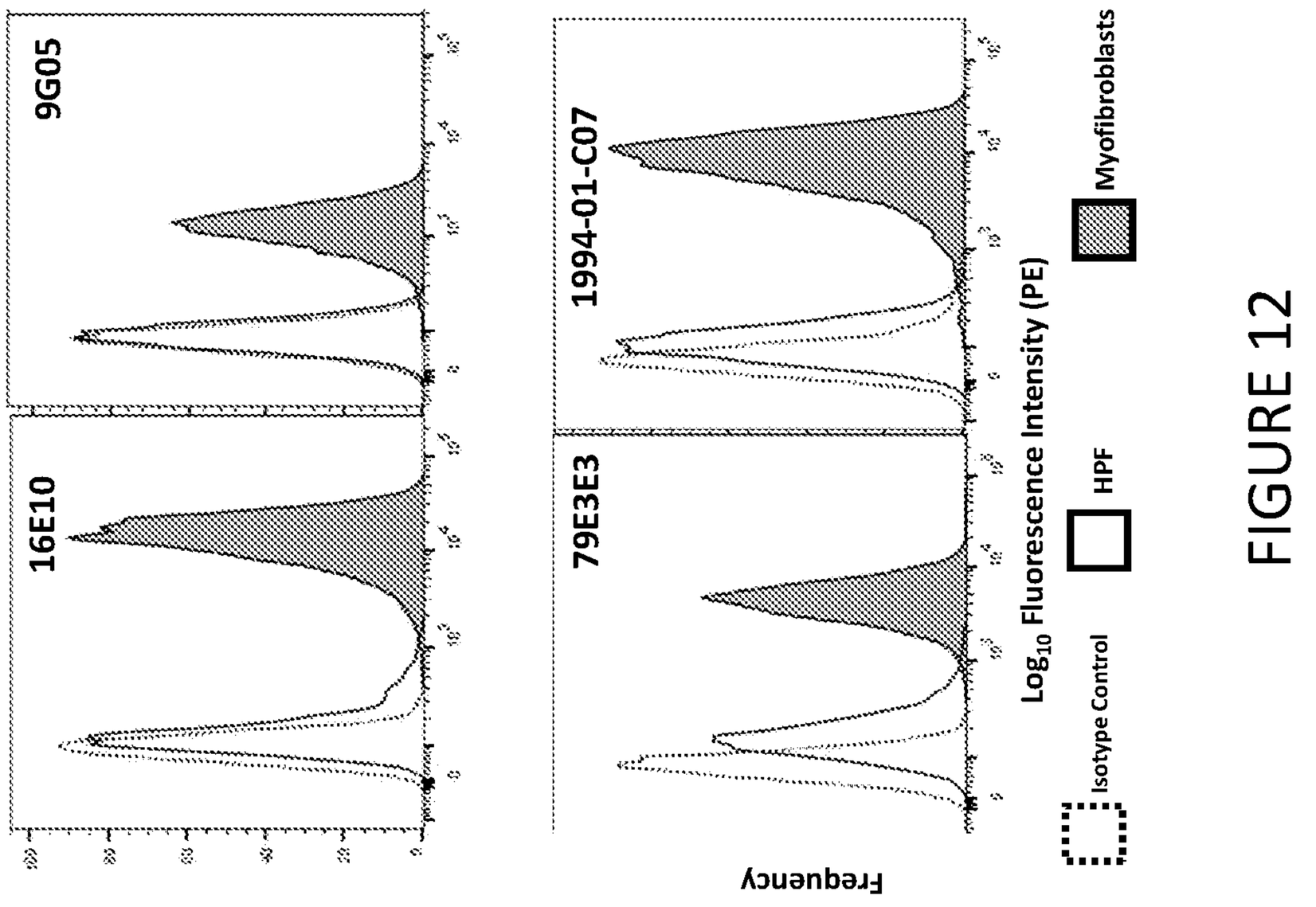
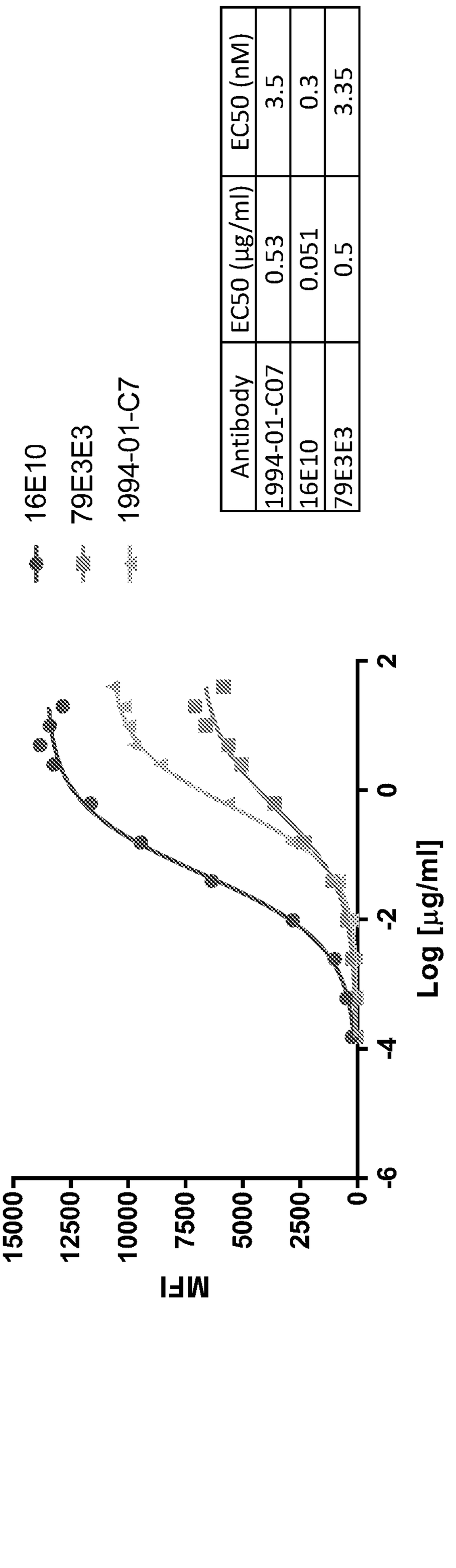

9G05
16E10
1994-01-C07
79E3E3
Frequency
Log_{10} Fluorescence Intensity (PE)
Myofibroblasts
HPF
Isotype Control

FIGURE 12



Antibody	EC50 (µg/ml)	EC50 (nM)
1994-01-C07	0.53	3.5
16E10	0.051	0.3
79E3E3	0.5	3.35

FIGURE 13

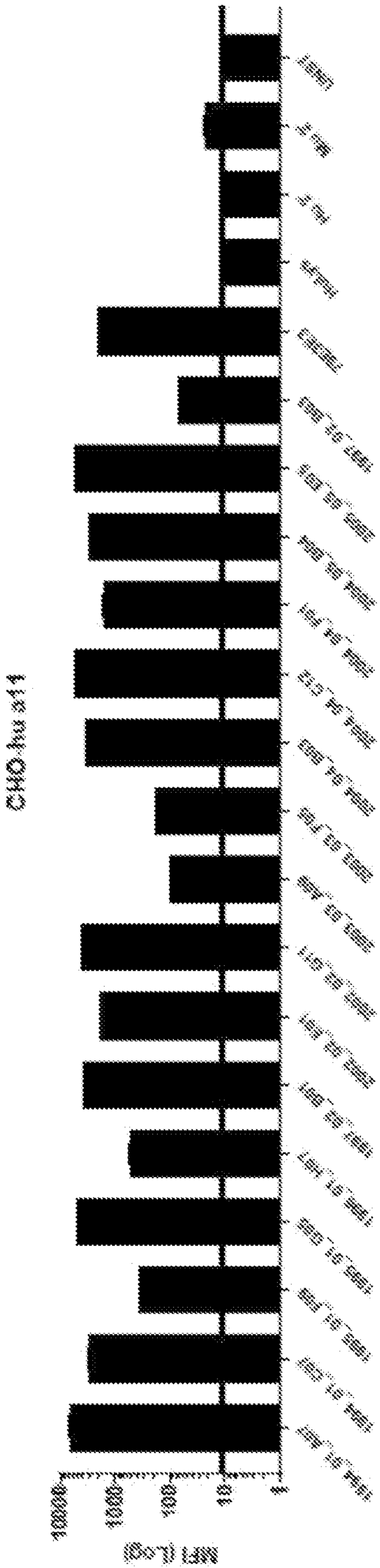

CHO-hu s11
MFI (a.u.)
0
10000
20000
30000
40000
50000
60000
70000
80000
90000
100000
110000
120000
130000
140000
150000
160000
170000
180000
190000
200000
210000
220000
230000
240000
250000
260000
270000
280000
290000
300000
310000
320000
330000
340000
350000
360000
370000
380000
390000
400000
410000
420000
430000
440000
450000
460000
470000
480000
490000
500000

FIGURE 14

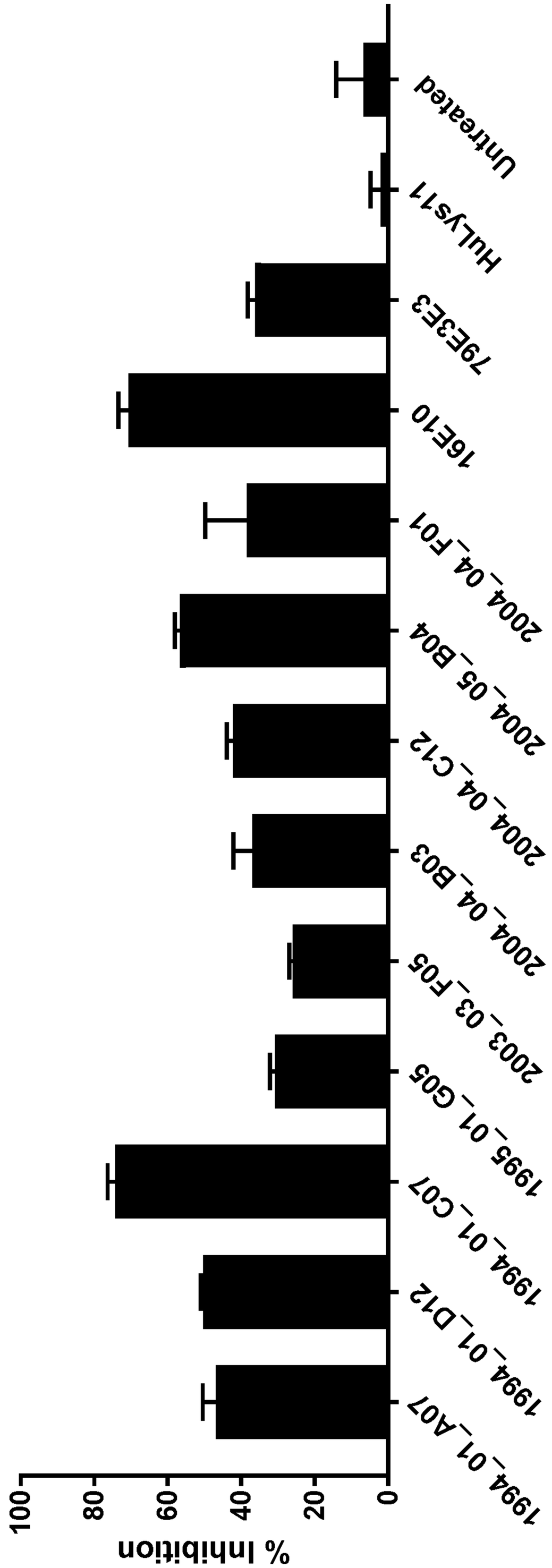

Untreated
HuLys11
79E3E3
16E10
2004_04_F01
2004_05_B04
2004_04_C12
2004_04_B03
2003_03_F05
1995_01_G05
1994_01_C07
1994_01_D12
1994_01_A07
100
80
60
40
20
0
% Inhibition

FIGURE 15A

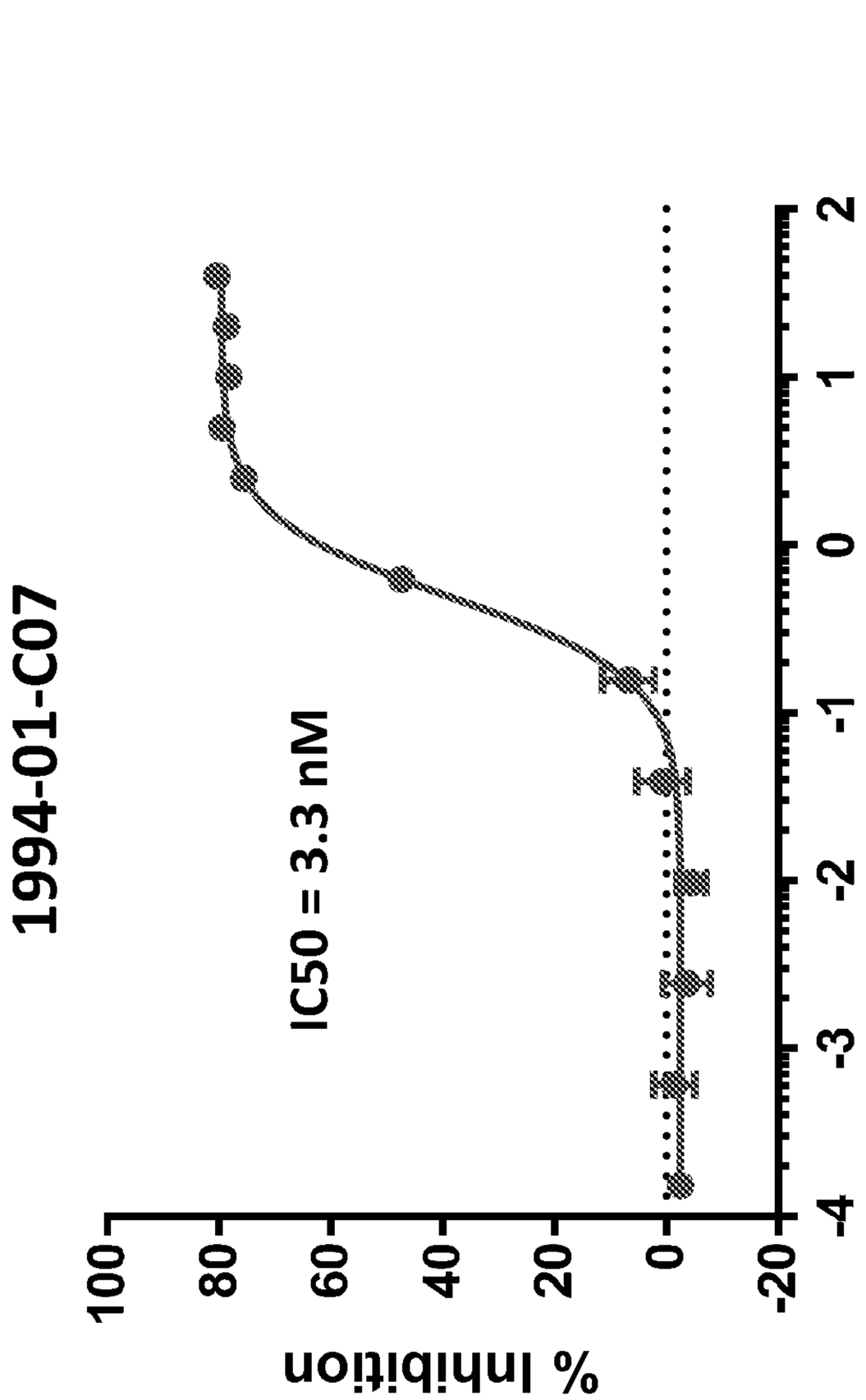

1994-01-C07
IC50 = 3.3 nM
% Inhibition
100
80
60
40
20
0
-20
-4
-3
-2
-1
0
1
2
Log [µg/ml]

FIGURE 15B

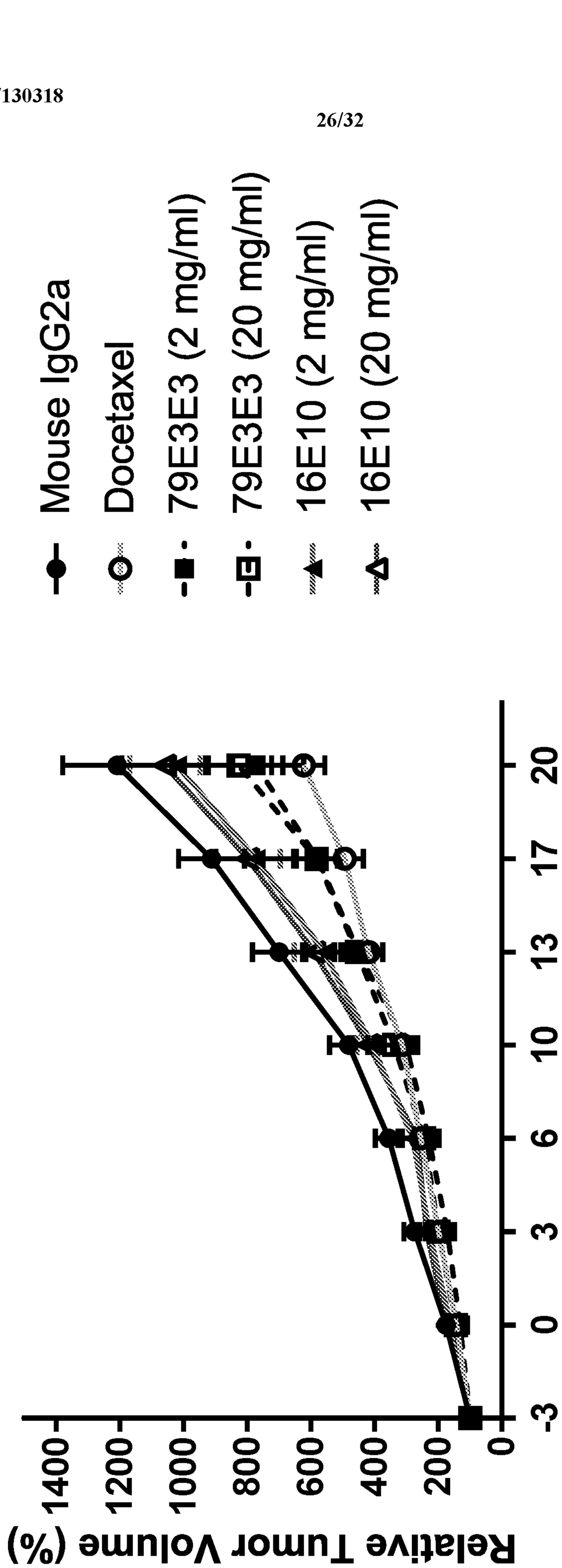

Mouse IgG2a
Docetaxel
79E3 (2 mg/ml)
79E3 (20 mg/ml)
16E10 (2 mg/ml)
16E10 (20 mg/ml)
Relative Tumor Volume (%)
1400
1200
1000
800
600
400
200
0
-3
0
3
6
10
13
17
20
Study treatment day

FIGURE 16

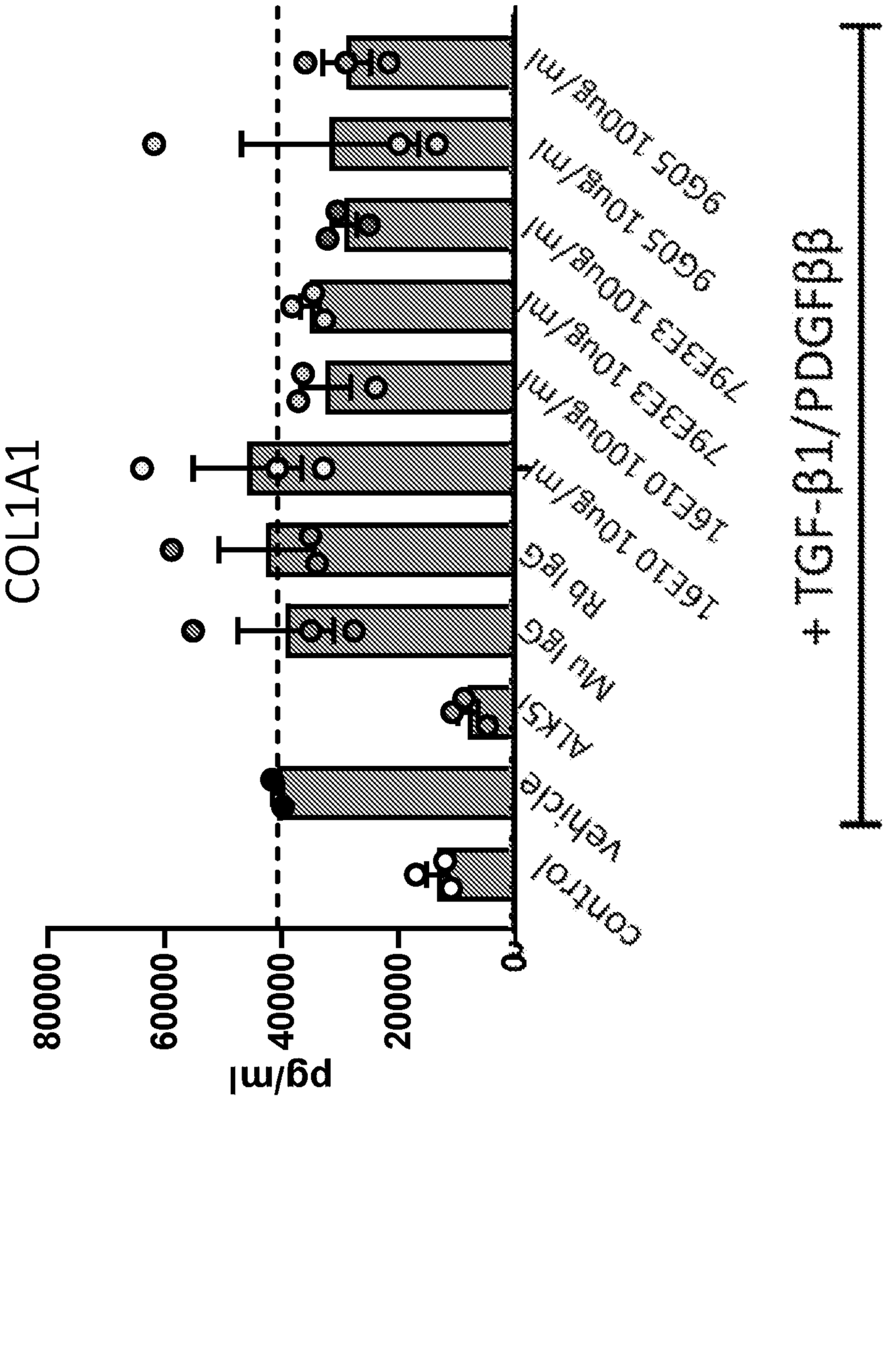

COL1A1
pg/ml
80000
60000
40000
20000
0
Control
Vehicle
ALK5i
Mu IgG
Rb IgG
16E10 10ug/ml
79E3E3 10ug/ml
79E3E3 100ug/ml
9G05 10ug/ml
9G05 100ug/ml
+ TGF-β1/PDGFBB

FIGURE 17A

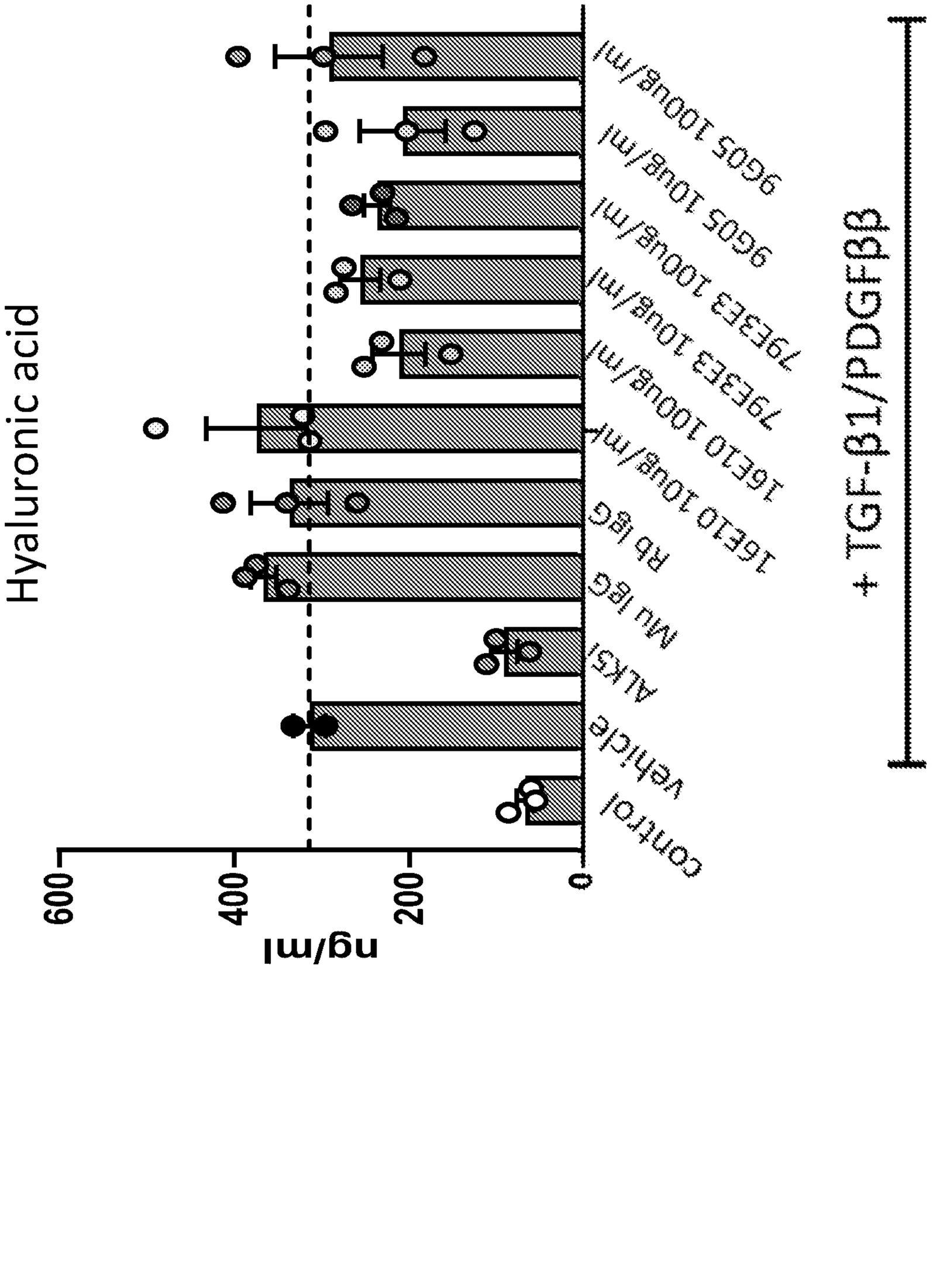

Hyaluronic acid
ng/ml
600
400
200
0
Control
Vehicle
ALK5i
Mu IgG
Rb IgG
16E10 10ug/ml
16E10 100ug/ml
79E3E3 10ug/ml
79E3E3 100ug/ml
9G05 10ug/ml
9G05 100ug/ml
+ TGF-β1/PDGFββ

FIGURE 17B

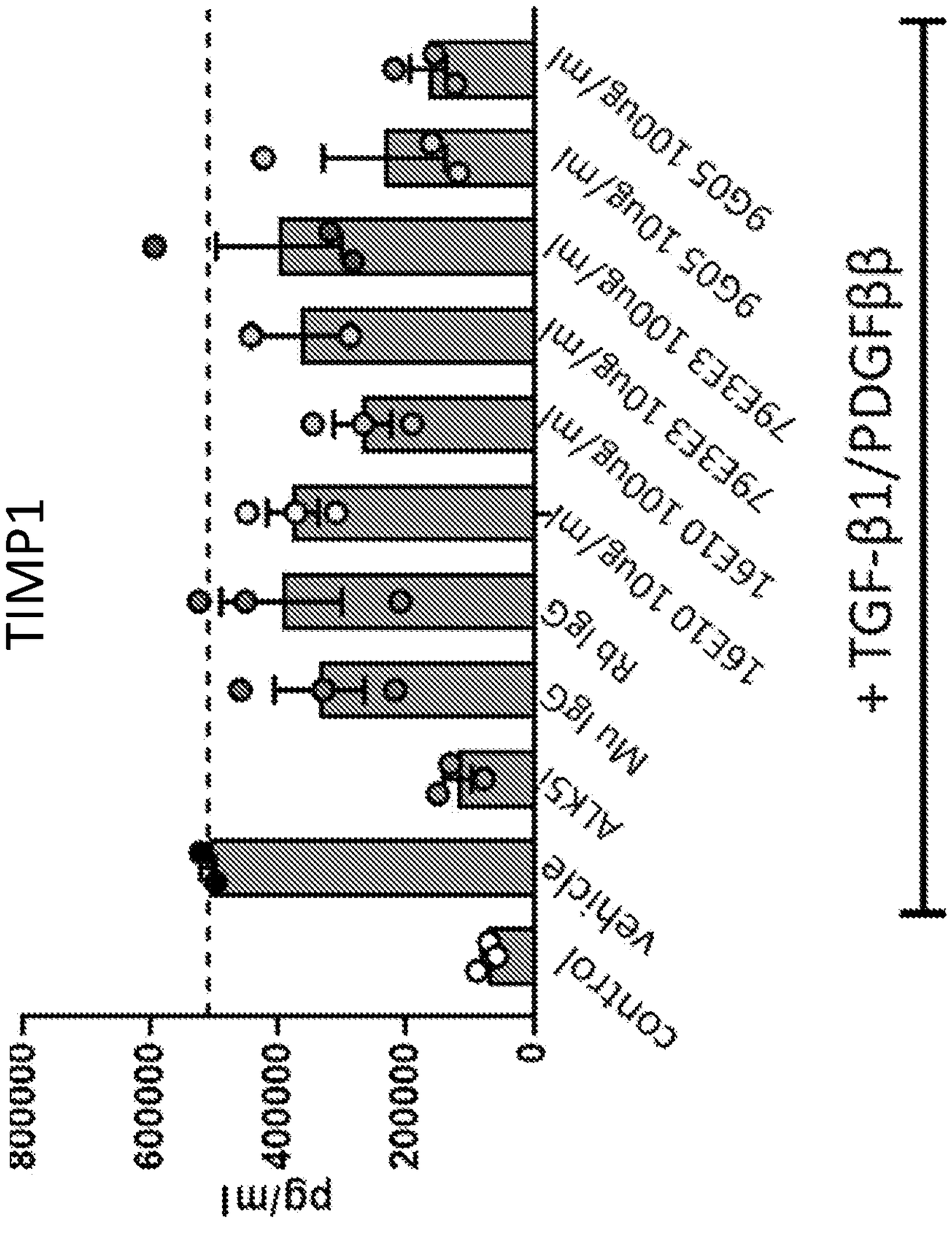

TIMP1
pg/ml
800000
600000
400000
200000
0
Control
Vehicle
ALK5i
Mu IgG
Rb IgG
16E10 10ug/ml
796E3 10ug/ml
796E3 10ug/ml
9G05 10ug/ml
9G05 10ug/ml
9G05 100ug/ml
+ TGF-β1/PDGFBB

FIGURE 17C

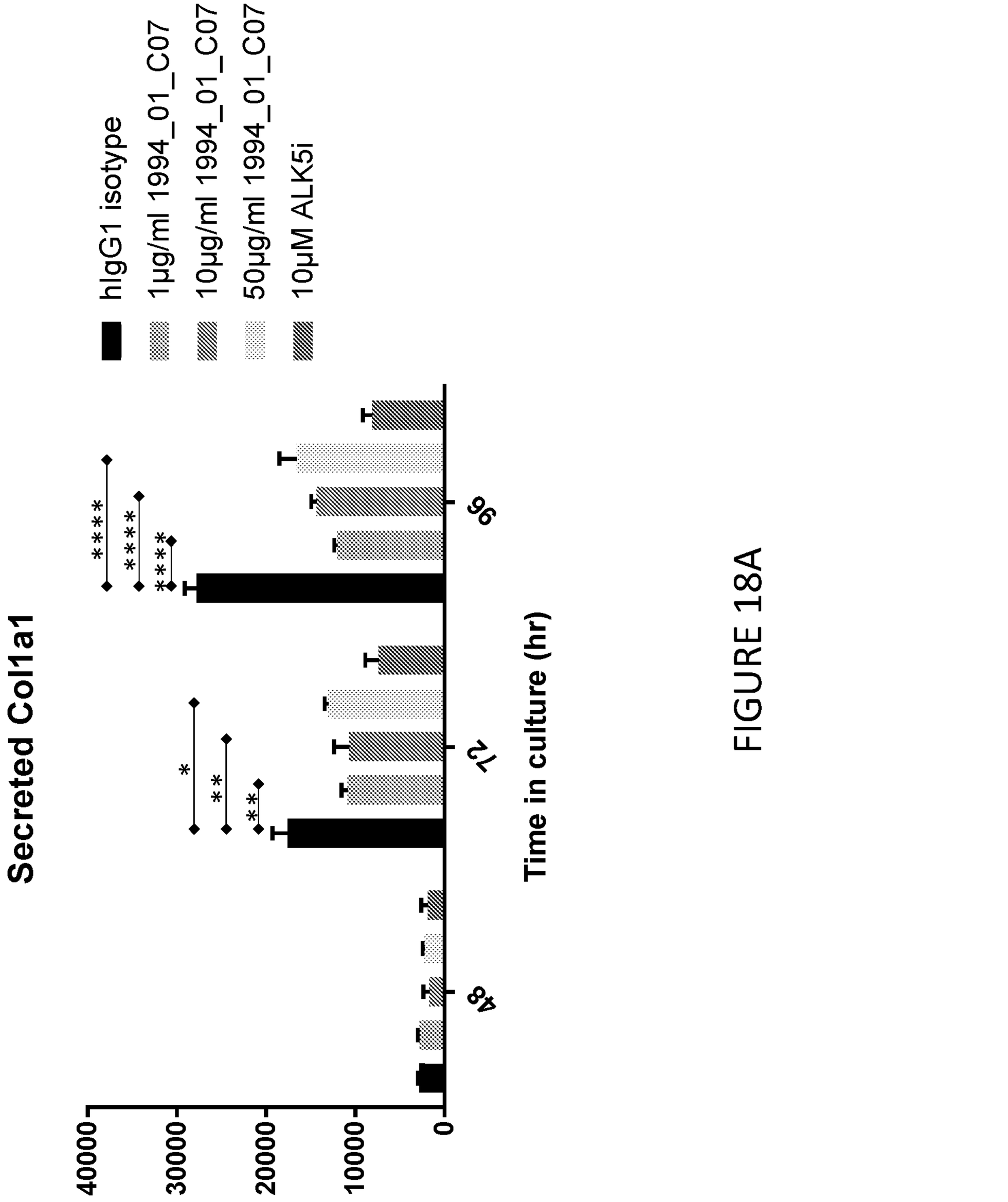

hIgG1 isotype
1µg/ml 1994_01_C07
10µg/ml 1994_01_C07
50µg/ml 1994_01_C07
10µM ALK5i
Secreted Col1a1
pg/ml
40000
30000
20000
10000
0
Time in culture (hr)
48
72
96
*
**
**
****
****
****

FIGURE 18A

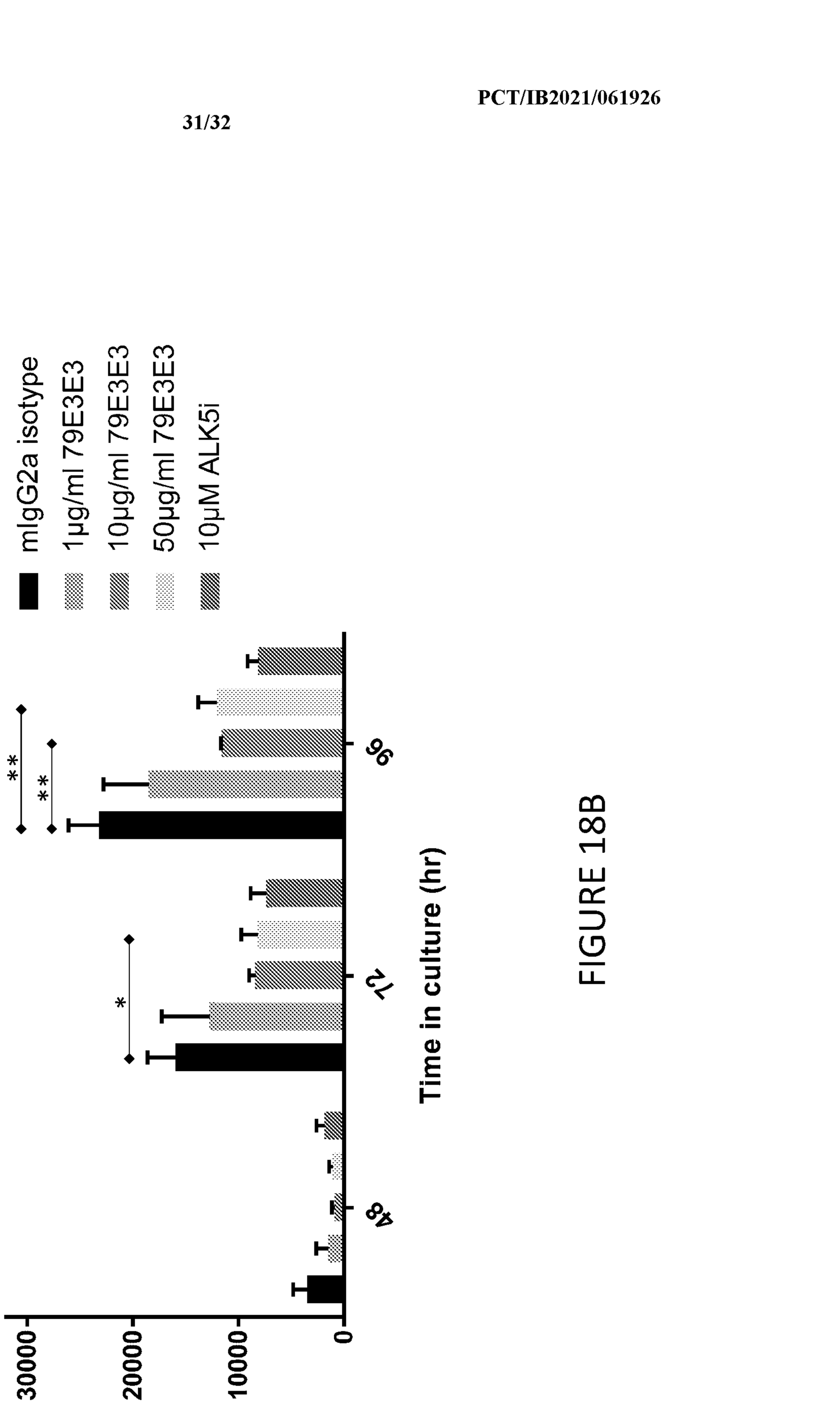

mIgG2a isotype
1µg/ml 79E3E3
10µg/ml 79E3E3
50µg/ml 79E3E3
10µM ALK5i
Secreted Col1a1
Time in culture (hr)
96
72
48
**
**
*
30000
20000
10000
0
pg/ml

FIGURE 18B

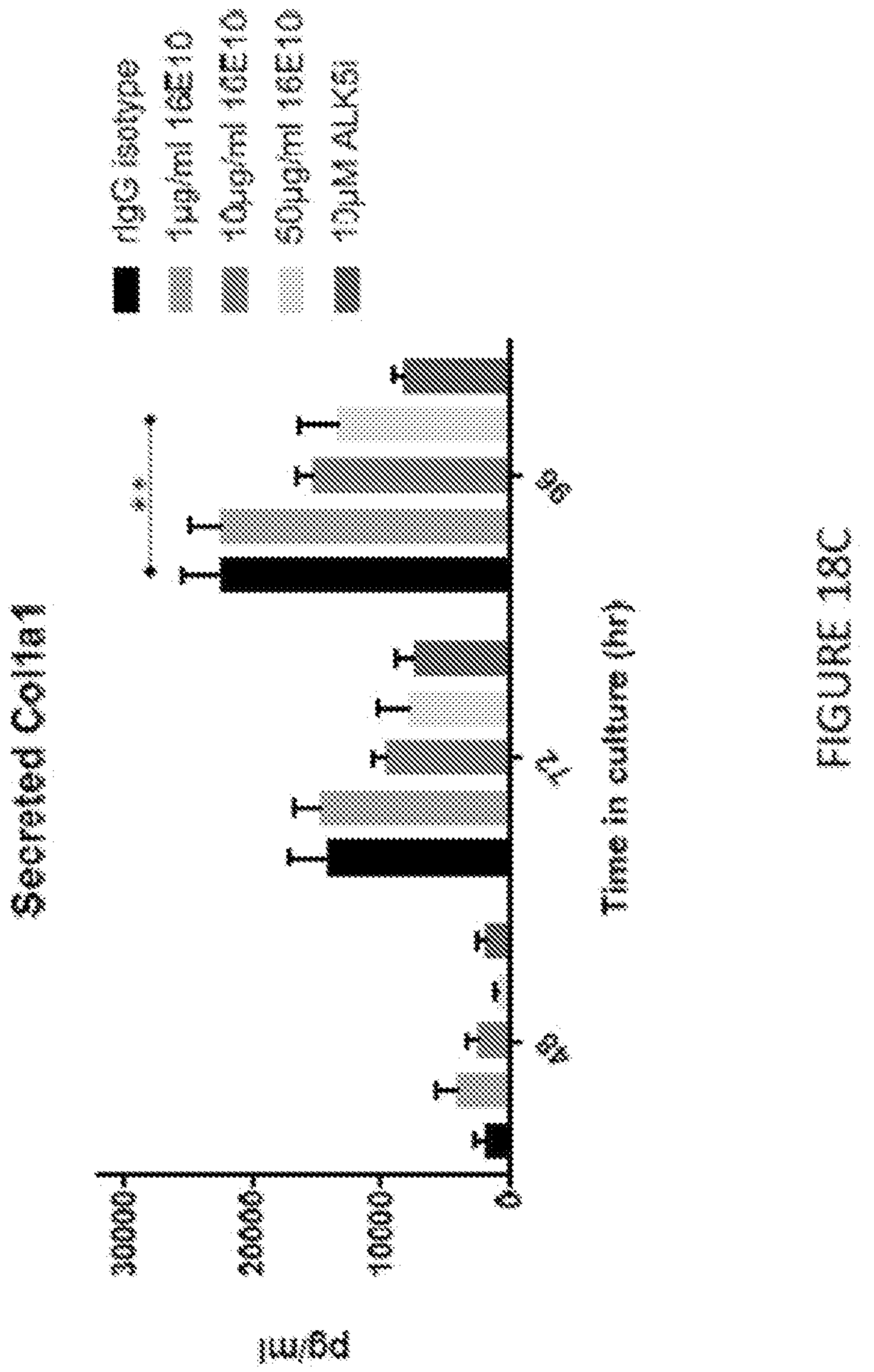

rIgG isotype
1µg/ml 16E1
10µg/ml 16E1
50µg/ml 16E1
10µM ALK5i
**
48
72
96
Time in culture (hr)
Secreted Col1a1
pg/ml
30000
20000
10000
0

FIGURE 18C

SEQUENCE LISTING

<110> JANSSEN BIOTECH, INC.

<120> ANTIBODIES AGAINST INTEGRIN ALPHA 11 BETA 1

<130> MPI6002WOPCT1

<140>
<141>

<150> 63/213,973
<151> 2021-06-23

<150> 63/127,849
<151> 2020-12-18

<160> 443

<170> PatentIn version 3.5

<210> 1
<211> 417
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 1
atggattggt tgtggaactt gctattcctg atggtagttg cccaaagtgc tcaagcacag 60

atccagttgg tacagtctgg acctgaagta aagaagcctg gagagtcagt gaagatctcc 120

tgcaaggcct ctgggtatac cttcacagac tatgcaatga actgggtgaa acaggctcca 180

ggaaatggcc tgaagtggat gggctggatc aacacccaaa ctggaaagcc aacatatgcg 240

gatgatttca aacaacggtt tgtcttctct ttggaaactt ctgccagaac tacatatttg 300

cagatcaaca acctcaatat tgaagacaca gctacatatt tctgtacgag attgggtaca 360

ggtaatacga aggggtttgc ttactggggc caaggcactc tggtcactgt ctcttca 417

<210> 2
<211> 399
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 2
atggaatcac agacgcatgt cctcatttcc cttctgctct gtgtatcagg tacctgtggg 60

gacattttga taaaccagtc tccagcctct ctgactgtgt cagcaggaga gagggtcact 120

atgagctgca agtccagtca gagtcttcta tacagtgaaa acaaccagga ctatttggct 180

tggtaccagc agaaaccagg acagtttcct aaattgctta tctatggggc atccaaccgg 240

cacactgggg tccctgatcg cttcacaggc agtggatctg ggacagactt cactctgacc 300

atcagcagtg tgcaggctga agacctggct gattattatt gtgagcagac ctacagatat 360

ccattcacgt tcggctcagg gacgaagttg gaaataaaa 399

<210> 3
<211> 414
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 3
atggagttgg aattgagctt aatttttatt ttttctcttt taaaagatgt ccagtgtgaa 60

gtacagctgg tggagtctgg aggaagcttg gttcaacctg ggggttctct gaaactctcc 120

tgtgtagcct caggatacac tttcagtaac tactggatgg actgggttcg gcagtctcct 180

ggaaagtccc tggaatggat tggagagatt aacacggatg gcagaaggac caactatgca 240

ccatccataa aggatcgatt cacaatctcc agagacaatg ccaagagcac cctgtatctg 300

cagatgagca atgtgaaatc agatgacaca gccatttatt actgtaccat actacgggta 360

taccccact actttgatta ctggggccaa ggagtcatgg tcacagtctc ctca 414

<210> 4

<211> 396
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 4
atgatgagtc ctgcccagtt cctgtttctg ctaatgctct ggatccagga agcccgcgga 60

gatgttgtga tgacccagac accaccgtct ttgtcggttg ccattggaca atcagtctcc 120

atctcttgca agtcaagtca gagcctcgta tatagtgatg gagagacata tttgcattgg 180

tttttacaga gtcctggcag gtctccgaag cgcctaattt atcacgtgtc taatctgggc 240

tctggagtcc ctgacaggtt cagtggcact ggatcactga cagattttac acttagaatc 300

agcagagtgg aggctgagga tttgggagtt tattactgcg cgcaaactac acattttcct 360

cccacgtttg gagctgggac caagctggaa ctgaaa 396

<210> 5
<211> 405
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 5
atggctgtcc tggtgctgtt gctctgcctg gtgacatttc caagctgtgc cctgtcccag 60

gtgcagttga aggagtcagg acctggtctg gtgcagccct cacagaccct gtccctcacc 120

tgcactgtct ctgggttctc attaaccagc aatagtgtta gctgggttcg ccaggctccg 180

ggaaagggtc tggagtggat gggagcaata tggagtggtg gaagcacaga ttataattca 240

gctctcaaat cccgactgag catcagcagg gacacctcca agagccaagt tttcttaaaa 300

atgaacagtc tgcaaactga agacacagcc atttacttct gtaccagatc tcactgggag 360

ccctttgatt actggggcca aggagtcatg gtcacagtct cctca 405

<210> 6
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 6
atggaatcac aaactcaggc cctcatatcc ctgctgctct gggtatatgg tacctgtggg 60

gacattgtga tgacccagtc tccattctcc ctggctgtgt cagaaggaga gatggtcact 120

ataaactgca agtccagtca gggtctttta tccagtggaa accaaaagaa ctacttggcc 180

tggtaccagc agagaccagg gcagtctcct aaactactga tctactatgc atccactagg 240

caatcagggg tccctgatcg cttcataggc ggtggatctg ggacagactt cactctgacc 300

atcagcgatg tgcaggctga agacctggca gattattact gcctgcagca ttacagctat 360

cctcccacgt tcggttctgg gaccaagctg gagatcaaa 399

<210> 7
<211> 405
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 7
atggctgtcc tggtgctgtt gctctgcctg gtgacatttc caagctgtgc cctgtcccag 60

gtgcagctga gggagtcagg acctggtctg gtgcagccct cacagaccct gtccctcacc 120

tgcactgtct ctgggttctc attgaccagc aatagtgtga cctgggttcg ccagcctccg 180

ggaaagggtc tggagtggat gggagcgata tggagtgatg gaagcacaga ttataattca 240

actctcaaat cccgactgag catcagtagg gacacctcca agagccaagt tttcttaaaa 300

atgagcagtc tgcaaactga agacacagcc atttacttct gtaccagatc ccactgggag 360

ccctttgatt actggggcca aggagtcatg gtcacagtct cctca 405

<210> 8
<211> 394
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 8
atggaatcac aaactcaggc cctcatatcc ctgctgctct gggtatatgg tacctgtggg 60

gacattgtga tgacccagtc tccactctcc ctggctgtgt cagaaggaga gacggtcact 120

atgaactgca agtccagtca gagtcttttt tccagtggaa atcaaaagaa ctacttggcc 180

tggtaccagc agaaaccagg gcagtctcct aaactactga tctactatgc atccactagg 240

caatcagggg tccctgatcg cttcataggc agtggatctg ggacagactt cactctgacc 300

atcagcgatg tgcagactga agacctggca gattattact gcctgcagca ttacaactat 360

cctcccacgt tcggttctgg gaccaagctg gaga 394

<210> 9
<211> 402
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 9
atggacttgc gactgactta tgtctttatt gttgctattt taaaaggtgt cttgtgtgag 60

gtgaaactgg aggaatctgg gggaggtttg gtgcaacctg gaatgtccgt gaaactctct 120

tgtgcaacct ctggattcat tttcagtgac tactggatgg aatgggtccg ccaggctcca 180

gggaaggggc tagaatgggt agccgaaatt agaaacaaag ctaataatta tgcaacatac 240

tatgggaagt ctatgaaagg cagattcacc atctcaagag atgattccaa aagtatagtc 300

tacctacaag tgaacagcat aagatctgaa gatactgcta tttattactg tgcaccgaat 360

tttgattact ggggccaagg agtcatggtc acggtctcct ca 402

<210> 10
<211> 393
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 10
atgagtcctg tccagtccct gtttttgcta ttgctttgga ttctgggaac ccatggtgat 60

gttgtgctga cccagactcc acccacttta tcggctacca ttggacaatc agtctctatc 120

tcttgcaggt caagtcagag tctcttacat agtactggaa acacctattt aaattggttg 180

ctacagaggc caggccaacc tccgcaactt ctaatttatt tggtttccag actggaatct 240

ggggtcccca acaggttcag tgccagtggg tcaggaactg atttcacact caaaatcagt 300

ggaatagagg ctgaggattt gggggtttat tactgcgtgc aaagttccca tactccgtac 360

acgtttggga ctgggaccaa gctggaactg aaa 393

<210> 11
<211> 405
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 11
atggacatca ggctcagctt ggttttcctt gtccttttta tgaaaggtgt ccagtgtgag 60

gtgcagttgg tggagtctgg gggaggctta gtgcagcctg gaaggtccct gaaactctcc 120

tgtgcagcct cacgattcac ttttagtgac tataacatgg cctgggtccg ccaggctcca 180

aagaagggtc tggagtgggt cgcaaccatt tatcatgatg atagtggttc ttactatcga 240

gactccgtga agggccgatt caccatctcc agaaataatg caaaaagcac tctgtacctg 300

cagatggaca gtctgaggtc tgaggacatg gccacttatt actgtgcaag acataacaat 360

ggctttgatt actggggcca aggagtcatg gtcacagtcg cctca 405

<210> 12
<211> 393
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 12
atgaagtggc ctgttaggct gttggtgctg ttcttctgga ttcctgcttc cgggggtgat 60

gttgtgatga cacaaactcc agtctccctg cctgtccgcc ttggaggtca agcctctatc 120

tcttgccggt caagtcagag cctggtacac agtaatggaa acacctactt gcattggtac 180

ctacagaagc caggccagtc tccacagctc ctcatcaatc gggtttccaa cagattttct 240

ggggtgccag acaggttcag tggcagtggg tcagggacag atttcaccct caagatcaac 300

agagtagagc ctgaggactt gggagattat tactgcttac aaagtacaca ttttccactc 360

acgttcggtt ctgggaccaa gctggagacc aaa 393

<210> 13
<211> 408
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 13
atggacatca ggctcagctt gggtttcctt gtccttttca taaaaggtga ccagtgtgcg 60

gtgcaactgg tggagtctgg gggaggctta gtgcagcctg gaaggtccct gaaactctcc 120

tgtgcagcct caagaatcac tttcactgac tattacatgg cctgggtccg ccaggctcca 180

acgaagggtc tggagtgggt cgcaaccatt agttctgatg gtggtgacac tttctatcga 240

gactccgtga agggccgatt tactatctcc agagacaatg caaaaagcac cctatatttg 300

caaatggtca gtctgaggtc tgaggacacg gccacttatt actgttcaac agatcgggga 360

gctcagtttg gttactgggg ccaaggcact ctggtcactg tctcttca 408

<210> 14
<211> 378
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 14
atggctccag tccagctctt agggctgctg ctgatttggc tcccagccat gagatgtgac 60

atccagatga cccagtctcc ttcattcctg tctgcatctg tgggagacag agtctctatc 120

aactgcaaag caagtcagaa tgttcacgag aacctaaact ggtatcagca aaagcttgga 180

gaagctccca aacgcctgat atataataca aacaatttgc aaacaggcat cccatcaagg 240

ttcagtggca gtggatctgg tgcagattac acactcacca tcagcagcct gcagcctgaa 300

gattttgcca catatttctg tttgcagcat aatgcttttc cgtacacgtt tggacctggg 360

acgaagctgg aactgaaa 378

<210> 15
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 15
gaggtccagc tgcaacagtc tggacctgag ctggtgaagc ctggggcttc agtgaagata 60

ccctgcaagg cttctggata cacattccct gactacaaca tggactgggt gaagcagagc 120

catggaaaga gccttgagtg gattggatat attaatcctg acaatggtgg tactatctac 180

aaccagaagt tcaagggcaa ggccacattg actgtagaca agtcctccag cacagcctac 240

atggagctcc gcagcctgac atctgaggac actgcagtct attactgtgc aagattagac 300

agctcaggct acggttacta tgctatggac tactggggtc aaggaacctc agtcaccgtc 360

tcctca 366

<210> 16
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 16
gacattgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc 60

atctcctgca gagccagcga aagtgttgat aattatggca ttagttttat gcactggtac 120

cagcagaaac caggacagcc acccaaactc ctcatctatc gtgcatccaa cctagactct 180

gagatccctg ccaggttcag tggcagtggg tctaggacag acttcaccct caccattgat 240

cctgtggaga ctgatgatgt tgcaacctat tactgtcagc aaagttataa ggatcctcgg 300

acgttcggtg gaggcaccaa gctggaaatc aaa 333

<210> 17
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 17
aaagtgatgc tggtggagtc tgggggagcc ttagtgaagc ctggagggtc cctgaaactc 60

tcctgtgtag cctctggatt cactttcagt aactatgcca tgtcttgggt tcgccagact 120

ccagagaaga ggctggagtg ggtcgcaacc attagtagtg gtggttatta cacttactat 180

ccagacagtg tgaagggtcg attcaccatc tccagagaca atgccaggaa caccctgttc 240

ctgcaaatga gcagtctgag gtctgaggac acggccatgt tttactgtgc aagagaggat 300

gattacggaa gatattccta tactatggac tactggggtc aaggaacctc agtcaccgtc 360

tcctca 366

<210> 18
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 18
gatgttgtga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagtctcc 60

atctcttgca gatgtagtca gagccttgta cacagtaatg gaaacaccta tttacattgg 120

tacctgcaga agccaggcca gtctccacag ctcctgatct acaaaatttc caaccgattt 180

tctggggtcc cagacaggtt cagtggcagt ggatcaggga cagatttcac actcaagatc 240

agcagagtgg aggctgagga tctgggagtt tatttctgct ctcaaagtac acatgttccg 300

tacacgttcg gaggggggac cgagctggaa ataaaa 336

<210> 19
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 19
gaggtccagc tgcagcagtc tggacctgag ctggtaaagc ctggggcttc agtgaggata 60

tcctgcaagg cttctggata cacattcact gactactaca tacactgggt gaagcagaag 120

cctgggcagg gccttgaatg cattggagag atttatcctg gaactgataa tacttactac 180

agtaaaaaat tcaggggcaa ggccacactg actgcagaca aatcctccga cacagcctac 240

atgcagctca gcagcctgac atctgaggac tctgcagtct atttctgtgc aagaggagac 300

tactataggg ggtacttcga tgtctggggc gcagggacca cggtcaccgt ctcctca 357

<210> 20
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 20
gatgttgtga tgactcagac ctcactcact ttgtcggtta ccattggaca accagcctcc 60

atctcttgca agtcaagtca gagcctctta catagtaatg gaaagacata tttgaattgg 120

ttattacaga ggccaggcca gtctccaaag ttcctaatct atctggtgtc taaactggaa 180

tctggagtcc ctgacaggtt cagtggcagt ggatcaggga cagatttcac actgaaaatc 240

agcagagtgg aggctgagga tttgggggtt tattactgct tgcaatctac acattttcct 300

tggacgttcg gtggaggcac caagctggaa atcaaa 336

<210> 21
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 21
gaggtccagc tgcagcagtc tggacctgag ctggtaaagc ctggggcttc agtgaagaaa 60

tcctgcaagg cttctggata cacattcact gactactaca tgcactgggt gaagcagaag 120

cctgggcagg gccttgagtg gattggaaag atttatcctg gaagtggtaa tactcactac 180

aatgagaagt tcaagggcaa ggccacactg actgcagaca aatcctccag cacagcctac 240

atgcagctca gcagcctgac atctgaggac tctgcagtct atttctgtgc aaccaattac 300

tacggctaca gggcaatgaa ctattggggt caaggatcct cagtcaccgt ctcctca 357

<210> 22
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 22
gacatccatt tgacccagtc tccatcctcc ttatctgcct ctctgggaga aagaatcagt 60

ctcacttgcc gggcaagtca ggacatttat attagcttaa actggtttca gcagaaacca 120

gatggaacta ttaaactcct gatctacggc acatccagtt tagattctgg tgtccccaaa 180

aggttcagtg gcagtaggtc tgggtcagat tattctctca ccatcagcag ccttgagtct 240

gaagattttg cagactatta ctgtctacaa tatgctagtt ctccgtacac gttcggaggg 300

gggaccaagc tggaaataaa a 321

<210> 23
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 23
gaggtccagc tgcagcagtc tggacctgag ctggtaaagc ctggggcttc agtgaagata 60

tcctgcaagg cttctggata cacattcact gactactaca tgcactgggt gaagcagaag 120

cctgggcagg gccttgagtg gattggagag atttatcctg gaagtggtaa tccttactac 180

aatgagaagt tcaagggcaa ggccacactg actgcagaca aatcatccag ctcagcctac 240

atgcagctca gcagcctgac atctgaggac tctgcagtct atttctgtgc aagaacctcc 300

tacggtagag tagggacagg gtttgcttac tggggccaag ggactctggt cactgtctct 360

gca 363

<210> 24
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 24
aattttgtga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc 60

atctcttgca gatctagtca gagccttcta cacagtaacg gaaacaccta tttacattgg 120

tacctgcaga agccaggcca gtctccaaag ctcctgatct acaaagtttc caaccgattt 180

tctggggtcc cagacaggtt cagtggcagt ggatcaggga cagatttcac actcaagatc 240

aacagagtgg agactgagga tctgggaatt tatttctgct ctcaaagttc acatgttccc 300

acgttcggtg ctgggaccaa gctggagctg aaa 333

<210> 25
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 25
caggtccagc tgcagcagtc tggggctgaa ctggcaaaac ctggggcctc agtgaagatg 60

tcctgcaagg cttctggcta cacctttact aactactgga tgcactgggt aaaacagagg 120

cctggacagg gtctggaatg gattggatac attaatccta acaatggtta tactgagtac 180

aatcagcgat tcaaggacaa ggccacattg actgcagaca gatcctccac cacagcctac 240

atgcaactaa gcagcctgac atctgaggac tctgcagtct attactgtgc aagatccgat 300

atcattacga cagactactg gggccaaggc accactctca cagtctcctc a 351

<210> 26
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 26
gatgttgtga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc 60

atctcttgca gatctagtca gagccttgta tatagtaatg gaaataccta tttacattgg 120

tacctgcaga agccaggcca gtctccaaag ctcctgatct acaaagtttc caaccgattt 180

tctggggtcc cagacaggtt cagtggcagt ggatcaggga cagatttcac actcaagata 240

agcagagtgg aggctgagga tctgggagtt tatttctgct ctcaaagtac acatgttccg 300

tggacgttcg gtggaggcac caagctggaa atcaaa 336

<210> 27
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 27
gaagtgaagc ttgaggagtc tggaggaggc ttggtgcaac ctggaggatc catgaaactc 60

tcttgtgctg cctctggatt cacttttagt gacgcctgga tggactgggt ccgccagtct 120

ccagaggcgg ggcttgagtg ggttgctgaa attagaaaca aagctcataa tcctgcaaca 180

tactatgctg agtctgtgaa agggagattc accatctcaa gagatgattc caaaagtagt 240

gtctacctgc aaatgaacag cttaagagct gaagacactg gcatttatta ctgtacctta 300

gtagcccctg atgctatgga ctactggggt caaggaacct cagtcaccgt ctcctca 357

<210> 28
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 28
gacattgtga tgtcactgtc tccatcctcc ctagctgtgt cagttggaga gaaggttact 60

atgagctgca agtccagtca gagcctttta tatagtcgca atcaaaagaa ctacttggcc 120

tggtaccagc agaaaccagg gcagtctcct aaactgctga tttactgggc atccactagg 180

gcatctggag tccctgatcg cttcacaggc agtggatctg ggacagattt cactctcacc 240

atcagcagtg tgaaggctga agacctggca gtttattact gtcagcaata ttatagctat 300

ccgtacacgt tcggaggggg gaccaagctg gaaataaaa 339

<210> 29
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 29
caggtccaac tgcagcagtc tgggcctgag ctggtgaggc ctggggcttc agtgaagatg 60

tcctgcaagg cttcaggcta taccttcacc agctactgga tgcactgggt gaaacagagg 120

cctggacaag gccttgagtg gattggcatg attgatcctt ccaatagtga aacttggtta 180

aatcagaagt tcaaggacaa ggccacattg aatgtagaca aatcctccaa cacagcctac 240

atgcagctca gcagcctgac atctgaggac tctgcagtct attactgtgc aagatatgat 300

ggttactacg actactgggg ccaaggcacc actctcacag tctcctca 348

<210> 30
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 30
aacattgtgc tgacccaatc tccagcttct ttggctgtgt ctctagggca gagggccacc 60

atatcctgca gagccagtga aagtgttgat agttatggca atagttttat gcactggtac 120

cagcagaaac caggacagcc acccaaactc ctcatctatc ttgcatccaa cgtagaatct 180

ggggtccctg ccaggttcag tggcagtggg tctaggacag acttcaccct caccattgat 240

cctgtggagg ctgatgatgc tgcaacctat tactgtcagc aaaataatga ggatccgtgg 300

acgttcggtg gaggcaccaa gctggaaatc aaa 333

<210> 31
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 31
caggtccaac tgcagcagcc tggggctgag ctggtgaggc ctggggcttc agtgaagctg 60

tcctgcaagc cttctggcta caccttcacc agctactgga tgaactgggt gaagcagagg 120

cctggacaag gccttgaatg gattggtatg attgatcctt cagacagtga aactcactac 180

aatcaaatgt tcaaggacaa ggccacattg actgttgaca aatcctccaa cacagcctac 240

atgcagctca gcagcctgac atctgaggac tctgcggtct attactgtgc gcagatctac 300

tatgcttacg acaaggctta ctggggccaa gggactctgg tcactgtctc tgca 354

<210> 32

<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 32
gacattgtga tgtcacagtc tccatcctcc ctagctgtgt cagttggaga gaaggttact 60

atgagctgca agtccagtca gagcctttta tatagtagcc atcaaaagaa ctacttggcc 120

tggtaccagc agaaaccagg gcagtctcct aaactgctga tttactgggc atccactagg 180

gaatctgggg tccctgatcg cttcacaggc agtggatctg ggacagattt cagtctcacc 240

atcagcagtg tgaaggctga agacctggca gtttattact gtcaggaata ttatagctgg 300

acgttcggtg gaggcaccaa gctggaaatc aaa 333

<210> 33
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 33
gaggtccagc tgcaacaatc tggacctgag ctggtgaagc ctggggcttc agtgaagata 60

tcctgtaagg cttctggata cacgttcact gactactaca tgaactgggt gaagcagagc 120

catggaaaga gccttgagtg gattggagat attaatcctc acaatggtgg tactagcttc 180

atccagaagt tcaagggcaa ggccacattg actgtagaca agtcctccag cacagcctac 240

atggagctcc gcagcctgac atctgaggac tctgcagtct attattgtgc ccctctggga 300

cgaaaggagg ggtttgctta ctggggccaa gggactctgg tcactgtctc tgca 354

<210> 34
<211> 333
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 34
gacactgtgc tgacacagtc tcctgcttcc ttagttgtat ctctggggca gagggccacc 60

atctcatgca gggccagcaa aagtgtcagt acatctggct atagttatat gcactggtac 120

caacagaaac caggacagcc acccaaactc ctcatctatc ttgcatccaa cctagaatct 180

ggggtccctg ccaggttcag tggcagtggg tctgggacag ccttcaccct caacatccat 240

cctgtggagg aggaggatgc tgcaacctat tactgtcagc acagtaggga gcttccgtac 300

acgttcggag gggggaccaa gctggaaata aaa 333

<210> 35
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 35
caggttactc tgaaagagtc tggccctggg atattgcagc cctcccagac cctcagtctg 60

acttgttctt tctctgggtt ttcactgagc acttttgcta tgggtgtagg ctggattcgt 120

cagccttcag ggaagggtct ggagtggctg gcacacattt ggtgggatga tgataagtac 180

tataacccag ccctgaagag ccggctcaca atctccaagg atacctccaa aaaccatgta 240

ttcctcaaga tcgccaatgt ggacactgca gatactgcca catactactg tgctcgaatg 300

ccgctaactt tctactttga ctactggggc caaggcacca ctctcacagt ctcctca 357

<210> 36
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 36
gatgttttgc tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc 60

atctcttgca gatctagtca gagcattgta catagtaatg gacacaccta tttagaatgg 120

tacctgcaga aaccaggcca gtctccaaag ctcctgatct acaaagtttc caaccgattt 180

tctggggtcc cagacaggtt cagtggcagt ggatcaggga cagatttcac actcaagatc 240

agcagagtgg aggctgagga tctgggagtt tattactgct ttcaaggttc acatgttccg 300

ttcacgttcg gaggggggac caagctggaa ataaaa 336

<210> 37
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 37
caggttactc tgaaagagtc tggccctggg atattgcagc cctcccagac cctcagtctg 60

acttgttctt tctctgggtt ttcactgaga acttttgcta tgggtgtagg ctggattcgt 120

cagccttcag ggaagggtct ggagtggctg gcacacattt ggtgggatga tgataagtac 180

tataacccag ccctgaagag ccggctcaca atctccaagg atacctccaa aaaccaggta 240

ttcctcaaga tcgccaatgt ggacactgca gatactgcca catactactg tgctcgaatg 300

ccgctaactt tctactttga ctactggggc caaggcacca ctctcacagt ctcctca 357

<210> 38
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 38
gatgttttga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc 60

atctcttgta gatctagtca gagcattgta catagtaatg gaaacaccta tttagaatgg 120

tacctgcaga aaccaggcca gtctccaaag ctcctgatct acaaagtttc cacccgattt 180

tctggggtcc cagacaggtt cagtggcagt ggatcaggga cagatttcac actcaagatc 240

agcagagtgg aggctgagga tctgggagtt tattactgct ttcaaggttc acatgttccg 300

ttcacgttcg gaggggggac caagctggaa ataaaa 336

<210> 39
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 39
caggtccaac tgcagcagcc tggggctgaa cttgtgatgc ctggggcttc agtgaagctg 60

tcctgcaagg cttctggcta caccttcacc aactactgga tgcactgggt gaaacagagg 120

cctggacaag gccttgagtg gatcggagag attgatcctt ctgatagtta tactaactac 180

aatcaaaagt tcaagggcaa ggccacattg actgtagaca aatcctccag cacagcctac 240

atgcagctca gcagcctgac atctgaggac tctgcggtct attactgtac aagacagggt 300

agtacctacg cgtggggtca aggaacctca gtcaccgtct cctca 345

<210> 40
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 40
gatattgtga tgacgcaggc tgcattctcc aatccagtca ctcttggaac atcagcttcc 60

atctcctgca ggtctagtaa gagtctccta catagtaatg gcatcactta tttgtattgg 120

tatctgcaga agccaggcca gtctcctcag ctcctgattt atcagatgtc caaccttgcc 180

tcaggagtcc cagacaggtt cagtagcagt gggtcaggaa ctgatttcac actgagaatc 240

agcagagtgg aggctgagga tgtgggtgtt tattactgtg ctcaaaatct agaacttcct 300

ccgacgttcg gtggaggcac caagctggaa atcaaa 336

<210> 41
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 41
gaggtccagc tgcaacaatc tggacctgag ctggtgaagc ctggggcttc agtgaagatg 60

tcctgtaagg cttctggata cacattcact gactactaca tgatgtgggt gaagcagagt 120

catggaaaga gccttgagtg gattggagat attaatcctt acaatggtgg ttctagctac 180

aacccgaagt tcaagggcag ggccacattg actgtagaca aatcctccag cacagcctac 240

atgcagctca acagcctgac atctgaggac tctgcagtct attactgtgc aagagggact 300

tactggggcc aagggactct ggtcactgtc tctgca 336

<210> 42
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 42

gatgttgtga tgacccagac tccactcact ttgtcggtta ccattggaca accagcctcc 60

atctcttgca agtcaagtca gagcctctta gatagtgctg gaaagacata tttgaattgg 120

ttgttacaga ggccaggcca gtctccaaag cgcctaatgt atctggtgtc taaactggac 180

tctggagtcc ctgacaggtt cactggcagc ggatcaggga cagatttcac actgaaaatc 240

agcagagtgg aggctgagga tttgggagtt tattattgct ggcaaggtac acattttccg 300

tacacgttcg gaggggggac caagctggaa ataaaa 336

<210> 43
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 43
caggtccaac tgcagcagcc tggggctgag cttgtgaagc ctggggcttc agtgaagttg 60

tcctgcaagg cttctggcta caccttcacc agctactgga tgcactggat aaagcagaga 120

cctggacaag gccttgagtg gattggagag attaacccta gcaatggtgg ttctaactac 180

aatgagaagt tcaagagcaa ggccacactg actgtagaca aatcctccag cacagcctac 240

atgcaactca gcagcctgac atctgaggac tctgcggtct atcactgtaa aagcagaggc 300

tactggggcc aaggcaccac tctcacagtc tcctca 336

<210> 44
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 44
gatgttgtga tgacccagac tccactcact ttgtcggtta ccattggaca accagcctcc 60

atctcttgca agtcaagtca gagcctctta gatagttatg gaaagacata tttgaattgg 120

ttgttacagc ggccaggcca gtctccaaag cgcctaatct atctggtgtc taaattggac 180

tctggagtcc ctgacaggtt cactggcagt ggatcaggga cagatttcac actgaaaatc 240

agcagagtgg aggctgagga tttgggaatt tattattgct ggcaaggtac acattttcct 300

cacacgttcg gctcggggac aaagttggaa ataaaa 336

<210> 45
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 45
caggttcagc tgcagcagtc tggagctgag ctggcgaggc ctggggcttc agtgaaactg 60

tcctgcaagg cttctggcta caccttcaca agctatggta taagctgggt gaaacagaga 120

actggacagg gccttgagtg gattggagag atttttccta gaagtagtaa tacttactat 180

aatgagaagt tcaagggcaa ggccacactg actgcagaca agtcctccag cacagtgtac 240

atggagttcc gcagcctgac atctgaggac tctgcggtct atttctgtgc aagagagggg 300

ggcctggcct ggtttgctta ctggggccaa gggactctgg tcactgtctc tgca 354

<210> 46
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 46
gatgttgtga tgacccagac tccactcact ttgtcggtta ccattggaca accagcttcc 60

atctcttgca agtcaagtca gagcctctta tatactaatg gaaacaccta tttgaattgg 120

ttattacaga ggccaggcca gtctccaaaa cgcctaatct atctggtgtc taaattggac 180

tctggaatcc ctgacaggtt cagtggcagt ggatcaggga cagatttcac actgagaatc 240

agcagagtgg aggctgagga tttgggagtt tattactgct tgcagagtac acattttcca 300

ttcacgttcg gctcggggac aaagttggaa ataaaa 336

<210> 47
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 47
gaggtccagc tgcaacaatc tggacctgag ctggtgaagc ctggggcttc agtgaagatg 60

tcctgtaagg cttctggata cacaatcact gactactaca tgatgtggtt gaagcagagt 120

catggaaaga gccttgaatg gattggagat attaatcctt acactggtgg tactagctac 180

aaccagaagt tcaagggcaa ggccacattg actgtagaca aatcctccag cacagcctac 240

ctgcagctcc acagcctgac atctgaggac tctgcagtct attactgtgc aagaggggcc 300

tactggggcc aaggcaccac tctcacagtc tcctca 336

<210> 48
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 48
gatgttgtga tgacccagac tccactcact ttgtcggtta ccattggaca accagcctcc 60

atctcttgca agtcaagtca gagcctctta gatagtgatg gaaagacata tttgaattgg 120

ttgttacaga ggccaggcca gtctccaaag cgcctaatct atctggtgtc taaactggac 180

tctggagtcc ctgacaggtt cactggcagt ggatcaggga cagatttcac actgaaaatc 240

agcagagtgg aggctgagga tttgggagtt tattattgct ggcaaggtac acattttccg 300

tacacgttcg gaggggggac caagctggaa ataaaa 336

<210> 49
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 49
gaggtccagc tgcaacaatc tggacctgag ctggtgaagc ctggggcttc agtgaagatg 60

tcctgtaagg cttctggata cacaatcact gactactaca tgatgtggtt gaagcagagt 120

catggaaaga gccttgaatg gattggagat attaatcctt acactggtgg tactagctac 180

aaccagaagt tcaagggcaa ggccacattg actgtagaca aatcctccag cacagcctac 240

atgcagctca acagcctgac atctgaggac tctgcagtct attactgtgc aagaggggcc 300

tactggggcc aaggcaccac tctcacagtc tcctca 336

<210> 50
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 50
gatgttgtga tgacccagac tccactcact ttgtcggtta ccattggaca accagcctcc 60

atctcttgca agtcaagtca gagcctctta gatagtgatg gaaagacata tttgaattgg 120

ttgttacaga ggccaggcca gtctccaaag cgcctaatct atctggtgtc taaactggac 180

tctggagtcc ctgacaggtt cactggcagt ggatcaggga cagatttcac actgaaaatc 240

agcagagtgg aggctgagga tttgggagtt tattattgct ggcaaggtac acattttccg 300

tacacgttcg gaggggggac caagctggaa ataaaa 336

<210> 51
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 51
gaggtccagc tgcaacaatc tggacctgag ctggtgaagc ctggggcttc agtgaagata 60

tcctgtaagg cttctggata cacgttcact gactactaca tgaactgggt gaagcagagc 120

catggcagga gccttgagtt gattggagat attaatccta acaatggtgg ttctaacttc 180

aaccagaagt tcaggggcaa ggccacattg actgtagaca agtcctccag cacagcctat 240

atggagctcc gcagcctgac atctgaggac tctgcaatct attactgtgc aagaatgggt 300

tactggggcc aagggactct ggtcactgtc tctgca 336

<210> 52
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 52
gatgttgtga tgacccagac tccactcact ttgtcggtta ccattggaca accagcctcc 60

atctcttgca agtcaagtca gagcctctta catagtgatg gaaagacata tttgaattgg 120

atgttccaga ggccaggcca gtctccaaag cgcctaatct atctggtgtc taaactggac 180

tctggagtcc cttacaggtt cactggcggt ggatcaggga cagatttcac actgcaaatc 240

agcagagtgg agactgagga tttgggagtt tattattgct ggcaaggtac acattttcct 300

cggacgttcg gtggaggcac caagctggaa atcaaa 336

<210> 53
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 53
gaggtccagc tgcagcagtc tggacctgaa ctggtcaagc ctggggcttc agtgaagatg 60

tcctgcaagg cttctggata cacattcact gactactaca tacactgggt gaagcagaag 120

cctgggcagg gccttgagta cattggagag atttatcctg gaagtggtaa tacttactac 180

aatgggaagt tcaggggcaa ggccacactg actgcagaca agtcctccag cacagcctac 240

atgcagctca gcagcctgac atctgaggac tctgcagtct atttctgtgg tagtggctac 300

tttgactact ggggccaagg caccactctc acagtctcct ca 342

<210> 54
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 54
gatgttgtga tgacccagac tccactcact ttgtctgtta ccattggaca gccagcttcc 60

atttcttgca agtcaagtca gagcctctta tatagtaatg gaaaaaccta tttgaattgg 120

ttattacaga gtccaggcca gtctccaaag ctcctaatct atctggtgtc taaactggaa 180

tctggagtcc ctgacagatt cagtggcagt ggatcaggga cagattttac actgaaactc 240

agcagagtgg aggctgagga tttgggagta tattactgcg tgcaaggtac acatttccca 300

ttcacgttcg gctcggggac aaagttggaa ataaaa 336

<210> 55
<211> 1368
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 55
atggagactg ggctgcgctg gcttctcctg gtcgctgtgt tcaaaggtgt ccagtgtcag 60

gagcaactgg tggagtccgg gggagacctg gtcaagcctg gggcatccct gacactcacc 120

tgcacagcct ctggattctc cttcaataag aattattgga tgtgctgggt ccgccaggct 180

ccagggaagg ggctggagtg gatcggatgc atttataatg gtgatggcaa cacatactac 240

gcgagctggg tgaatggccg attcaccatc tccaaaacct cgtcgaccac ggtgactctg 300

caaatgacca gtctgacagt cgcggacacg gccatctatt tctgtgcgag actacttaat 360

atgtggggcc caggcaccct ggtcaccgtc tcctcagggc aacctaaggc tccatcagtc 420

ttcccactgg ccccctgctg cggggacaca cccagctcca cggtgaccct gggctgcctg 480

gtcaaaggct acctcccgga gccagtgacc gtgacctgga actcgggcac cctcaccaat 540

ggggtacgca ccttcccgtc cgtccggcag tcctcaggcc tctactcgct gagcagcgtg 600

gtgagcgtga cctcaagcag ccagcccgtc acctgcaacg tggcccaccc agccaccaac 660

accaaagtgg acaagaccgt tgcgccctcg acatgcagca agcccatgtg cccacccccc 720

gaactcccgg ggggaccgtc tgtcttcatc ttcccccccaa aacccaagga caccctcatg 780

atctcacgca cccccgaggt cacatgcgtg gtggtggacg tgagccagga tgaccccgag 840

gtgcagttca catggtacat aaacaacgag caggtgcgca ccgcccggcc gccgctacgg 900

gagcagcagt tcaacagcac gatccgcgtg gtcagcaccc tccccatcgc gcaccaggac 960

tggctgaggg gcaaggagtt caagtgcaaa gtccacaaca aggcactccc ggcccccatc 1020

gagaaaacca tctccaaagc cagagggcag cccctggagc cgaaggtcta caccatgggc 1080

cctccccggg aggagctgag cagcaggtcg gtcagcctga cctgcatgat caacggcttc 1140

taccttccg acatctcggt ggagtgggag aagaacggga aggcagagga caactacaag 1200

accacgccga ccgtgctgga cagcgacggc tcctacttcc tctacagcaa gctctcagtg 1260

cccacgagtg agtggcagcg gggcgacgtc ttcacctgct ccgtgatgca cgaggccttg 1320

cacaaccact acacgcagaa gtccatctcc cgctctccgg gtaaatag 1368

<210> 56
<211> 720
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 56
atggacacga gggcccccac tcagctgctg gggctcctac tgctctggct cccaggtgcc 60

agatgtgctg acattgtgat gacccagact ccagcctccg tggaggcagc tgtgggaggc 120

acagtcacca tcaagtgcca ggccagtgag agcattggca atgcattagc ctggtatcag 180

cagaaaccag ggcagcctcc caagctcctg atctatactg cagccactct ggcatctggg 240

gtcccatcgc ggttcagcgg cagtggatct gggacagagt tcactctcac catcagtggc 300

gtgcagtgtg acgatgctgc cacttactac tgtcaaagct attattttac tagtgttagt 360

agttatggca atgctttcgg cggagggacc gaggtggtgg tcaaaggtga tccagttgca 420

cctactgtcc tcatcttccc accagctgct gatcaggtgg caactggaac agtcaccatc 480

gtgtgtgtgg cgaataaata ctttcccgat gtcaccgtca cctgggaggt ggatggcacc 540

acccaaacaa ctggcatcga gaacagtaaa acaccgcaga attctgcaga ttgtacctac 600

aacctcagca gcactctgac actgaccagc acacagtaca acagccacaa agagtacacc 660

tgcaaggtga cccagggcac gacctcagtc gtccagagct tcaatagggg tgactgttag 720

<210> 57
<211> 1401
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 57
atggagactg ggctgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag 60

tcgttggagg agtccggggg agacctggtc aagcctgggg catccctgac actcacctgc 120

agagtctctg gattctcctt cagtagcagt tattatatgt gttgggtccg ccaggctcca 180

gggaaggggc tggaatggat cgcatgtatt ggtactactc gtggtagcac ttactacgcg 240

acctgggcga aaggccgatt caccatttct aaaatctcgt cgaccacggt gactctacaa 300

atgaccagtc tgacagacgc ggacacggcc acctatttct gtgcgagaga tgctactggt 360

tataggatta acacgattgg cctctatttt aatttgtggg gcccaggcac cctggtcacc 420

gtctcctcag ggcaacctaa ggctccatca gtcttcccac tggccccctg ctgcggggac 480

acacccagct ccacggtgac cctgggctgc ctggtcaaag gctacctccc ggagccagtg 540

accgtgacct ggaactcggg caccctcacc aatggggtac gcaccttccc gtccgtccgg 600

cagtcctcag gcctctactc gctgagcagc gtggtgagcg tgacctcaag cagccagccc 660

gtcacctgca acgtggccca cccagccacc aacaccaaag tggacaagac cgttgcgccc 720

tcgacatgca gcaagcccat gtgcccaccc cctgaactcc cgggggggacc gtctgtcttc 780

atcttccccc caaaacccaa ggacaccctc atgatctcac gcacccccga ggtcacatgc 840

gtggtggtgg acgtgagcca ggatgacccc gaggtgcagt tcacatggta cataaacaac 900

gagcaggtgc gcaccgcccg gccgccgcta cgggagcagc agttcaacag cacgatccgc 960

gtggtcagca ccctccccat cgcgcaccag gactggctga ggggcaagga gttcaagtgc 1020

aaagtccaca acaaggcact cccggccccc atcgagaaaa ccatctccaa agccagaggg 1080

cagcccctgg agccgaaggt ctacaccatg ggccctcccc gggaggagct gagcagcagg 1140

tcggtcagcc tgacctgcat gatcaacggc ttctaccctt ccgacatctc ggtggagtgg 1200

gagaagaacg ggaaggcaga ggacaactac aagaccacgc cgaccgtgct ggacagcgac 1260

ggctcctact tcctctacag caagctctca gtgcccacga gtgagtggca gcggggcgac 1320

gtcttcacct gctccgtgat gcacgaggcc ttgcacaacc actacacgca gaagtccatc 1380

tcccgctctc cgggtaaata g 1401

<210> 58
<211> 714
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 58
atggacacga gggcccccac tcagctgctg gggctcctgc tgctctggct cccaggtgcc 60

agatgtgcgt tcgaattgac ccagactcca tcctccgtgg aggctgctgt gggaggcacg 120

cccaccatca agtgccaggc cagtcagacc atttacagtt acttatcctg gtatcagcag 180

aaaccagggc agcctcccaa gctcctgatc tatgaagcgt ccaaactggc ctctggggtc 240

ccatcgcggt tcagcggcag tggatctggg acagactaca ctctcaccat cagcgacctg 300

gagtgtgccg atgctgccac ttactactgt caaagctatc atggtactgc tagtactgaa 360

tataatactt tcggcggggg gaccgaggtg gtggtcagag gtgatccagt tgcacctact 420

gtcctcatct tcccaccagc tgctgatcag gtggcaactg gaacagtcac catcgtgtgt 480

gtggcgaata aatactttcc cgatgtcacc gtcacctggg aggtggatgg caccacccaa 540

acaactggca tcgagaacag taaaacaccg cagaattctg cagattgtac ctacaacctc 600

agcagcactc tgacactgac cagcacacag tacaacagcc acaaagagta cacctgcaag 660

gtgacccagg gcacgacctc agtcgtccag agcttcaata ggggtgactg ttag 714

<210> 59
<211> 1401
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 59
atggagactg ggctgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag 60

cagcagctgg tggagtccgg gggaggcctg gtcaagcctg gggcagccct gacattcacc 120

tgcacagcct ctggattctc cttcagtggc aattattgga tatgctgggt ccgccaggct 180

ccagggaagg ggttggagtg gatcgcgtgc attggtacta ttactagtag gacatactac 240

gcgagctggg cgaaaggccg attcaccatt tccaaaacct cgtcgaccac ggtgactctg 300

caaatgacca gtctgacagc cgcggacacg gccacgtatt tctgtgcgag aggtgcggtt 360

gttagtagtg gtaatgctcc ctactacttt accttgtggg gcccaggcac cctggtcacc 420

gtctcctcag ggcaacctaa ggctccatca gtcttcccac tggccccctg ctgcggggac 480

acacccagct ccacggtgac cctgggctgc ctggtcaaag gctacctccc ggagccagtg 540

accgtgacct ggaactcggg caccctcacc aatggggtac gcaccttccc gtccgtccgg 600

cagtcctcag gcctctactc gctgagcagc gtggtgagcg tgacctcaag cagccagccc 660

gtcacctgca acgtggccca cccagccacc aacaccaaag tggacaagac cgttgcgccc 720

tcgacatgca gcaagcccat gtgcccaccc cctgaactcc cgggggggacc gtctgtcttc 780

atcttccccc caaaacccaa ggacaccctc atgatctcac gcacccccga ggtcacatgc 840

gtggtggtgg acgtgagcca ggatgacccc gaggtgcagt tcacatggta cataaacaac 900

gagcaggtgc gcaccgcccg gccgccgcta cgggagcagc agttcaacag cacgatccgc 960

gtggtcagca ccctccccat cgcgcaccag gactggctga ggggcaagga gttcaagtgc 1020

aaagtccaca acaaggcact cccggccccc atcgagaaaa ccatctccaa agccagaggg 1080

cagcccctgg agccgaaggt ctacaccatg ggccctcccc gggaggagct gagcagcagg 1140

tcggtcagcc tgacctgcat gatcaacggc ttctaccctt ccgacatctc ggtggagtgg 1200

gagaagaacg ggaaggcaga ggacaactac aagaccacgc cgaccgtgct ggacagcgac 1260

ggctcctact tcctctacag caagctctca gtgcccacga gtgagtggca gcggggcgac 1320

gtcttcacct gctccgtgat gcacgaggcc ttgcacaacc actacacgca gaagtccatc 1380

tcccgctctc cgggtaaata g 1401

<210> 60
<211> 711
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 60
atggacacga gggcccccac tcagctgctg gggctcctgc tgctctggct cccaggtgcc 60

agatgtgcat tcgaattgac gcagactcca tcctccgtgg aggcagctgt gggaggcaca 120

gtcaccatca agtgccaggc cagtcagagc attagtagtt acttatcctg gtatcagcag 180

aaaccagggc agcctcccaa gctcctgatc tacagggcat ccactctgga atctggggtc 240

ccatcgcggt ttaaaggcag tggatctggg acagagttca ctctcaccat cagcgacctg 300

gagtgtgccg atgctgccac ttacttctgt caaagctatt atggtgttac ttttagtggt 360

tttgctttcg gcggagggac cgaggtggtg gtcaaaggtg atccagttgc acctactgtc 420

ctcatcttcc caccagctgc tgatcaggtg gcaactggaa cagtcaccat cgtgtgtgtg 480

gcgaataaat actttcccga tgtcaccgtc acctgggagg tggatggcac cacccaaaca 540

actggcatcg agaacagtaa aacaccgcag aattctgcag attgtaccta caacctcagc 600

agcactctga cactgaccag cacacagtac aacagccaca aagagtacac ctgcaaggtg 660

acccagggca cgacctcagt cgtccagagc ttcaataggg gtgactgtta g 711

<210> 61
<211> 1383
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 61
atggagactg ggctgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag 60

tcgttggagg agtccggggg agacctggtc aagcctgggg catccctgac actcacctgc 120

aaagcctctg gaatcgactt caataactat tggataacct gggtccgcca ggctccaggg 180

aaggggctgg agtggatcgc atgcatttat gttggaatta ccggccgcac atggtacgcg 240

aactgggcga aaggccgatt caccatctcc aaggcctcga gcacggtgga tctgaaaatg 300

accagtctga cagccgcgga cacggccacc tatttctgtg cgaggaatgg tgatggtggt 360

atttatgctc ttaacttgtg gggcccaggc accctggtca ccgtctcctc agggcaacct 420

aaggctccat cagtcttccc actggccccc tgctgcgggg acacacccag ctccacggtg 480

accctgggct gcctggtcaa aggctacctc ccggagccag tgaccgtgac ctggaactcg 540

ggcaccctca ccaatggggt acgcaccttc ccgtccgtcc ggcagtcctc aggcctctac 600

tcgctgagca gcgtggtgag cgtgacctca agcagccagc ccgtcacctg caacgtggcc 660

cacccagcca ccaacaccaa agtggacaag accgttgcgc cctcgacatg cagcaagccc 720

atgtgcccac cccctgaact cccgggggga ccgtctgtct tcatcttccc cccaaaaccc 780

aaggacaccc tcatgatctc acgcaccccc gaggtcacat gcgtggtggt ggacgtgagc 840

caggatgacc ccgaggtgca gttcacatgg tacataaaca acgagcaggt gcgcaccgcc 900

cggccgccgc tacgggagca gcagttcaac agcacgatcc gcgtggtcag caccctcccc 960

atcgcgcacc aggactggct gaggggcaag gagttcaagt gcaaagtcca caacaaggca 1020

ctcccggccc ccatcgagaa aaccatctcc aaagccagag ggcagcccct ggagccgaag 1080

gtctacacca tgggccctcc ccgggaggag ctgagcagca ggtcggtcag cctgacctgc 1140

atgatcaacg gcttctaccc ttccgacatc tcggtggagt gggagaagaa cgggaaggca 1200

gaggacaact acaagaccac gccgaccgtg ctggacagcg acggctccta cttcctctac 1260

agcaagctct cagtgcccac gagtgagtgg cagcggggcg acgtcttcac ctgctccgtg 1320

atgcacgagg ccttgcacaa ccactacacg cagaagtcca tctcccgctc tccgggtaaa 1380

tag 1383

<210> 62
<211> 717
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 62
atggacacga gggcccccac tcagctgctg gggctcctgc tgctctggct cccaggtgcc 60

acatttgcac aagtgctgac ccagactgca tcgtccgtgt ctgcagctgt gggaggcaca 120

gtcaccatca gttgccagtc cagtcagagt gtttataata ataattggtt agcctggtat 180

cagcagaaac cagggcagcc tcccaagctc ctgatctaca gggcatccac tctgacatct 240

ggggtcccat cgcggttcaa aggcagtgga tctgggacac agttcactct caccatcagc 300

gacctggagt gtgacgatgc tgccacttac tactgtgcag gcggttatag tggtaatatt 360

tacgtaaatg atttcggcgg agggaccgag gtggtggtca aaggtgatcc agttgcacct 420

actgtcctca tcttcccacc agctgctgat caggtggcaa ctggaacagt caccatcgtg 480

tgtgtggcga ataaatactt tcccgatgtc accgtcacct gggaggtgga tggcaccacc 540

caaacaactg gcatcgagaa cagtaaaaca ccgcagaatt ctgcagattg tacctacaac 600

ctcagcagca ctctgacact gaccagcaca cagtacaaca gccacaaaga gtacacctgc 660

aaggtgaccc agggcacgac ctcagtcgtc cagagcttca ataggggtga ctgttag 717

<210> 63
<211> 1380
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 63
atggagactg ggctgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag 60

gagcagctgg aggagtccgg gggagacctg gtcaagcctg ggggatccct gacactcacc 120

tgcaaagcct ctggattctc cttcagtaat acctactggg catgctgggt ccgccaggct 180

ccagggaagg ggctggagtg gatcgcatgc atgaatcctg ctagtagtgg tagctcttac 240

tacgcgagct gggcgaaagg ccgattcacc atctccaaaa cctcgtcgac cacggtgact 300

ctgcacatgc ccagtctgac agccgcggac acggccacct atttctgtgc gaaatgggat 360

actgctttcg atgtgtgggg cccaggcacc ctggtcaccg tctcctcagg gcaacctaag 420

gctccatcag tcttcccact ggccccctgc tgcggggaca cacccagctc cacggtgacc 480

ctgggctgcc tggtcaaagg ctacctcccg gagccagtga ccgtgacctg gaactcgggc 540

accctcacca atggggtacg caccttcccg tccgtccggc agtcctcagg cctctactcg 600

ctgagcagcg tggtgagcgt gacctcaagc agccagcccg tcacctgcaa cgtggcccac 660

ccagccacca acaccaaagt ggacaagacc gttgcgccct cgacatgcag caagcccatg 720

tgcccacccc ctgaactccc ggggggaccg tctgtcttca tcttcccccc aaaacccaag 780

gacaccctca tgatctcacg cacccccgag gtcacatgcg tggtggtgga cgtgagccag 840

gatgaccccg aggtgcagtt cacatggtac ataaacaacg agcaggtgcg caccgcccgg 900

ccgccgctac gggagcagca gttcaacagc acgatccgcg tggtcagcac cctccccatc 960

gcgcaccagg actggctgag gggcaaggag ttcaagtgca aagtccacaa caaggcactc 1020

ccggccccca tcgagaaaac catctccaaa gccagagggc agcccctgga gccgaaggtc 1080

tacaccatgg gccctccccg ggaggagctg agcagcaggt cggtcagcct gacctgcatg 1140

atcaacggct tctacccttc cgacatctcg gtggagtggg agaagaacgg gaaggcagag 1200

gacaactaca agaccacgcc gaccgtgctg gacagcgacg gctcctactt cctctacagc 1260

aagctctcag tgcccacgag tgagtggcag cggggcgacg tcttcacctg ctccgtgatg 1320

cacgaggcct tgcacaacca ctacacgcag aagtccatct cccgctctcc gggtaaatag 1380

<210> 64
<211> 714
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 64
atggacacga gggcccccac tcagctgctg gggctcctgc tgctctggct cccaggtgcc 60

agatgtgccg atgttgtgat gacccagact ccatcctccg tggaggcagc tgtgggaggc 120

acagtcacca tcaagtgcca ggccagtcag agcattagta gctacttagc ctggtatcag 180

cagaaaccag ggcagcctcc caagctcctg atctatggtg catccaatct ggagtctggg 240

gtcccatcgc ggttcaaagg cagtggatct gggacagagt acactctcac catcagcggc 300

gtgcagtgtg acgatgctgc cacttactac tgtcaaaact attatgctat tgatacttat 360

ggtcatgctt tcggcggagg gaccgaggtg gtggtcaaag gtgatccagt tgcacctact 420

gtcctcatct tcccaccagc tgctgatcag gtggcaactg gaacagtcac catcgtgtgt 480

gtggcgaata aatactttcc cgatgtcacc gtcacctggg aggtggatgg caccacccaa 540

acaactggca tcgagaacag taaaacaccg cagaattctg cagattgtac ctacaacctc 600

agcagcactc tgacactgac cagcacacag tacaacagcc acaaagagta cacctgcaag 660

gtgacccagg gcacgacctc agtcgtccag agcttcaata ggggtgactg ttag 714

<210> 65
<211> 1368
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 65
atggagactg ggctgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag 60

gagcagctgg aggagtccgg gggagacctg gtcaagcctg gggcatccct gacactcacc 120

tgcacagcct ctggattctc ctttagtagc aactatcaca tctgctgggt ccgccaggct 180

ccaggaaagg ggctggagtt gatcgcatgc atttatgttg gtgatggcag cacatactac 240

gcgagctggg cgaaaggccg attcaccatc tccaaatcct cgtcgaccac ggtagctctg 300

caaatgacca gtctgacagc cgcggacacg gccacctatt tctgtgggag aatgtttaac 360

ttgtggggcc caggcaccct ggtcaccgtc tcctcagggc aacctaaggc tccatcagtc 420

ttcccactgg ccccctgctg cggggacaca cccagctcca cggtgaccct gggctgcctg 480

gtcaaaggct acctcccgga gccagtgacc gtgacctgga actcgggcac cctcaccaat 540

ggggtacgca ccttcccgtc cgtccggcag tcctcaggcc tctactcgct gagcagcgtg 600

gtgagcgtga cctcaagcag ccagcccgtc acctgcaacg tggcccaccc agccaccaac 660

accaaagtgg acaagaccgt tgcgccctcg acatgcagca agcccatgtg cccacccccc 720

gaactcccgg ggggaccgtc tgtcttcatc ttcccccccaa aacccaagga caccctcatg 780

atctcacgca cccccgaggt cacatgcgtg gtggtggacg tgagccagga tgaccccgag 840

gtgcagttca catggtacat aaacaacgag caggtgcgca ccgcccggcc gccgctacgg 900

gagcagcagt tcaacagcac gatccgcgtg gtcagcaccc tccccatcgc gcaccaggac 960

tggctgaggg gcaaggagtt caagtgcaaa gtccacaaca aggcactccc ggcccccatc 1020

gagaaaacca tctccaaagc cagagggcag cccctggagc cgaaggtcta caccatgggc 1080

cctccccggg aggagctgag cagcaggtcg gtcagcctga cctgcatgat caacggcttc 1140

taccttccg acatctcggt ggagtgggag aagaacggga aggcagagga caactacaag 1200

accacgccga ccgtgctgga cagcgacggc tcctacttcc tctacagcaa gctctcagtg 1260

cccacgagtg agtggcagcg gggcgacgtc ttcacctgct ccgtgatgca cgaggccttg 1320

cacaaccact acacgcagaa gtccatctcc cgctctccgg gtaaatag 1368

<210> 66
<211> 708
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 66
atggacacga gggcccccac tcagctgctg gggctcctgc tgctctggct cccaggtgcc 60

atatgtgacc ctgtgctgac ccagactcca tcctccgtgt ctgcggctgt gggagtcaca 120

gtcaccatca actgccagtc cagtccgagt gtttatagta actacttatc ctggtatcag 180

cagaaaccag ggcagcctcc caagctcctc atctatctgg catctactct ggcatctggg 240

gtcccatcgc ggttcaaagg cagtggatct gggacacagt tcactctcac catcagcgac 300

gtgcagtgtg acgatgctgc cacttactac tgtgcaggca cttatagtgg taatatttgg 360

tctttcggcg gagggaccga ggtggtggtc aaaggtgatc cagttgcacc tactgtcctc 420

atcttcccac cagctgctga tcaggtggca actggaacag tcaccatcgt gtgtgtggcg 480

aataaatact ttcccgatgt caccgtcacc tgggaggtgg atggcaccac ccaaacaact 540

ggcatcgaga acagtaaaac accgcagaat tctgcagatt gtacctacaa cctcagcagc 600

actctgacac tgaccagcac acagtacaac agccacaaag agtacacctg caaggtgacc 660

cagggcacga cctcagtcgt ccagagcttc aataggggtg actgttag 708

<210> 67
<211> 1383
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 67
atggagactg ggctgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag 60

cagcagctgg tggagtccgg gggaggcctg gtcaagcctg gggcatccct gacactcacc 120

tgcacagcct ctggattctc cttcagtagc ggctatcaca tgtgctgggt ccgccaggct 180

ccagggaagg ggctggagtg gatcgcatgc tttggtgttt atactggtac cactacctac 240

gcgagctggg cgaaaggtcg attcaccatc tccaaaacct cgtcgaccac ggtgactcta 300

caaatgacca gtctaacagt cgcggacacg gccacctatt tctgtgcgag aatcagtgct 360

gaaaatggtg gggacttgtg gggcccaggc accctggtca ccgtctcctc agggcaacct 420

aaggctccat cagtcttccc actggccccc tgctgcgggg acacacccag ctccacggtg 480

accctgggct gcctggtcaa aggctacctc ccggagccag tgaccgtgac ctggaactcg 540

ggcaccctca ccaatggggt acgcaccttc ccgtccgtcc ggcagtcctc aggcctctac 600

tcgctgagca gcgtggtgag cgtgacctca agcagccagc ccgtcacctg caacgtggcc 660

cacccagcca ccaacaccaa agtggacaag accgttgcgc cctcgacatg cagcaagccc 720

atgtgcccac cccctgaact cccgggggga ccgtctgtct tcatcttccc cccaaaaccc 780

aaggacaccc tcatgatctc acgcaccccc gaggtcacat gcgtggtggt ggacgtgagc 840

caggatgacc ccgaggtgca gttcacatgg tacataaaca acgagcaggt gcgcaccgcc 900

cggccgccgc tacgggagca gcagttcaac agcacgatcc gcgtggtcag caccctcccc 960

atcgcgcacc aggactggct gaggggcaag gagttcaagt gcaaagtcca caacaaggca 1020

ctcccggccc ccatcgagaa aaccatctcc aaagccagag ggcagcccct ggagccgaag 1080

gtctacacca tgggccctcc ccgggaggag ctgagcagca ggtcggtcag cctgacctgc 1140

atgatcaacg gcttctaccc ttccgacatc tcggtggagt gggagaagaa cgggaaggca 1200

gaggacaact acaagaccac gccgaccgtg ctggacagcg acggctccta cttcctctac 1260

agcaagctct cagtgcccac gagtgagtgg cagcggggcg acgtcttcac ctgctccgtg 1320

atgcacgagg ccttgcacaa ccactacacg cagaagtcca tctcccgctc tccgggtaaa 1380

tag 1383

<210> 68
<211> 711
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 68
atggacacga gggcccccac tcagctgctg gggctcctgc tgctctggct cccaggtgcc 60

agatgtgatg ttgtgatgac ccagactcca gcctccgtgg aggcagctgt gggaggcaca 120

gtcaccatca agtgccaggc cagtcagagc attagcaact acttttcttg gtatcagcag 180

aaaccagggc agcctcccaa gctcctgatc tacagggcgt ccactctggc atctggggtc 240

ccatcgcggt tcagcggcag tggatctggg acagagttca ctctcaccat cagcgacctg 300

gagtgtgccg attctgccac ttactactgt cagtgcactt atggtagtag tagtactggt 360

tttggtttcg gcggagggac cgaggtggtg gtcaaaggtg atccagttgc acctactgtc 420

cccatcttcc caccagctgc tgatcaggtg gcaactggaa cagtcaccat cgtgtgtgtg 480

gcgaataaat actttcccga tgtcaccgtc acctgggagg tggatggcac cacccaaaca 540

actggcatcg agaacagtaa aacaccgcag aattctgcag attgtaccta caacctcagc 600

agcactctga cactgaccag cacacagtac aacagccaca aagagtacac ctgcaaggtg 660

acccagggca cgacctcagt cgtccagagc ttcaataggg gtgactgtta g 711

<210> 69
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 69
atggagactg ggctgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag 60

tcgttggagg agtccggggg agacctggtc aagcctgggg catccctgac actcacctgc 120

atggcctctg gaatcgactt cagtagcggc tacggcatgt ggtgggtccg ccaggctcca 180

gggaagggac tggagtatat cggatacatt gatactggtg atgataacac atactacgcg 240

aactgggcga aaggccgatt caccatctcc aaaacctcgt cgaccacggt gactctgcaa 300

atgaccagtc tgacagtcgc ggacacggcc acctatttct gtgcgaaagg gggcgccata 360

gacctctggg gcccagggac cctcgtcacc gtctcttcag ggcaacctaa ggctccatca 420

gtcttcccac tggcccctg ctgcggggac acacccagct ccacggtgac cctgggctgc 480

ctggtcaaag gctacctccc ggagccagtg accgtgacct ggaactcggg caccctcacc 540

aatggggtac gcaccttccc gtccgtccgg cagtcctcag gcctctactc gctgagcagc 600

gtggtgagcg tgacctcaag cagccagccc gtcacctgca acgtggccca cccagccacc 660

aacaccaaag tggacaagac cgttgcgccc tcgacatgca gcaagcccat gtgcccaccc 720

cctgaactcc cgggggggacc gtctgtcttc atcttccccc caaaacccaa ggacaccctc 780

atgatctcac gcacccccga ggtcacatgc gtggtggtgg acgtgagcca ggatgacccc 840

gaggtgcagt tcacatggta cataaacaac gagcaggtgc gcaccgcccg gccgccgcta 900

cgggagcagc agttcaacag cacgatccgc gtggtcagca ccctccccat cgcgcaccag 960

gactggctga ggggcaagga gttcaagtgc aaagtccaca acaaggcact cccggccccc 1020

atcgagaaaa ccatctccaa agccagaggg cagcccctgg agccgaaggt ctacaccatg 1080

ggccctcccc gggaggagct gagcagcagg tcggtcagcc tgacctgcat gatcaacggc 1140

ttctaccctt ccgacatctc ggtggagtgg gagaagaacg ggaaggcaga ggacaactac 1200

aagaccacgc cgaccgtgct ggacagcgac ggctcctact tcctctacag caagctctca 1260

gtgcccacga gtgagtggca gcggggcgac gtcttcacct gctccgtgat gcacgaggcc 1320

ttgcacaacc actacacgca gaagtccatc tcccgctctc cgggtaaata g 1371

<210> 70
<211> 720
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 70
atggacacga gggcccccac tcagctgctg ggactcctac tgctctggct cccaggtgcc 60

agatgtgctg acattgtgat gacccagact ccagcctccg tggaggcagc tgtgggaggc 120

acagtcacca tcaagtgcca ggccagtcag agcattagta gttacttagc ctggtatcag 180

cagaaaccag ggcagcgtcc caagctcctg atctacaggg catccactct aaaatctggg 240

gtcccatcgc ggttcaaagg cagtggatct gggacagagt acactctcac catcagcgac 300

ctggagtgtg ccgatgctgc cacttattat tgtcaagcgt attatcttag tagtagtatc 360

agttatggta atactttcgg cggagggacc gaggtggtgg tcaaaggtga tccagttgca 420

cctactgtcc tcatcttccc accagctgct gatcaggtgg caactggaac agtcaccatc 480

gtgtgtgtgg cgaataaata ctttcccgat gtcaccgtca cctgggaggt ggatggcacc 540

acccaaacaa ctggcatcga gaacagtaaa acaccgcaga attctgcaga ttgtacctac 600

aacctcagca gcactctgac actgaccagc acacagtaca acagccacaa agagtacacc 660

tgcaaggtga cccagggcac gacctcagtc gtccagagct tcaatagggg tgactgttag 720

<210> 71
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 71
atggagactg ggctgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag 60

tcgttggagg agtccggggg agacctggtc aagcctgggg cgtccctgac actcacctgc 120

acagcctctg gattctccct cagtagcggg tatggcatgt gctgggtccg ccaggctcca 180

gggaagggac tggagtggat cggatacact gatactgcta ctggtaccat tcactacgcg 240

agctgggcga aaggccgatt caccatctcc aaaacctcgt cgaccacggt gactctgcaa 300

atgaccagtc tgacagccgc ggacacggcc acctatttct gtgcgaaagg gggcgccatg 360

gacctctggg gcccagggac cctcgtcacc gtctcttcag ggcaacctaa ggctccatca 420

gtcttcccac tggccccctg ctgcggggac acacccagct ccacggtgac cctgggctgc 480

ctggtcaaag gctacctccc ggagccagtg accgtgacct ggaactcggg caccctcacc 540

aatggggtac gcaccttccc gtccgtccgg cagtcctcag gcctctactc gctgagcagc 600

gtggtgagcg tgacctcaag cagccagccc gtcacctgca acgtggccca cccagccacc 660

aacaccaaag tggacaagac cgttgcgccc tcgacatgca gcaagcccat gtgcccaccc 720

cctgaactcc cgggggggacc gtctgtcttc atcttccccc caaaacccaa ggacaccctc 780

atgatctcac gcacccccga ggtcacatgc gtggtggtgg acgtgagcca ggatgacccc 840

gaggtgcagt tcacatggta cataaacaac gagcaggtgc gcaccgcccg gccgccgcta 900

cgggagcagc agttcaacag cacgatccgc gtggtcagca ccctccccat cgcgcaccag 960

gactggctga ggggcaagga gttcaagtgc aaagtccaca acaaggcact cccggccccc 1020

atcgagaaaa ccatctccaa agccagaggg cagcccctgg agccgaaggt ctacaccatg 1080

ggccctcccc gggaggagct gagcagcagg tcggtcagcc tgacctgcat gatcaacggc 1140

ttctaccctt ccgacatctc ggtggagtgg gagaagaacg ggaaggcaga ggacaactac 1200

aagaccacgc cgaccgtgct ggacagcgac ggctcctact tcctctacag caagctctca 1260

gtgcccacga gtgagtggca gcggggcgac gtcttcacct gctccgtgat gcacgaggcc 1320

ttgcacaacc actacacgca gaagtccatc tcccgctctc cgggtaaata g 1371

<210> 72
<211> 720
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 72
atggacacga gggcccccac tcagctgctg gggctcctac tgctctggct cccaggtgcc 60

agatgtgctg acattgtgat gacccagact ccagcctccg tggaggcagc tgtgggaggc 120

acagtcacca tcaagtgcca ggccagtcag agcattagta gctacttagc ctggtatcag 180

cagaaaccag ggcagcctcc caagctcctg atctacagga catccactct ggcatctggg 240

gtcccatcgc ggttcaaagg cagtggatct gggacagagt acactctcac catcagcgac 300

ctggagtgtg ccgatgctgc cacttactat tgtcaaagct atgcttatag tagtagtagc 360

agttatggta atgctttcgg cggagggacc gaggtggtgg tcaaaggtga tccagttgca 420

cctactgtcc tcatcttccc accagctgct gatcaggtgg caactggaac agtcaccatc 480

gtgtgtgtgg cgaataaata ctttcccgat gtcaccgtca cctgggaggt ggatggcacc 540

acccaaacaa ctggcatcga gaacagtaaa acaccgcaga attctgcaga ttgtacctac 600

aacctcagca gcactctgac actgaccagc acacagtaca acagccacaa agagtacacc 660

tgcaaggtga cccagggcac gacctcagtc gtccagagct tcaatagggg tgactgttag 720

<210> 73
<211> 1365
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 73
atggagactg ggctgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag 60

tcgttggagg agtccggggg agacctggtc aagcctgggg catccctgac actcacctgc 120

acaggctctg gaatcgactt cagtagcagc tactggatat gctgggtccg ccaggctcca 180

gggaaggggc tggagtggat cgcatgcatc gatggtagtg atggtaacac ttactacgcg 240

agctgggcga gaggccgatt caccatctcc aaaacctcgt cgaccacggt gactctgcaa 300

atggccagtc tgacagccgc ggacacggcc acctatttct gtacgagaga tctcaggttg 360

tggggcccag gcaccctggt caccgtctcc tcagggcaac ctaaggctcc atcagtcttc 420

ccactggccc cctgctgcgg ggacacaccc agctccacgg tgaccctggg ctgcctggtc 480

aaaggctacc tcccggagcc agtgaccgtg acctggaact cgggcaccct caccaatggg 540

gtacgcacct tcccgtccgt ccggcagtcc tcaggcctct actcgctgag cagcgtggtg 600

agcgtgacct caagcagcca gcccgtcacc tgcaacgtgg cccacccagc caccaacacc 660

aaagtggaca agaccgttgc gccctcgaca tgcagcaagc ccatgtgccc acccctgaa 720

ctcccggggg gaccgtctgt cttcatcttc cccccaaaac ccaaggacac cctcatgatc 780

tcacgcaccc ccgaggtcac atgcgtggtg gtggacgtga gccaggatga ccccgaggtg 840

cagttcacat ggtacataaa caacgagcag gtgcgcaccg cccggccgcc gctacgggag 900

cagcagttca acagcacgat ccgcgtggtc agcaccctcc ccatcgcgca ccaggactgg 960

ctgaggggca aggagttcaa gtgcaaagtc cacaacaagg cactcccggc ccccatcgag 1020

aaaaccatct ccaaagccag agggcagccc ctggagccga aggtctacac catgggccct 1080

ccccgggagg agctgagcag caggtcggtc agcctgacct gcatgatcaa cggcttctac 1140

ccttccgaca tctcggtgga gtgggagaag aacgggaagg cagaggacaa ctacaagacc 1200

acgccgaccg tgctggacag cgacggctcc tacttcctct acagcaagct ctcagtgccc 1260

acgagtgagt ggcagcgggg cgacgtcttc acctgctccg tgatgcacga ggccttgcac 1320

aaccactaca cgcagaagtc catctcccgc tctccgggta aatag 1365

<210> 74
<211> 723
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 74
atggacacga gggcccccac tcagctgctg gggctcctgc tgctctggct cccaggtgcc 60

agatgtgctg acattgtgct gacccagact ccagcctcgg tgtctgcagc tgtgggaggc 120

acagtcacca tcaactgcca ggccagtcag aatgtttata gtaacaatgc cttagcctgg 180

catcagcaga aaccagggca gcgtcccaac ctcctgatct acaaggcttc cactctggca 240

tctggggtcc catcgcggtt caaaggcagt ggatctggga cacagtttac tctcaccatc 300

agcgacgtgc agtgtgacga tgctgccact tactactgtc taggcgaatt tagttgtagt 360

agtggtgatt gttttgtttt cggcggaggg accgaggtgg tggtcaaagg tgatccagtt 420

gcacctactg tcctcatctt cccaccagct gctgatcagg tggcaactgg aacagtcacc 480

atcgtgtgtg tggcgaataa atactttccc gatgtcaccg tcacctggga ggtggatggc 540

accacccaaa caactggcat cgagaacagt aaaacaccgc agaattctgc agattgtacc 600

tacaacctca gcagcactct gacactgacc agcacacagt acaacagcca caaagagtac 660

acctgcaagg tgacccaggg cacgacctca gtcgtccaga gcttcaatag gggtgactgt 720

tag 723

<210> 75
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 75
atggagactg ggctgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag 60

tcgttggagg agtccggggg agacctggtc aagcctgggg catccctgac actcacctgc 120

atggcctctg gaatcgactt cagtagcggc tacggcatgt ggtgggtccg ccaggctcca 180

gggaagggac tggagtatat cggatacatt gatactggtg atgataacac atactacgcg 240

aactgggcga aaggccgatt caccatctcc aaaacctcgt cgaccacggt gactctgcaa 300

atgaccagtc tgacagtcgc ggacacggcc acctatttct gtgcgaaagg gggcgccata 360

gacctctggg gcccagggac cctcgtcacc gtctcttcag ggcaacctaa ggctccatca 420

gtcttcccac tggccccctg ctgcggggac acacccagct ccacggtgac cctgggctgc 480

ctggtcaaag gctacctccc ggagccagtg accgtgacct ggaactcggg caccctcacc 540

aatggggtac gcaccttccc gtccgtccgg cagtcctcag gcctctactc gctgagcagc 600

gtggtgagcg tgacctcaag cagccagccc gtcacctgca acgtggccca cccagccacc 660

aacaccaaag tggacaagac cgttgcgccc tcgacatgca gcaagcccat gtgcccaccc 720

cctgaactcc cgggggggacc gtctgtcttc atcttccccc caaaacccaa ggacaccctc 780

atgatctcac gcacccccga ggtcacatgc gtggtggtgg acgtgagcca ggatgacccc 840

gaggtgcagt tcacatggta cataaacaac gagcaggtgc gcaccgcccg gccgccgcta 900

cgggagcagc agttcaacag cacgatccgc gtggtcagca ccctccccat cgcgcaccag 960

gactggctga ggggcaagga gttcaagtgc aaagtccaca acaaggcact cccggccccc 1020

atcgagaaaa ccatctccaa agccagaggg cagcccctgg agccgaaggt ctacaccatg 1080

ggccctcccc gggaggagct gagcagcagg tcggtcagcc tgacctgcat gatcaacggc 1140

ttctaccctt ccgacatctc ggtggagtgg gagaagaacg ggaaggcaga ggacaactac 1200

aagaccacgc cgaccgtgct ggacagcgac ggctcctact tcctctacag caagctctca 1260

gtgcccacga gtgagtggca gcggggcgac gtcttcacct gctccgtgat gcacgaggcc 1320

ttgcacaacc actacacgca gaagtccatc tcccgctctc cgggtaaata g 1371

<210> 76
<211> 720
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 76
atggacacga gggcccccac tcagctgctg ggactcctac tgctctggct cccaggtgcc 60

agatgtgctg acattgtgat gacccagact ccagcctccg tggaggcagc tgtgggaggc 120

acagtcacca tcaagtgcca ggccagtcag agcattagta gttacttagc ctggtatcag 180

cagaaaccag ggcagcgtcc caagctcctg atctacaggg catccactct aaaatctggg 240

gtcccatcgc ggttcaaagg cagtggatct gggacagagt acactctcac catcagcgac 300

ctggagtgtg ccgatgctgc cacttattat tgtcaagcgt attatcttag tagtagtatc 360

agttatggta atactttcgg cggagggacc gaggtggtgg tcaaaggtga tccagttgca 420

cctactgtcc tcatcttccc accagctgct gatcaggtgg caactggaac agtcaccatc 480

gtgtgtgtgg cgaataaata ctttcccgat gtcaccgtca cctgggaggt ggatggcacc 540

acccaaacaa ctggcatcga gaacagtaaa acaccgcaga attctgcaga ttgtacctac 600

aacctcagca gcactctgac actgaccagc acacagtaca acagccacaa agagtacacc 660

tgcaaggtga cccagggcac gacctcagtc gtccagagct tcaatagggg tgactgttag 720

<210> 77
<211> 1416
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 77
atggagactg ggctgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag 60

cagcagctgg aggagtccgg gggaggcctg gtcaagcctg gaggaaccct gacactcacc 120

tgcaaagcct ctggagtcgc cctcaatccc tactactata tgtgctgggt ccgccaggct 180

ccagggaagg ggctggagtg gatcgcatgc gtggatgctg atagtagtgg tagcacttac 240

tacgcgagct gggcgaaagg ccgattcacc atctccaaaa cctcgtcgac cacggtgact 300

ctgaaaatga ccagtctgac agccgcggac acggccacct atttctgtgc gagagaatcg 360

gttgactata gttctgttgg tattggctat gtacatggta cggatggctt gtggggccca 420

ggcaccctgg tcaccgtctc ctcagggcaa cctaaggctc catcagtctt cccactggcc 480

ccctgctgcg gggacacacc cagctccacg gtgaccctgg gctgcctggt caaaggctac 540

ctcccggagc cagtgaccgt gacctggaac tcgggcaccc tcaccaatgg ggtacgcacc 600

ttcccgtccg tccggcagtc ctcaggcctc tactcgctga gcagcgtggt gagcgtgacc 660

tcaagcagcc agcccgtcac ctgcaacgtg gcccacccag ccaccaacac caaagtggac 720

aagaccgttg cgccctcgac atgcagcaag cccatgtgcc caccccctga actcccgggg 780

ggaccgtctg tcttcatctt ccccccaaaa cccaaggaca ccctcatgat ctcacgcacc 840

cccgaggtca catgcgtggt ggtggacgtg agccaggatg accccgaggt gcagttcaca 900

tggtacataa acaacgagca ggtgcgcacc gcccggccgc cgctacggga gcagcagttc 960

aacagcacga tccgcgtggt cagcaccctc cccatcgcgc accaggactg gctgaggggc 1020

aaggagttca agtgcaaagt ccacaacaag gcactcccgg cccccatcga gaaaaccatc 1080

tccaaagcca gagggcagcc cctggagccg aaggtctaca ccatgggccc tccccgggag 1140

gagctgagca gcaggtcggt cagcctgacc tgcatgatca acggcttcta cccttccgac 1200

atctcggtgg agtgggagaa gaacgggaag gcagaggaca actacaagac cacgccgacc 1260

gtgctggaca gcgacggctc ctacttcctc tacagcaagc tctcagtgcc cacgagtgag 1320

tggcagcggg gcgacgtctt cacctgctcc gtgatgcacg aggccttgca caaccactac 1380

acgcagaagt ccatctcccg ctctccgggt aaatag 1416

<210> 78
<211> 720
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 78
atggacacga gggcccccac tcagctgctg gggctcctgc tgctctggct cccaggtgcc 60

agatgtgccg acatcgtggt gacccagact ccatcctccg tgtctgcagc tgtgggaggc 120

acagtcacca tcaagtgcca ggccagtcag agcattagca actacttttc ttggtatcag 180

cagaaaccag ggcagcctcc caagctcctg atctacaggg cgtccactct ggcatctggg 240

gtcccatcgc ggttcaaagg cagtggatct gggacagagt tcactctcac catcagcgac 300

ctggagtgtg ccgatgctgc cacttactac tgtcaatgca cttacggtag aagtaatagt 360

aatttttttt atggtttcgg cggagggacc gaggtggtgg tcaaaggtga tccagttgca 420

cctactgtcc tcatcttccc accagctgct gatcaggtgg caactggaac agtcaccatc 480

gtgtgtgtgg cgaataaata ctttcccgat gtcaccgtca cctgggaggt ggatggcacc 540

acccaaacaa ctggcatcga gaacagtaaa acaccgcaga attctgcaga ttgtacctac 600

aacctcagca gcactctgac actgaccagc acacagtaca acagccacaa agagtacacc 660

tgcaaggtga cccagggcac gacctcagtc gtccagagct tcaatagggg tgactgttag 720

<210> 79
<211> 1395
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 79
atggagactg ggctgcgctg gcttctcctg gtcgccgtgc tcaaaggtgt ccagtgtcag 60

tcgttggagg agtccggggg agacctggtc aagcctgggg cctccctgac actcacctgc 120

acagcctctg gatcctcctt cagtagtacc tactggaact gctgggtccg ccaggctcca 180

gggaaggggc tggagtggat cgcatgcatt aatgctggta gtggtaccac ttactacgcg 240

agctgggcga aaggccgatt caccgtctcc aaaacctcgt cgaccacggt gactctgcaa 300

atgaccagtc tgacagccgc ggacacggcc acctatttct gtacgagaga tagtgatggt 360

cgttttagta gtggctacta ttttaacttg tggggcccag gcaccctggt caccgtctcc 420

tcagggcaac ctaaggctcc atcagtcttc ccactggccc cctgctgcgg ggacacaccc 480

agctccacgg tgaccctggg ctgcctggtc aaaggctacc tcccggagcc agtgaccgtg 540

acctggaact cgggcaccct caccaatggg gtacgcacct tcccgtccgt ccggcagtcc 600

tcaggcctct actcgctgag cagcgtggtg agcgtgacct caagcagcca gcccgtcacc 660

tgcaacgtgg cccacccagc caccaacacc aaagtggaca agaccgttgc gccctcgaca 720

tgcagcaagc ccatgtgccc acccccctgaa ctcccggggg gaccgtctgt cttcatcttc 780

cccccaaaac ccaaggacac cctcatgatc tcacgcaccc ccgaggtcac atgcgtggtg 840

gtggacgtga gccaggatga ccccgaggtg cagttcacat ggtacataaa caacgagcag 900

gtgcgcaccg cccggccgcc gctacgggag cagcagttca acagcacgat ccgcgtggtc 960

agcaccctcc ccatcgcgca ccaggactgg ctgaggggca aggagttcaa gtgcaaagtc 1020

cacaacaagg cactcccggc ccccatcgag aaaaccatct ccaaagccag agggcagccc 1080

ctggagccga aggtctacac catgggccct ccccgggagg agctgagcag caggtcggtc 1140

agcctgacct gcatgatcaa cggcttctac ccttccgaca tctcggtgga gtgggagaag 1200

aacgggaagg cagaggacaa ctacaagacc acgccgaccg tgctggacag cgacggctcc 1260

tacttcctct acagcaagct ctcagtgccc acgagtgagt ggcagcgggg cgacgtcttc 1320

acctgctccg tgatgcacga ggccttgcac aaccactaca cgcagaagtc catctcccgc 1380

tctccgggta aatag 1395

<210> 80
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 80
atggacacga gggcccccac tcagctgctg gggctcctgc tgctctggct cccaggtgcc 60

acatttgccc aagtgctgac ccagactgca tcccctgtgt ctgcagctgt gggaggcaca 120

gtcaccatca attgtcagtc cagtcagagt gtttatgata acaactggtt agcctggtat 180

cagcaaaaac cagggcagcc tcccaaactc ttgatcgacg atgcatccaa attgacatct 240

ggggtctcat cgcggttcaa aggcagtgga tctgggacgc agttcactct caccatcagc 300

ggcgtgcagt gtgacgatgc tgccacttac tactgtcaag gcgcttatta tagtagtggt 360

tggtactggg ctttcggcgg agggaccgag gtggtggtca aaggtgatcc agttgcacct 420

actgtcctca tcttcccacc agctgctgat caggtggcaa ctggaacagt caccatcgtg 480

tgtgtggcga ataaatactt tcccgatgtc accgtcacct gggaggtgga tggcaccacc 540

caaacaactg gcatcgagaa cagtaaaaca ccgcagaatt ctgcagattg tacctacaac 600

ctcagcagca ctctgacact gaccagcaca cagtacaaca gccacaaaga gtacacctgc 660

aaggtgaccc agggcacgac ctcagtcgtc cagagcttca ataggggtga ctgttag 717

<210> 81
<211> 1404
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 81
atggagactg ggctgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag 60

cagcagctgg aggagtccgg gggaggcctg gtcaagcctg gaggaaccct gacactcacc 120

tgcaaagcct ctggaatcga cttcagtagc tactactaca tgtgttgggt ccgccaggct 180

ccagggaagg ggctggagtt gatcgtatgt atttatacta gtagtggtgg cacatggtac 240

gcgagctggg tgaatggccg actcaccatc tccagaagca ccagcctaaa cacggtggat 300

ctgaaaatga ccagtctgac agccgcggac acggccacct atttctgtgc cagaggggtt 360

tattctggta gtagtgatta tccaactcgg ttggatctct ggggccaggg caccctggtc 420

accgtctcct tagggcaacc taaggctcca tcagtcttcc cactggcccc ctgctgcggg 480

gacacaccca gctccacggt gaccctgggc tgcctggtca aaggctacct cccggagcca 540

gtgaccgtga cctggaactc gggcaccctc accaatgggg tacgcacctt cccgtccgtc 600

cggcagtcct caggcctcta ctcgctgagc agcgtggtga gcgtgacctc aagcagccag 660

cccgtcacct gcaacgtggc ccacccagcc accaacacca aagtggacaa gaccgttgcg 720

ccctcgacat gcagcaagcc catgtgccca ccccctgaac tcccgggggg accgtctgtc 780

ttcatcttcc ccccaaaacc caaggacacc ctcatgatct cacgcacccc cgaggtcaca 840

tgcgtggtgg tggacgtgag ccaggatgac cccgaggtgc agttcacatg gtacataaac 900

aacgagcagg tgcgcaccgc ccggccgccg ctacgggagc agcagttcaa cagcacgatc 960

cgcgtggtca gcaccctccc catcgcgcac caggactggc tgaggggcaa ggagttcaag 1020

tgcaaagtcc acaacaaggc actcccggcc cccatcgaga aaaccatctc caaagccaga 1080

gggcagcccc tggagccgaa ggtctacacc atgggccctc cccgggagga gctgagcagc 1140

aggtcggtca gcctgacctg catgatcaac ggcttctacc cttccgacat ctcggtggag 1200

tgggagaaga acgggaaggc agaggacaac tacaagacca cgccgaccgt gctggacagc 1260

gacggctcct acttcctcta cagcaagctc tcagtgccca cgagtgagtg gcagcggggc 1320

gacgtcttca cctgctccgt gatgcacgag gccttgcaca accactacac gcagaagtcc 1380

atctcccgct ctccgggtaa atag 1404

<210> 82
<211> 711
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 82
atggacacga gcacctccac tgcgctcctg gggctcctgc tgctctggct cacaggtgcc 60

agatgtgcca tcgagatgac ccagtctcca ccctccctgt ctgcatctgt gggagaaact 120

gtcaggatta ggtgcctggc cagtgaggac atttacagtg gtatatcctg gtaccaacag 180

aagccagaga aacctcctac actcctgatc tctggtgcat ccaatttaga atctggggtc 240

ccaccacggt tcagtggcgg tggatccggg acagattaca ccctcaccat cggcggcgtg 300

caggctgaag atgttgccac ctactactgt ctaggcggtt atagtttcag tagtaccggt 360

ttgacttttg gagctggcac caaggtggaa atcaaacgtg atccagttgc gccttctgtc 420

ctcctcttcc caccatctaa ggaggagctg acaactggaa cagccaccat cgtgtgtgtg 480

gcgaataaat actttcccga tgtcaccgtc acctgggagg tggatggcac cacccaaaca 540

actggcatcg agaacagtaa aacaccgcag aattctgcag attgtaccta caacctcagc 600

agcactctga cactgaccag cacacagtac aacagccaca aagagtacac ctgcaaggtg 660

acccagggca cgacctcagt cgtccagagc ttcaataggg gtgactgtta g 711

<210> 83
<211> 1383
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 83
atggagactg ggctgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag 60

caacatctgg tggagtccgg gggaggcctg gtcaagcctg gggcatccct gacactcacc 120

tgcacagcct ctggattctc cttcactacc ggctatcaca tgtgctgggt ccgccaggct 180

ccagggaagg ggctggagtg gatcgcatgt tttggtgttt atactagtac cactacctac 240

gcgagctggg cgaaaggtcg attcaccatc tccaaaacct cgtcgaccac ggtgactcta 300

caaatgacca gtctaacagt cgcggacacg gccacctatt tctgtgcgag aatcagtgct 360

gaagatggtg gggacttgtg gggcccaggc accctggtca ccgtctcctc agggcaacct 420

aaggctccat cagtcttccc actggccccc tgctgcgggg acacacccag ctccacggtg 480

accctgggct gcctggtcaa aggctacctc ccggagccag tgaccgtgac ctggaactcg 540

ggcaccctca ccaatggggt acgcaccttc ccgtccgtcc ggcagtcctc aggcctctac 600

tcgctgagca gcgtggtgag cgtgacctca agcagccagc ccgtcacctg caacgtggcc 660

cacccagcca ccaacaccaa agtggacaag accgttgcgc cctcgacatg cagcaagccc 720

atgtgcccac cccctgaact cccgggggga ccgtctgtct tcatcttccc cccaaaaccc 780

aaggacaccc tcatgatctc acgcaccccc gaggtcacat gcgtggtggt ggacgtgagc 840

caggatgacc ccgaggtgca gttcacatgg tacataaaca acgagcaggt gcgcaccgcc 900

cggccgccgc tacgggagca gcagttcaac agcacgatcc gcgtggtcag caccctcccc 960

atcgcgcacc aggactggct gaggggcaag gagttcaagt gcaaagtcca caacaaggca 1020

ctcccggccc ccatcgagaa aaccatctcc aaagccagag ggcagcccct ggagccgaag 1080

gtctacacca tgggccctcc ccgggaggag ctgagcagca ggtcggtcag cctgacctgc 1140

atgatcaacg gcttctaccc ttccgacatc tcggtggagt gggagaagaa cgggaaggca 1200

gaggacaact acaagaccac gccgaccgtg ctggacagcg acggctccta cttcctctac 1260

agcaagctct cagtgcccac gagtgagtgg cagcggggcg acgtcttcac ctgctccgtg 1320

atgcacgagg ccttgcacaa ccactacacg cagaagtcca tctcccgctc tccgggtaaa 1380

tag 1383

<210> 84
<211> 711
<212> DNA
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 84
atggacacga gggcccccac tcagctgctg gggctcctgc tgctctggct cccaggtgcc 60

agatgtgatg ttgtgatgac ccagactcca gcctccgtgg aggcagctgt gggaggcaca 120

gtcaccatca cgtgccaggc cagtcagagc attagcaact acttttcttg gtatcagcag 180

aaaccagggc agcctcccaa gctcctgatc tacagggcgt ccactctggc atctggggtc 240

ccatcgcggt tcagcggcag tggatctggg acacagttca ctctcaccat cagcgacctg 300

gagtgtgccg attctgccac ttacgcctgt cagtgcactt atggtagtag tagtactggt 360

tttggtttcg gcggagggac cgaggtggtg gtcaaaggtg atccagttgc acctactgtc 420

ctcatcttcc caccagctgc tgatcaggtg gcaactggaa cagtcaccat cgtgtgtgtg 480

gcgaataaat actttcccga tgtcaccgtc acctgggagg tggatggcac cacccaaaca 540

actggcatcg agaacagtaa aacaccgcag aattctgcag attgtaccta caacctcagc 600

agcactctga cactgaccag cacacagtac aacagccaca aagagtacac ctgcaaggtg 660

acccagggca cgacctcagt cgtccagagc ttcaataggg gtgactgtta g 711

<210> 85
<211> 1389
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 85
atggagactg ggctgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag 60

tcgttggagg agtccggggg agacctggtc aagcctgggg catccctgac actcacctgc 120

aaagcctctg gattctcctt cagtagttac ttctggatat gctgggtccg ccaggctcca 180

gggaaggggc tggagtggag cgcatgcatc tatggtgata gtagtggtag tagttactac 240

gcgagctggg cgaaaggccg attcaccatc tccaaaacct cgtcgaccac ggtgactctg 300

caaatgacca gtctgacagc cgcggacacg gccacctatt tctgtgcgag ttatggtagt 360

agtagttatt actactctaa tttatggggc ccaggcaccc tggtcaccgt ctcctcaggg 420

caacctaagg ctccatcagt cttcccactg gccccctgct gcggggacac acccagctcc 480

acggtgaccc tgggctgcct ggtcaaaggc tacctcccgg agccagtgac cgtgacctgg 540

aactcgggca ccctcaccaa tggggtacgc accttcccgt ccgtccggca gtcctcaggc 600

ctctactcgc tgagcagcgt ggtgagcgtg acctcaagca gccagcccgt cacctgcaac 660

gtggcccacc cagccaccaa caccaaagtg gacaagaccg ttgcgccctc gacatgcagc 720

aagcccatgt gcccaccccc tgaactcccg gggggaccgt ctgtcttcat cttcccccca 780

aaacccaagg acaccctcat gatctcacgc acccccgagg tcacatgcgt ggtggtggac 840

gtgagccagg atgaccccga ggtgcagttc acatggtaca taaacaacga gcaggtgcgc 900

accgcccggc cgccgctacg ggagcagcag ttcaacagca cgatccgcgt ggtcagcacc 960

ctccccatcg cgcaccagga ctggctgagg ggcaaggagt tcaagtgcaa agtccacaac 1020

aaggcactcc cggcccccat cgagaaaacc atctccaaag ccagagggca gcccctggag 1080

ccgaaggtct acaccatggg ccctccccgg gaggagctga gcagcaggtc ggtcagcctg 1140

acctgcatga tcaacggctt ctacccttcc gacatctcgg tggagtggga gaagaacggg 1200

aaggcagagg acaactacaa gaccacgccg accgtgctgg acagcgacgg ctcctacttc 1260

ctctacagca agctctcagt gcccacgagt gagtggcagc ggggcgacgt cttcacctgc 1320

tccgtgatgc acgaggcctt gcacaaccac tacacgcaga agtccatctc ccgctctccg 1380

ggtaaatag 1389

<210> 86
<211> 708
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 86

atggacacga gggcccccac tcagctgctg gggctcctgc tgctctggct cccaggtgcc 60

atatgtgacc ctgtgatgac ccagactcca tcttccacgt ctgcggctgt gggaggcaca 120

gtcaccatca gttgccagtc cagtcagagt gtttataata acaactactt agcctggtat 180

cagcagaaac cagggcagcc tcccaaacgc ctgatctacg aatcatccaa actggcatct 240

ggggtcccat cgcggttcag aggcagtgga tctggggcac agttcactct caccatcagc 300

gacctggagt gtgacgatgc tgccacttac tactgtctag gcgcatatta tactactctt 360

gatttcggcg gagggaccga ggtggtggtc agaggtgatc cagttgcacc tactgtcctc 420

atcttcccac cagctgctga tcaggtggca actggaacag tcaccatcgt gtgtgtggcg 480

aataaatact ttcccgatgt caccgtcacc tgggaggtgg atggcaccac ccaaacaact 540

ggcatcgaga acagtaaaac accgcagaat tctgcagatt gtacctacaa cctcagcagc 600

actctgacac tgaccagcac acagtacaac agccacaaag agtacacctg caaggtgacc 660

cagggcacga cctcagtcgt ccagagcttc aataggggtg actgttag 708

<210> 87
<211> 1383
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 87
atggagactg ggctgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag 60

gagcagttgg tggagtccgg gggaggcctg gtccagcctg agggatccct gacactcacc 120

tgcaaagcct ctggattcga cttcagtagc aatgcaatgt gctgggtccg ccaggctcca 180

gggaaggggc tggagtggat cgcatgcatt tataatggtg atggcagcac atactacgcg 240

agctgggtga atggccgatt caccatctcc aagacctcgt cgaccacggt gactctgcaa 300

atgaccagtc tgacagccgc ggacacggcc acctatttct gtgcgagagg tctctctaat 360

tggaataggg ataacttatg gggccctggc accctggtca ccgtctcctc agggcaacct 420

aaggctccat cagtcttccc actggccccc tgctgcgggg acacacccag ctccacggtg 480

accctgggct gcctggtcaa aggctacctc ccggagccag tgaccgtgac ctggaactcg 540

ggcaccctca ccaatggggt acgcaccttc ccgtccgtcc ggcagtcctc aggcctctac 600

tcgctgagca gcgtggtgag cgtgacctca agcagccagc ccgtcacctg caacgtggcc 660

cacccagcca ccaacaccaa agtggacaag accgttgcgc cctcgacatg cagcaagccc 720

atgtgcccac cccctgaact cccgggggga ccgtctgtct tcatcttccc cccaaaaccc 780

aaggacaccc tcatgatctc acgcaccccc gaggtcacat gcgtggtggt ggacgtgagc 840

caggatgacc ccgaggtgca gttcacatgg tacataaaca acgagcaggt gcgcaccgcc 900

cggccgccgc tacgggagca gcagttcaac agcacgatcc gcgtggtcag caccctcccc 960

atcgcgcacc aggactggct gaggggcaag gagttcaagt gcaaagtcca caacaaggca 1020

ctcccggccc ccatcgagaa aaccatctcc aaagccagag ggcagcccct ggagccgaag 1080

gtctacacca tgggccctcc ccgggaggag ctgagcagca ggtcggtcag cctgacctgc 1140

atgatcaacg gcttctaccc ttccgacatc tcggtggagt gggagaagaa cgggaaggca 1200

gaggacaact acaagaccac gccgaccgtg ctggacagcg acggctccta cttcctctac 1260

agcaagctct cagtgcccac gagtgagtgg cagcggggcg acgtcttcac ctgctccgtg 1320

atgcacgagg ccttgcacaa ccactacacg cagaagtcca tctcccgctc tccgggtaaa 1380

tag 1383

<210> 88
<211> 720
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 88
atggacacga gggcccccac tcagctgctg gggctcctgc tgctctggct cccaggtgcc 60

acatttgccc aagtgctgac ccagactcca tcctccgtgt ctgcagctgt gggaggcaca 120

gccaccatca actgccaggc cagtcagagt ctttatagtc ccaagaattt agcctggtat 180

cagcagacac cagggcagcc tcccaagctc ctgatctatt ctgcatcgaa actggcatct 240

ggggtcccat cgcggttcaa aggcagtgga tctgggacac agttcactct caccatcagc 300

ggcgtgcagt gtgacgatgc tgcaatttac tactgtcaag gcgaatttag ttgtactact 360

gctgcttgtt ttgcttttgg cggagggacc gaggtggtgg tcaaaggtga tccagttgca 420

cctactgtcc tcatcttccc accagctgct gatcaggtgg caactggaac agtcaccatc 480

gtgtgtgtgg cgaataaata ctttcccgat gtcaccgtca cctgggaggt ggatggcacc 540

acccaaacaa ctggcatcga gaacagtaaa acaccgcaga attctgcaga ttgtacctac 600

aacctcagca gcactctgac actgaccagc acacagtaca acagccacaa agagtacacc 660

tgcaaggtga cccagggcac gacctcagtc gtccagagct tcaatagggg tgactgttag 720

<210> 89
<211> 1386
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 89
atggagactg ggctgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag 60

tctttggagg agtccggggg aggcctggtc cagcctgagg gatccctgac actcgcctgc 120

acagcttcgg gattctcctt cagtagctac tactacatct gctgggtccg ccaggctcca 180

gggacggggc tggagtggat cggatgcatt aatactggta gtgatgacac tcactacgcg 240

agctggttga aaggccgatt caccttctcc aaggcctcgt cgaccacgtt gactctgcaa 300

atgaccagtc tgacagccgc ggacacggcc acctatttct gtgcgagatc atctggtagt 360

agtgatgatg cttatgatct ctggggccca ggcaccctgg tcactgtctc ctcagggcaa 420

cctaaggctc catcagtctt cccactggcc ccctgctgcg gggacacacc cagctccacg 480

gtgaccctgg gctgcctggt caaaggctac ctcccggagc cagtgaccgt gacctggaac 540

tcgggcaccc tcaccaatgg ggtacgcacc ttcccgtccg tccggcagtc ctcaggcctc 600

tactcgctga gcagcgtggt gagcgtgacc tcaagcagcc agcccgtcac ctgcaacgtg 660

gcccacccag ccaccaacac caaagtggac aagaccgttg cgccctcgac atgcagcaag 720

cccatgtgcc cacccccctga actcccgggg ggaccgtctg tcttcatctt cccccccaaaa 780

cccaaggaca ccctcatgat ctcacgcacc cccgaggtca catgcgtggt ggtggacgtg 840

agccaggatg accccgaggt gcagttcaca tggtacataa acaacgagca ggtgcgcacc 900

gcccggccgc cgctacggga gcagcagttc aacagcacga tccgcgtggt cagcaccctc 960

cccatcgcgc accaggactg gctgaggggc aaggagttca agtgcaaagt ccacaacaag 1020

gcactcccgg cccccatcga gaaaaccatc tccaaagcca gagggcagcc cctggagccg 1080

aaggtctaca ccatgggccc tccccgggag gagctgagca gcaggtcggt cagcctgacc 1140

tgcatgatca acggcttcta cccttccgac atctcggtgg agtgggagaa gaacgggaag 1200

gcagaggaca actacaagac cacgccgacc gtgctggaca gcgacggctc ctacttcctc 1260

tacagcaagc tctcagtgcc cacgagtgag tggcagcggg gcgacgtctt cacctgctcc 1320

gtgatgcacg aggccttgca caaccactac acgcagaagt ccatctcccg ctctccgggt 1380

aaatag 1386

<210> 90
<211> 708
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 90
atggacacga gggcccccac tcagctgctg gggctcctgc tgctctggct cccaggtgcc 60

agatgtgatg ttgtgatgac ccagactcca gcctccgtgt ctgaacctgt gggaggcgca 120

gtcaccatca agtgccaggc cagtcagagc attggtagta atttagcctg gtatcagcac 180

aaaccagggc agcctcccaa gctcctgatc tattttgcat ccagcctggc atctggggtc 240

tcgtcgcggt tcaagggcgg tagatctggg acacagttca ctctcaccat cagcgacctg 300

gagtgtgccg atgctgccac ttactactgt cactgtactt attatcctct tagttatgtt 360

actttcggcg gagggaccga ggtggtggtc aaaggtgatc cagttgcacc tactgtcctc 420

atcttcccac cagctgctga tcaggtggca actggaacag tcaccatcgt gtgtgtggcg 480

aataaatact ttcccgatgt caccgtcacc tgggaggtgg atggcaccac ccaaacaact 540

ggcatcgaga acagtaaaac accgcagaat tctgcagatt gtacctacaa cctcagcagc 600

actctgacac tgaccagcac acagtacaac agccacaaag agtacacctg caaggtgacc 660

cagggcacga cctcagtcgt ccagagcttc aataggggtg actgttag 708

<210> 91
<211> 1395
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 91
atggagactg ggctgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag 60

tcgttggagg agtccggggg agacctggtc aagcctggga catccctgac actctcctgc 120

acagcctctg gattctcctt cggtagctat tattatatgt gctgggtccg ccaggctcca 180

gggaaggggc tggagtggat cgcatgcatt gatgttggta gtagtggtga cacatactac 240

gcgagctggg tgaatggccg attcaccatc tccaaaacct cgtcgaccac ggtgactctg 300

caaatgacca gtctgacagc cgcggacacg gccacctatt tctgtgcgag agatgatact 360

gctgctggtg gttttggtaa tttggaattg tggggcccag gcaccctggt caccgtctcc 420

tcagggcaac ctaaggctcc atcagtcttc ccactggccc cctgctgcgg ggacacaccc 480

agctccacgg tgaccctggg ctgcctggtc aaaggctacc tcccggagcc agtgaccgtg 540

acctggaact cgggcaccct caccaatggg gtacgcacct tcccgtccgt ccggcagtcc 600

tcaggcctct actcgctgag cagcgtggtg agcgtgacct caagcagcca gcccgtcacc 660

tgcaacgtgg cccacccagc caccaacacc aaagtggaca agaccgttgc gccctcgaca 720

tgcagcaagc ccatgtgccc acccccctgaa ctcccggggg gaccgtctgt cttcatcttc 780

cccccaaaac ccaaggacac cctcatgatc tcacgcaccc ccgaggtcac atgcgtggtg 840

gtggacgtga gccaggatga ccccgaggtg cagttcacat ggtacataaa caacgagcag 900

gtgcgcaccg cccggccgcc gctacgggag cagcagttca acagcacgat ccgcgtggtc 960

agcaccctcc ccatcgcgca ccaggactgg ctgaggggca aggagttcaa gtgcaaagtc 1020

cacaacaagg cactcccggc ccccatcgag aaaaccatct ccaaagccag agggcagccc 1080

ctggagccga aggtctacac catgggccct ccccgggagg agctgagcag caggtcggtc 1140

agcctgacct gcatgatcaa cggcttctac ccttccgaca tctcggtgga gtgggagaag 1200

aacgggaagg cagaggacaa ctacaagacc acgccgaccg tgctggacag cgacggctcc 1260

tacttcctct acagcaagct ctcagtgccc acgagtgagt ggcagcgggg cgacgtcttc 1320

acctgctccg tgatgcacga ggccttgcac aaccactaca cgcagaagtc catctcccgc 1380

tctccgggta aatag 1395

<210> 92
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 92
atggacacga gggcccccac tcagctgctg gggctcctgc tgctctggct cccaggtgcc 60

agatgtgcat tcgaattgac ccagactcca tcctccgtgt ctgaacctgt gggaggcaca 120

gtcaccatca agtgccaggc cagtcagagc atttacagct acttttcctg gtatcagcag 180

aaaccagggc agcctcccaa gcgcctgatt taccaggcat ccactctggc ttctggggtc 240

ccatcgcggt tcaaaggcag tggatctggg acagatttca ctctcaccat cagcgacctg 300

gagtgtgccg atgctgccac ttactactgt caaaacaatt atggtagggg tagtggtagt 360

tatttttttg gtttcggcgg agggaccgag gtggtggtca aaggtgatcc agttgcacct 420

actgtcctca tcttcccacc agctgctgat caggtggcaa ctggaacagt caccatcgtg 480

tgtgtggcga ataaatactt tcccgatgtc accgtcacct gggaggtgga tggcaccacc 540

caaacaactg gcatcgagaa cagtaaaaca ccgcagaatt ctgcagattg tacctacaac 600

ctcagcagca ctctgacact gaccagcaca cagtacaaca gccacaaaga gtacacctgc 660

aaggtgaccc agggcacgac ctcagtcgtc cagagcttca ataggggtga ctgttag 717

<210> 93
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 93
atggagactg ggctgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag 60

tcgttggagg agtccggggg agacctggtc aagcctgggg catccctgac actcacctgc 120

aaagcctctg gaatcgactt cagtagcggc tacggcatgt ggtgggtccg ccaggctcca 180

gggaagggac tggagtatat cggatacatt gatactggta gtggtagcac ttactacgcg 240

aactgggcga aaggccgatt caccatctcc aaaacctcgt cgaccatggt gactctgcaa 300

atgaccagtc tgacagtcgc ggacacggcc acctatttct gtgcgaaagg gggcgccata 360

gacctctggg gcccagggac cctcgtcacc gtctcttcag ggcaacctaa ggctccatca 420

gtcttcccac tggccccctg ctgcggggac acacccagct ccacggtgac cctgggctgc 480

ctggtcaaag gctacctccc ggagccagtg accgtgacct ggaactcggg caccctcacc 540

aatggggtac gcaccttccc gtccgtccgg cagtcctcag gcctctactc gctgagcagc 600

gtggtgagcg tgacctcaag cagccagccc gtcacctgca acgtggccca cccagccacc 660

aacaccaaag tggacaagac cgttgcgccc tcgacatgca gcaagcccat gtgcccaccc 720

cctgaactcc cgggggggacc gtctgtcttc atcttccccc caaaacccaa ggacaccctc 780

atgatctcac gcacccccga ggtcacatgc gtggtggtgg acgtgagcca ggatgacccc 840

gaggtgcagt tcacatggta cataaacaac gagcaggtgc gcaccgcccg gccgccgcta 900

cgggagcagc agttcaacag cacgatccgc gtggtcagca ccctccccat cgcgcaccag 960

gactggctga ggggcaagga gttcaagtgc aaagtccaca acaaggcact cccggccccc 1020

atcgagaaaa ccatctccaa agccagaggg cagcccctgg agccgaaggt ctacaccatg 1080

ggccctcccc gggaggagct gagcagcagg tcggtcagcc tgacctgcat gatcaacggc 1140

ttctaccctt ccgacatctc ggtggagtgg gagaagaacg ggaaggcaga ggacaactac 1200

aagaccacgc cgaccgtgct ggacagcgac ggctcctact tcctctacag caagctctca 1260

gtgcccacga gtgagtggca gcggggcgac gtcttcacct gctccgtgat gcacgaggcc 1320

ttgcacaacc actacacgca gaagtccatc tcccgctctc cgggtaaata g 1371

<210> 94
<211> 720
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 94
atggacacga gggcccccac tcagctgctg ggactcctac tgctctggct cccaggtgcc 60

agatgtgctg acattgtgat gacccagact ccagcctccg tggaggcagc tgtgggaggc 120

acagtcacca tcaagtgcca ggccagtcag agcattagta gttacttagc ctggtatcag 180

cagaaaccag ggcagcgtcc caagctcctg atctacaggg catccactct ggcatctggg 240

gtcccatcgc ggttcaaagg cagtggatct gggacagact acactctcac catcagcgac 300

ctggagtgtg ccgatgctgc cacttattat tgtcatacct attatcttag tagtagtatc 360

agttatggta atactttcgg cggagggacc gaggtggtgg tcaaaggtga tccagttgca 420

cctactgtcc tcatcttccc accagctgct gatcaggtgg caactggaac agtcaccatc 480

gtgtgtgtgg cgaataaata ctttcccgat gtcaccgtca cctgggaggt ggatggcacc 540

acccaaacaa ctggcatcga gaacagtaaa acaccgcaga attctgcaga ttgtacctac 600

aacctcagca gcactctgac actgaccagc acacagtaca acagccacaa agagtacacc 660

tgcaaggtga cccagggcac gacctcagtc gtccagagct tcaatagggg tgactgttag 720

<210> 95
<211> 1398
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 95
atggagactg ggctgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag 60

gagcagctgg aggagtccgg gggagacctg gtcaagcctg agggatccct gacactcacc 120

tgcaaagcct ctggattctc cttcagtagc atctactgga tttgctgggt ccgccaggct 180

ccagggaagg ggctggagtg gatcgcatgc actactgttg tcaaaagtgg tagaacttac 240

tacgcgaact gggcgaaagg ccgattcacc atctccaaaa cctcgtcgac cacggtgact 300

ctgcaaatga ccagtctgac agccgcggac acggccacct atttctgtgc gagagaattt 360

gttgatggtg gtggtagtag tggtagggac ttgtggggcc caggcaccct ggtcaccgtc 420

tcctcagggc aacctaaggc tccatcagtc ttcccactgg ccccctgctg cggggacaca 480

cccagctcca cggtgaccct gggctgcctg gtcaaaggct acctcccgga gccagtgacc 540

gtgacctgga actcgggcac cctcaccaat ggggtacgca ccttcccgtc cgtccggcag 600

tcctcaggcc tctactcgct gagcagcgtg gtgagcgtga cctcaagcag ccagcccgtc 660

acctgcaacg tggcccaccc agccaccaac accaaagtgg acaagaccgt tgcgccctcg 720

acatgcagca agcccatgtg cccacccccc gaactcccgg ggggaccgtc tgtcttcatc 780

ttcccccccaa aacccaagga caccctcatg atctcacgca cccccgaggt cacatgcgtg 840

gtggtggacg tgagccagga tgaccccgag gtgcagttca catggtacat aaacaacgag 900

caggtgcgca ccgcccggcc gccgctacgg gagcagcagt tcaacagcac gatccgcgtg 960

gtcagcaccc tccccatcgc gcaccaggac tggctgaggg gcaaggagtt caagtgcaaa 1020

gtccacaaca aggcactccc ggcccccatc gagaaaacca tctccaaagc cagagggcag 1080

cccctggagc cgaaggtcta caccatgggc cctccccggg aggagctgag cagcaggtcg 1140

gtcagcctga cctgcatgat caacggcttc tacccttccg acatctcggt ggagtgggag 1200

aagaacggga aggcagagga caactacaag accacgccga ccgtgctgga cagcgacggc 1260

tcctacttcc tctacagcaa gctctcagtg cccacgagtg agtggcagcg gggcgacgtc 1320

ttcacctgct ccgtgatgca cgaggccttg cacaaccact acacgcagaa gtccatctcc 1380

cgctctccgg gtaaatag 1398

<210> 96
<211> 711
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 96
atggacacga gggcccccac tcagctgctg gggctcctgc tgctctggct cccaggtgcc 60

agatgtgcct atgatatgac ccagactcca gcctccgtgg aggcagctgt gggaggcaca 120

gtcaccatca agtgccaggc cagtcagagc attagtaggg acttatcctg gtatcagcag 180

aaacctggac agcctcccaa gcgcctaatc tacaaggcat ccactctggc atctggggtc 240

ccatcgcggt tcaaaggcag tggatctggg acagatttca ctctcaccat cagcgacctg 300

gagtgtgccg atgctgccac ttactactgt caacagggtt atagtagtat tgatgttgat 360

aatgatttcg gcggagggac cgaggtggtg gtcaaaggtg atccagttgc acctactgtc 420

ctcatcttcc caccagctgc tgatcaggtg gcaactggaa cagtcaccat cgtgtgtgtg 480

gcgaataaat actttcccga tgtcaccgtc acctgggagg tggatggcac cacccaaaca 540

actggcatcg agaacagtaa aacaccgcag aattctgcag attgtaccta caacctcagc 600

agcactctga cactgaccag cacacagtac aacagccaca aagagtacac ctgcaaggtg 660

acccagggca cgacctcagt cgtccagagc ttcaataggg gtgactgtta g 711

<210> 97
<211> 1404
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 97
atggagactg ggctgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag 60

gagcagctgg aggagtccgg gggaggcctg gtcaagcctg agggatccct gacactcacc 120

tgcaaagcct ctggattcga cctcagtagc ggctatgaca tgtgctgggt ccgccaggct 180

ccagggaagg ggctggagtg gatcgcatgc atttatgctg attatagtgg tagcacatac 240

tacgcgagct gggtgaatgg ccgattcacc atctccagca gcaccagcct aaacacggtg 300

gatctgaaaa tgaccagtct gacagccgcg gacacggcca cctatttctg tgccagaggg 360

gctactggta atggtggtta tggatactac tttaacttgt ggggcccagg caccctggtc 420

accgtctcct cagggcaacc taaggctcca tcagtcttcc cactggcccc ctgctgcggg 480

gacacaccca gctccacggt gaccctgggc tgcctggtca aaggctacct cccggagcca 540

gtgaccgtga cctggaactc gggcaccctc accaatgggg tacgcacctt cccgtccgtc 600

cggcagtcct caggcctcta ctcgctgagc agcgtggtga gcgtgacctc aagcagccag 660

cccgtcacct gcaacgtggc ccacccagcc accaacacca aagtggacaa gaccgttgcg 720

ccctcgacat gcagcaagcc catgtgccca ccccctgaac tcccgggggg accgtctgtc 780

ttcatcttcc ccccaaaacc caaggacacc ctcatgatct cacgcacccc cgaggtcaca 840

tgcgtggtgg tggacgtgag ccaggatgac cccgaggtgc agttcacatg gtacataaac 900

aacgagcagg tgcgcaccgc ccggccgccg ctacgggagc agcagttcaa cagcacgatc 960

cgcgtggtca gcaccctccc catcgcgcac caggactggc tgaggggcaa ggagttcaag 1020

tgcaaagtcc acaacaaggc actcccggcc cccatcgaga aaaccatctc caaagccaga 1080

gggcagcccc tggagccgaa ggtctacacc atgggccctc cccgggagga gctgagcagc 1140

aggtcggtca gcctgacctg catgatcaac ggcttctacc cttccgacat ctcggtggag 1200

tgggagaaga acgggaaggc agaggacaac tacaagacca cgccgaccgt gctggacagc 1260

gacggctcct acttcctcta cagcaagctc tcagtgccca cgagtgagtg gcagcggggc 1320

gacgtcttca cctgctccgt gatgcacgag gccttgcaca accactacac gcagaagtcc 1380

atctcccgct ctccgggtaa atag 1404

<210> 98
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 98
atggacacga gggcccccac tcagctgctg gggctcctac tgctctggct cccaggtgcc 60

agatgtgctg acattgtgat gacccagact ccagcctccg tgtctgaacc tgtgggaggc 120

acagtcacca tcaagtgtca ggccagtcag aacattaata gcggcttagc ctggtatcag 180

cagaaaccag ggcagcctcc caagctcctg atctacaagg catccactct ggcatctggg 240

gtctcatcgc ggttcaaagg cagtggatct gggacagaat tcactctcac catcagcgac 300

ctggagtgtg ccgatgctgc cacttactac tgtcaaacct attattatag tagtagtagt 360

agtgataatg ctttcggcgg agggaccgag gtggtggtca aaggtgatcc agttgcacct 420

actgtcctca tcttcccacc agctgctgat caggtggcaa ctggaacagt caccatcgtg 480

tgtgtggcga ataaatactt tcccgatgtc accgtcacct gggaggtgga tggcaccacc 540

caaacaactg gcatcgagaa cagtaaaaca ccgcagaatt ctgcagattg tacctacaac 600

ctcagcagca ctctgacact gaccagcaca cagtacaaca gccacaaaga gtacacctgc 660

aaggtgaccc agggcacgac ctcagtcgtc cagagcttca ataggggtga ctgttag 717

<210> 99

<211> 1389
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 99
atggagactg ggctgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag 60

tcgttggagg agtccggggg agacctggtc aagcctgggg catccctgac actcacctgc 120

acagcttctg gattctcctt cagtagcagt tattggatat gctgggtccg ccaggctcca 180

gggaaggggc tggagtggat cgcatgtatt tatggtggta gtagtggtaa cattgcctac 240

gcgagctggg cgaaaggccg attcaccatc tccaaaacct cgtcgaccac ggtgactcta 300

caaatgacca gtctgacagc cgcggacacg gccacctatt tctgtgcgag agatattcct 360

agtgatgctt tcaccttaga cttgtggggc ccaggcaccc tggtcaccgt ctcctcaggg 420

caacctaagg ctccatcagt cttcccactg gccccctgct gcggggacac acccagctcc 480

acggtgaccc tgggctgcct ggtcaaaggc tacctcccgg agccagtgac cgtgacctgg 540

aactcgggca ccctcaccaa tggggtacgc accttcccgt ccgtccggca gtcctcaggc 600

ctctactcgc tgagcagcgt ggtgagcgtg acctcaagca gccagcccgt cacctgcaac 660

gtggcccacc cagccaccaa caccaaagtg gacaagaccg ttgcgccctc gacatgcagc 720

aagcccatgt gcccaccccc tgaactcccg gggggaccgt ctgtcttcat cttcccccca 780

aaacccaagg acaccctcat gatctcacgc acccccgagg tcacatgcgt ggtggtggac 840

gtgagccagg atgaccccga ggtgcagttc acatggtaca taaacaacga gcaggtgcgc 900

accgcccggc cgccgctacg ggagcagcag ttcaacagca cgatccgcgt ggtcagcacc 960

ctccccatcg cgcaccagga ctggctgagg ggcaaggagt tcaagtgcaa agtccacaac 1020

aaggcactcc cggcccccat cgagaaaacc atctccaaag ccagagggca gcccctggag 1080

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acctgcatga tcaacggctt ctacccttcc gacatctcgg tggagtggga gaagaacggg 1200

aaggcagagg acaactacaa gaccacgccg accgtgctgg acagcgacgg ctcctacttc 1260

ctctacagca agctctcagt gcccacgagt gagtggcagc ggggcgacgt cttcacctgc 1320

tccgtgatgc acgaggcctt gcacaaccac tacacgcaga agtccatctc ccgctctccg 1380

ggtaaatag 1389

<210> 100
<211> 720
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 100
atggacacga gggcccccac tcagctgctg gggctcctgc tgctctggct cccaggtgcc 60

acatttgccc aagtgctgac ccagactcca tcctccgtgt ctgcagctgt gggaagcaca 120

gtcaccatca attgccaggc cagtcagagt gtttataaag acaacaattt agcctggtat 180

cagcagaaac cagggcagcc tcccaagctc ctgatctaca aggcttccac tctggcatct 240

ggggtcccat cgcggttcaa aggcagtgga tctgggacac agttcactct caccatcagc 300

ggcgtgcagt gtgaagatgc tgccacttac tactgtcaag gcgaattcag ttgtggtagt 360

gctgattgta ttgctttcgg cggagggacc gaggtggtgg tcaaaggtga tccagttgca 420

cctactgtcc tcatcttccc accagctgct gatcaggtgg caactggaac agtcaccatc 480

gtgtgtgtgg cgaataaata ctttcccgat gtcaccgtca cctgggaggt ggatggcacc 540

acccaaacaa ctggcatcga gaacagtaaa acaccgcaga attctgcaga ttgtacctac 600

aacctcagca gcactctgac actgaccagc acacagtaca acagccacaa agagtacacc 660

tgcaaggtga cccagggcac gacctcagtc gtccagagct tcaatagggg tgactgttag 720

<210> 101
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 101
atggagactg ggctgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag 60

tcgttggagg agtccggggg agacctggtc aagcctgggg catccctgac actcacctgc 120

aaaggctctg gaatcgactt cagtagcggc tacggcatgt ggtgggtccg ccaggctcca 180

gggaagggac tggagtatat cggatacatt gatactggtt atggtagcac ttactacgcg 240

agctgggcga aaggccgatt caccatctcc aagacctcgt cgaccacggt gactctgcaa 300

atgaccagtc tgacagtcgc ggacacggcc acctatttct gtgcgaaagg gggcgccata 360

gacctctggg gcccagggac cctcgtcacc gtctcttcag ggcaacctaa ggctccatca 420

gtcttcccac tggcccctg ctgcggggac acacccagct ccacggtgac cctgggctgc 480

ctggtcaaag gctacctccc ggagccagtg accgtgacct ggaactcggg caccctcacc 540

aatggggtac gcaccttccc gtccgtccgg cagtcctcag gcctctactc gctgagcagc 600

gtggtgagcg tgacctcaag cagccagccc gtcacctgca acgtggccca cccagccacc 660

aacaccaaag tggacaagac cgttgcgccc tcgacatgca gcaagcccat gtgcccaccc 720

cctgaactcc cgggggggacc gtctgtcttc atcttccccc caaaacccaa ggacaccctc 780

atgatctcac gcacccccga ggtcacatgc gtggtggtgg acgtgagcca ggatgacccc 840

gaggtgcagt tcacatggta cataaacaac gagcaggtgc gcaccgcccg gccgccgcta 900

cgggagcagc agttcaacag cacgatccgc gtggtcagca ccctccccat cgcgcaccag 960

gactggctga ggggcaagga gttcaagtgc aaagtccaca acaaggcact cccggccccc 1020

atcgagaaaa ccatctccaa agccagaggg cagcccctgg agccgaaggt ctacaccatg 1080

ggccctcccc gggaggagct gagcagcagg tcggtcagcc tgacctgcat gatcaacggc 1140

ttctaccctt ccgacatctc ggtggagtgg gagaagaacg ggaaggcaga ggacaactac 1200

aagaccacgc cgaccgtgct ggacagcgac ggctcctact tcctctacag caagctctca 1260

gtgcccacga gtgagtggca gcggggcgac gtcttcacct gctccgtgat gcacgaggcc 1320

ttgcacaacc actacacgca gaagtccatc tcccgctctc cgggtaaata g 1371

<210> 102
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 102
atggacacga gggcccccac tcagctgctg gggctcctgc tgctctggct cccaggtgcc 60

acatttgcag ccgtgctgac ccagactccg gcttccacgt ctgcagctgt gggaggcaca 120

gtcaccatca attgtcagtc cagtcagagc gtgtatcgta gcaactggtt agcctggtat 180

cagcagaaac cagggcagcc tcccaagctc ctgatctatg atgtatttaa tttggcatct 240

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ggcgtgcagt gtgccgatgc tgccacttac tactgtcaag gcagttatta tagtggtaat 360

tggtacagtg ctttcggcgg agggaccgag gtggtggtca aaggtgatcc agttgcacct 420

actgtcctca tcttcccacc agctgctgat caggtggcaa ctggaacagt caccatcgtg 480

tgtgtggcga ataaatactt tcccgatgtc accgtcacct gggaggtgga tggcaccacc 540

caaacaactg gcatcgagaa cagtaaaaca ccgcagaatt ctgcagattg tacctacaac 600

ctcagcagca ctctgacact gaccagcaca cagtacaaca gccacaaaga gtacacctgc 660

aaggtgaccc agggcacgac ctcagtcgtc cagagcttca ataggggtga ctgttag 717

<210> 103
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 103

```
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Ile Pro Cys Lys Ala Ser Gly Tyr Thr Phe Pro Asp Tyr
            20                  25                  30


Asn Met Asp Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
        35                  40                  45


Gly Tyr Ile Asn Pro Asp Asn Gly Gly Thr Ile Tyr Asn Gln Lys Phe
    50                  55                  60


Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Leu Asp Ser Ser Gly Tyr Gly Tyr Tyr Ala Met Asp Tyr Trp
            100                 105                 110


Gly Gln Gly Thr Ser Val Thr Val Ser Ser
        115                 120


<210> 104
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 104
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15


Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Asn Tyr
            20                  25                  30
```

Gly Ile Ser Phe Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45

Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Asp Ser Glu Ile Pro Ala
    50   55   60

Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asp
65   70   75   80

Pro Val Glu Thr Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr
                85   90   95

Lys Asp Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105   110

<210> 105
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 105
Lys Val Met Leu Val Glu Ser Gly Gly Ala Leu Val Lys Pro Gly Gly
1   5   10   15

Ser Leu Lys Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20   25   30

Ala Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
        35   40   45

Ala Thr Ile Ser Ser Gly Gly Tyr Tyr Thr Tyr Tyr Pro Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Arg Asn Thr Leu Phe
65   70   75   80

```
Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Phe Tyr Cys
                85                  90                  95


Ala Arg Glu Asp Asp Tyr Gly Arg Tyr Ser Tyr Thr Met Asp Tyr Trp
            100                 105                 110


Gly Gln Gly Thr Ser Val Thr Val Ser Ser
        115                 120


<210> 106
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 106
Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1               5                   10                  15


Asp Gln Val Ser Ile Ser Cys Arg Cys Ser Gln Ser Leu Val His Ser
            20                  25                  30


Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35                  40                  45


Pro Gln Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
    50                  55                  60


Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80


Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
                85                  90                  95


Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Glu Leu Glu Ile Lys
```

100 105 110

<210> 107
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 107
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Arg Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Ile His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Cys Ile
35 40 45

Gly Glu Ile Tyr Pro Gly Thr Asp Asn Thr Tyr Tyr Ser Lys Lys Phe
50 55 60

Arg Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Asp Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Gly Asp Tyr Tyr Arg Gly Tyr Phe Asp Val Trp Gly Ala Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 108
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 108
Asp Val Val Met Thr Gln Thr Ser Leu Thr Leu Ser Val Thr Ile Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asn Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser
35 40 45

Pro Lys Phe Leu Ile Tyr Leu Val Ser Lys Leu Glu Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Leu Gln Ser
85 90 95

Thr His Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 109
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 109
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

```
Ser Val Lys Lys Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20                  25                  30


Tyr Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Lys Ile Tyr Pro Gly Ser Gly Asn Thr His Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80


Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
                85                  90                  95


Ala Thr Asn Tyr Tyr Gly Tyr Arg Ala Met Asn Tyr Trp Gly Gln Gly
            100                 105                 110


Ser Ser Val Thr Val Ser Ser
        115


<210> 110
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 110
Asp Ile His Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1               5                   10                  15


Glu Arg Ile Ser Leu Thr Cys Arg Ala Ser Gln Asp Ile Tyr Ile Ser
            20                  25                  30


Leu Asn Trp Phe Gln Gln Lys Pro Asp Gly Thr Ile Lys Leu Leu Ile
        35                  40                  45
```

```
Tyr Gly Thr Ser Ser Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly
    50                  55                  60


Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
65                  70                  75                  80


Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Tyr Ala Ser Ser Pro Tyr
                85                  90                  95


Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105


<210> 111
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 111
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20                  25                  30


Tyr Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Glu Ile Tyr Pro Gly Ser Gly Asn Pro Tyr Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Ser Ala Tyr
65                  70                  75                  80


Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
                85                  90                  95
```

Ala Arg Thr Ser Tyr Gly Arg Val Gly Thr Gly Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ala
115 120

<210> 112
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 112
Asn Phe Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1 5 10 15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Asn Arg Val Glu Thr Glu Asp Leu Gly Ile Tyr Phe Cys Ser Gln Ser
85 90 95

Ser His Val Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105 110

<210> 113

<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 113
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Asn Asn Gly Tyr Thr Glu Tyr Asn Gln Arg Phe
50 55 60

Lys Asp Lys Ala Thr Leu Thr Ala Asp Arg Ser Ser Thr Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Asp Ile Ile Thr Thr Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Leu Thr Val Ser Ser
115

<210> 114
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<400> 114
Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1 5 10 15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Ser
20 25 30

Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
85 90 95

Thr His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 115
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 115
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Arg Pro Gly Thr
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

```
Trp Met His Trp Val Gln Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Val Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60


Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser Ser Ala Tyr
65                  70                  75                  80


Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Asp Val Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val
            100                 105                 110


Thr Val Ser Ser
        115


<210> 116
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 116
Asp Ile Val Val Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15


Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Ser Tyr
            20                  25                  30


Gly Asn Ser Phe Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45


Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Lys Ser Gly Ile Pro Ala
    50                  55                  60
```

```
Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asn
65                  70                  75                  80


Pro Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ser Asn
                85                  90                  95


Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110


<210> 117
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 117
Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Met Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Ala
            20                  25                  30


Trp Met Asp Trp Val Arg Gln Ser Pro Glu Ala Gly Leu Glu Trp Val
        35                  40                  45


Ala Glu Ile Arg Asn Lys Ala His Asn Pro Ala Thr Tyr Tyr Ala Glu
    50                  55                  60


Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ser
65                  70                  75                  80


Val Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Gly Ile Tyr
                85                  90                  95


Tyr Cys Thr Leu Val Ala Pro Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100                 105                 110
```

Thr Ser Val Thr Val Ser Ser
        115

<210> 118
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 118
Asp Ile Val Met Ser Leu Ser Pro Ser Ser Leu Ala Val Ser Val Gly
1   5   10   15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
            20   25   30

Arg Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Ala Ser Gly Val
    50   55   60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80

Ile Ser Ser Val Lys Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln
                85   90   95

Tyr Tyr Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
            100   105   110

Lys

<210> 119

<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 119
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Met Ile Asp Pro Ser Asn Ser Glu Thr Trp Leu Asn Gln Lys Phe
50 55 60

Lys Asp Lys Ala Thr Leu Asn Val Asp Lys Ser Ser Asn Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Asp Gly Tyr Tyr Asp Tyr Trp Gly Gln Gly Thr Thr Leu
100 105 110

Thr Val Ser Ser
115

<210> 120
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<400> 120
Asn Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Ser Tyr
20 25 30

Gly Asn Ser Phe Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Leu Ala Ser Asn Val Glu Ser Gly Val Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asp
65 70 75 80

Pro Val Glu Ala Asp Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Asn Asn
85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 121
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 121
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Arg Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Pro Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

```
Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Met Ile Asp Pro Ser Asp Ser Glu Thr His Tyr Asn Gln Met Phe
    50                  55                  60


Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Asn Thr Ala Tyr
65                  70                  75                  80


Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Gln Ile Tyr Tyr Ala Tyr Asp Lys Ala Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ala
        115


<210> 122
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 122
Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val Ser Val Gly
1               5                   10                  15


Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
            20                  25                  30


Ser His Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45


Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60
```

```
Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Thr
65                  70                  75                  80


Ile Ser Ser Val Lys Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Glu
                85                  90                  95


Tyr Tyr Ser Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110


<210> 123
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 123
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20                  25                  30


Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
        35                  40                  45


Gly Asp Ile Asn Pro His Asn Gly Gly Thr Ser Phe Ile Gln Lys Phe
    50                  55                  60


Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Pro Leu Gly Arg Lys Glu Gly Phe Ala Tyr Trp Gly Gln Gly Thr
            100                 105                 110
```

Leu Val Thr Val Ser Ala
        115

<210> 124
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 124
Asp Thr Val Leu Thr Gln Ser Pro Ala Ser Leu Val Val Ser Leu Gly
1   5   10   15

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20   25   30

Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45

Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
    50   55   60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Ala Phe Thr Leu Asn Ile His
65   70   75   80

Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg
                85   90   95

Glu Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105   110

<210> 125
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 125
Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Ser Thr Phe
20 25 30

Ala Met Gly Val Gly Trp Ile Arg Gln Pro Ser Gly Lys Gly Leu Glu
35 40 45

Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ala
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn His Val
65 70 75 80

Phe Leu Lys Ile Ala Asn Val Asp Thr Ala Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Met Pro Leu Thr Phe Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Leu Thr Val Ser Ser
115

<210> 126
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 126
Asp Val Leu Leu Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly

1 5 10 15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
20 25 30

Asn Gly His Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly
85 90 95

Ser His Val Pro Phe Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 127
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 127
Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Arg Thr Phe
20 25 30

Ala Met Gly Val Gly Trp Ile Arg Gln Pro Ser Gly Lys Gly Leu Glu
35 40 45

```
Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Tyr Tyr Asn Pro Ala
    50                  55                  60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65                  70                  75                  80

Phe Leu Lys Ile Ala Asn Val Asp Thr Ala Asp Thr Ala Thr Tyr Tyr
                85                  90                  95

Cys Ala Arg Met Pro Leu Thr Phe Tyr Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Thr Leu Thr Val Ser Ser
        115
```

<210> 128
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 128

```
Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1               5                   10                  15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
            20                  25                  30

Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35                  40                  45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Thr Arg Phe Ser Gly Val Pro
    50                  55                  60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80
```

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly
85 90 95

Ser His Val Pro Phe Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 129
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 129
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Met Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Gln Gly Ser Thr Tyr Ala Trp Gly Gln Gly Thr Ser Val Thr
100 105 110

Val Ser Ser
115

<210> 130
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 130
Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro Val Thr Leu Gly
1 5 10 15

Thr Ser Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu His Ser
20 25 30

Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe Thr Leu Arg Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Ala Gln Asn
85 90 95

Leu Glu Leu Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 131
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 131
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20   25   30

Tyr Met Met Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
        35   40   45

Gly Asp Ile Asn Pro Tyr Asn Gly Gly Ser Ser Tyr Asn Pro Lys Phe
    50   55   60

Lys Gly Arg Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Gly Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
            100   105   110

<210> 132
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 132
Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Val Thr Ile Gly
1   5   10   15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
            20   25   30

Ala Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser

```
        35                  40                  45

Pro Lys Arg Leu Met Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
    50                  55                  60

Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly
                85                  90                  95

Thr His Phe Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
```

<210> 133
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 133

```
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30

Trp Met His Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45

Gly Glu Ile Asn Pro Ser Asn Gly Gly Ser Asn Tyr Asn Glu Lys Phe
    50                  55                  60

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80
```

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr His Cys
85 90 95

Lys Ser Arg Gly Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
100 105 110

<210> 134
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 134
Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Val Thr Ile Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Tyr Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser
35 40 45

Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60

Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Phe Pro His Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 135
<211> 118
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 135
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Gly Ile Ser Trp Val Lys Gln Arg Thr Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Phe Pro Arg Ser Ser Asn Thr Tyr Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Val Tyr
65 70 75 80

Met Glu Phe Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Glu Gly Gly Leu Ala Trp Phe Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ala
115

<210> 136
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 136
Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Val Thr Ile Gly
1   5   10   15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Thr
            20   25   30

Asn Gly Asn Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser
        35   40   45

Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Ile Pro
    50   55   60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Arg Ile
65   70   75   80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Leu Gln Ser
                85   90   95

Thr His Phe Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
            100   105   110

<210> 137
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 137
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Ile Thr Asp Tyr
            20   25   30

Tyr Met Met Trp Leu Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
        35   40   45

```
Gly Asp Ile Asn Pro Tyr Thr Gly Gly Thr Ser Tyr Asn Gln Lys Phe
    50                  55                  60


Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80


Leu Gln Leu His Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Gly Ala Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
            100                 105                 110


<210> 138
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 138
Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Val Thr Ile Gly
1               5                   10                  15


Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
            20                  25                  30


Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser
        35                  40                  45


Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
    50                  55                  60


Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80


Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly
```

85 90 95

Thr His Phe Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 139
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 139
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Ile Thr Asp Tyr
20 25 30

Tyr Met Met Trp Leu Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Asp Ile Asn Pro Tyr Thr Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Ala Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
100 105 110

<210> 140
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 140
Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Val Thr Ile Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser
35 40 45

Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
50 55 60

Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Phe Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 141
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 141
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

```
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20                  25                  30

Tyr Met Asn Trp Val Lys Gln Ser His Gly Arg Ser Leu Glu Leu Ile
        35                  40                  45

Gly Asp Ile Asn Pro Asn Asn Gly Gly Ser Asn Phe Asn Gln Lys Phe
    50                  55                  60

Arg Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys
                85                  90                  95

Ala Arg Met Gly Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
            100                 105                 110


<210> 142
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 142
Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Val Thr Ile Gly
1               5                   10                  15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
            20                  25                  30

Asp Gly Lys Thr Tyr Leu Asn Trp Met Phe Gln Arg Pro Gly Gln Ser
        35                  40                  45

Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser Gly Val Pro
    50                  55                  60
```

Tyr Arg Phe Thr Gly Gly Gly Ser Gly Thr Asp Phe Thr Leu Gln Ile
65 70 75 80

Ser Arg Val Glu Thr Glu Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Phe Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 143
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 143
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Ile His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Tyr Ile
35 40 45

Gly Glu Ile Tyr Pro Gly Ser Gly Asn Thr Tyr Tyr Asn Gly Lys Phe
50 55 60

Arg Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Gly Ser Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val
100 105 110

Ser Ser

<210> 144
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 144
Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Val Thr Ile Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
20 25 30

Asn Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Ser Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Leu Val Ser Lys Leu Glu Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Leu
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Val Gln Gly
85 90 95

Thr His Phe Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 145
<211> 139
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 145
Met Asp Trp Leu Trp Asn Leu Leu Phe Leu Met Val Val Ala Gln Ser
1   5   10   15

Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys
            20   25   30

Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35   40   45

Thr Asp Tyr Ala Met Asn Trp Val Lys Gln Ala Pro Gly Asn Gly Leu
    50   55   60

Lys Trp Met Gly Trp Ile Asn Thr Gln Thr Gly Lys Pro Thr Tyr Ala
65   70   75   80

Asp Asp Phe Lys Gln Arg Phe Val Phe Ser Leu Glu Thr Ser Ala Arg
                85   90   95

Thr Thr Tyr Leu Gln Ile Asn Asn Leu Asn Ile Glu Asp Thr Ala Thr
            100   105   110

Tyr Phe Cys Thr Arg Leu Gly Thr Gly Asn Thr Lys Gly Phe Ala Tyr
        115   120   125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
    130   135

<210> 146
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<400> 146
Met Glu Ser Gln Thr His Val Leu Ile Ser Leu Leu Leu Cys Val Ser
1   5   10   15

Gly Thr Cys Gly Asp Ile Leu Ile Asn Gln Ser Pro Ala Ser Leu Thr
            20   25   30

Val Ser Ala Gly Glu Arg Val Thr Met Ser Cys Lys Ser Ser Gln Ser
        35   40   45

Leu Leu Tyr Ser Glu Asn Asn Gln Asp Tyr Leu Ala Trp Tyr Gln Gln
    50   55   60

Lys Pro Gly Gln Phe Pro Lys Leu Leu Ile Tyr Gly Ala Ser Asn Arg
65   70   75   80

His Thr Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
                85   90   95

Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr
            100   105   110

Tyr Cys Glu Gln Thr Tyr Arg Tyr Pro Phe Thr Phe Gly Ser Gly Thr
        115   120   125

Lys Leu Glu Ile Lys
    130

<210> 147
<211> 138
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 147

```
Met Glu Leu Glu Leu Ser Leu Ile Phe Ile Phe Ser Leu Leu Lys Asp
1               5                   10                  15


Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Ser Leu Val Gln
            20                  25                  30


Pro Gly Gly Ser Leu Lys Leu Ser Cys Val Ala Ser Gly Tyr Thr Phe
        35                  40                  45


Ser Asn Tyr Trp Met Asp Trp Val Arg Gln Ser Pro Gly Lys Ser Leu
    50                  55                  60


Glu Trp Ile Gly Glu Ile Asn Thr Asp Gly Arg Arg Thr Asn Tyr Ala
65                  70                  75                  80


Pro Ser Ile Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser
                85                  90                  95


Thr Leu Tyr Leu Gln Met Ser Asn Val Lys Ser Asp Asp Thr Ala Ile
            100                 105                 110


Tyr Tyr Cys Thr Ile Leu Arg Val Tyr Pro His Tyr Phe Asp Tyr Trp
        115                 120                 125


Gly Gln Gly Val Met Val Thr Val Ser Ser
    130                 135


<210> 148
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 148
Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Met Leu Trp Ile Gln
1               5                   10                  15
```

```
Glu Ala Arg Gly Asp Val Val Met Thr Gln Thr Pro Pro Ser Leu Ser
            20                  25                  30


Val Ala Ile Gly Gln Ser Val Ser Ile Ser Cys Lys Ser Ser Gln Ser
        35                  40                  45


Leu Val Tyr Ser Asp Gly Glu Thr Tyr Leu His Trp Phe Leu Gln Ser
    50                  55                  60


Pro Gly Arg Ser Pro Lys Arg Leu Ile Tyr His Val Ser Asn Leu Gly
65                  70                  75                  80


Ser Gly Val Pro Asp Arg Phe Ser Gly Thr Gly Ser Leu Thr Asp Phe
                85                  90                  95


Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr
            100                 105                 110


Cys Ala Gln Thr Thr His Phe Pro Pro Thr Phe Gly Ala Gly Thr Lys
        115                 120                 125


Leu Glu Leu Lys
    130


<210> 149
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 149
Met Ala Val Leu Val Leu Leu Leu Cys Leu Val Thr Phe Pro Ser Cys
1               5                   10                  15


Ala Leu Ser Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Gln
            20                  25                  30
```

```
Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu
        35                  40                  45

Thr Ser Asn Ser Val Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60

Glu Trp Met Gly Ala Ile Trp Ser Gly Gly Ser Thr Asp Tyr Asn Ser
65                  70                  75                  80

Ala Leu Lys Ser Arg Leu Ser Ile Ser Arg Asp Thr Ser Lys Ser Gln
                85                  90                  95

Val Phe Leu Lys Met Asn Ser Leu Gln Thr Glu Asp Thr Ala Ile Tyr
            100                 105                 110

Phe Cys Thr Arg Ser His Trp Glu Pro Phe Asp Tyr Trp Gly Gln Gly
        115                 120                 125

Val Met Val Thr Val Ser Ser
    130                 135


<210> 150
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 150
Met Glu Ser Gln Thr Gln Ala Leu Ile Ser Leu Leu Leu Trp Val Tyr
1               5                   10                  15

Gly Thr Cys Gly Asp Ile Val Met Thr Gln Ser Pro Phe Ser Leu Ala
            20                  25                  30

Val Ser Glu Gly Glu Met Val Thr Ile Asn Cys Lys Ser Ser Gln Gly
```

```
        35                  40                  45

Leu Leu Ser Ser Gly Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
    50                  55                  60

Arg Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Tyr Ala Ser Thr Arg
65                  70                  75                  80

Gln Ser Gly Val Pro Asp Arg Phe Ile Gly Gly Gly Ser Gly Thr Asp
                85                  90                  95

Phe Thr Leu Thr Ile Ser Asp Val Gln Ala Glu Asp Leu Ala Asp Tyr
            100                 105                 110

Tyr Cys Leu Gln His Tyr Ser Tyr Pro Pro Thr Phe Gly Ser Gly Thr
        115                 120                 125

Lys Leu Glu Ile Lys
    130


<210> 151
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 151
Met Ala Val Leu Val Leu Leu Leu Cys Leu Val Thr Phe Pro Ser Cys
1               5                   10                  15

Ala Leu Ser Gln Val Gln Leu Arg Glu Ser Gly Pro Gly Leu Val Gln
            20                  25                  30

Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu
        35                  40                  45
```

```
Thr Ser Asn Ser Val Thr Trp Val Arg Gln Pro Pro Gly Lys Gly Leu
    50                  55                  60

Glu Trp Met Gly Ala Ile Trp Ser Asp Gly Ser Thr Asp Tyr Asn Ser
65                  70                  75                  80

Thr Leu Lys Ser Arg Leu Ser Ile Ser Arg Asp Thr Ser Lys Ser Gln
                85                  90                  95

Val Phe Leu Lys Met Ser Ser Leu Gln Thr Glu Asp Thr Ala Ile Tyr
            100                 105                 110

Phe Cys Thr Arg Ser His Trp Glu Pro Phe Asp Tyr Trp Gly Gln Gly
        115                 120                 125

Val Met Val Thr Val Ser Ser
    130                 135


<210> 152
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 152
Met Glu Ser Gln Thr Gln Ala Leu Ile Ser Leu Leu Leu Trp Val Tyr
1               5                   10                  15

Gly Thr Cys Gly Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Ala
            20                  25                  30

Val Ser Glu Gly Glu Thr Val Thr Met Asn Cys Lys Ser Ser Gln Ser
        35                  40                  45

Leu Phe Ser Ser Gly Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
    50                  55                  60
```

```
Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Tyr Ala Ser Thr Arg
65                  70                  75                  80


Gln Ser Gly Val Pro Asp Arg Phe Ile Gly Ser Gly Ser Gly Thr Asp
                85                  90                  95


Phe Thr Leu Thr Ile Ser Asp Val Gln Thr Glu Asp Leu Ala Asp Tyr
            100                 105                 110


Tyr Cys Leu Gln His Tyr Asn Tyr Pro Pro Thr Phe Gly Ser Gly Thr
        115                 120                 125


Lys Leu Glu Ile Lys
    130


<210> 153
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 153
Met Asp Leu Arg Leu Thr Tyr Val Phe Ile Val Ala Ile Leu Lys Gly
1               5                   10                  15


Val Leu Cys Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln
            20                  25                  30


Pro Gly Met Ser Val Lys Leu Ser Cys Ala Thr Ser Gly Phe Ile Phe
        35                  40                  45


Ser Asp Tyr Trp Met Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60


Glu Trp Val Ala Glu Ile Arg Asn Lys Ala Asn Asn Tyr Ala Thr Tyr
65                  70                  75                  80
```

Tyr Gly Lys Ser Met Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
85 90 95

Lys Ser Ile Val Tyr Leu Gln Val Asn Ser Ile Arg Ser Glu Asp Thr
100 105 110

Ala Ile Tyr Tyr Cys Ala Pro Asn Phe Asp Tyr Trp Gly Gln Gly Val
115 120 125

Met Val Thr Val Ser Ser
130

<210> 154
<211> 131
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 154
Met Ser Pro Val Gln Ser Leu Phe Leu Leu Leu Leu Trp Ile Leu Gly
1 5 10 15

Thr His Gly Asp Val Val Leu Thr Gln Thr Pro Pro Thr Leu Ser Ala
20 25 30

Thr Ile Gly Gln Ser Val Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
35 40 45

Leu His Ser Thr Gly Asn Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro
50 55 60

Gly Gln Pro Pro Gln Leu Leu Ile Tyr Leu Val Ser Arg Leu Glu Ser
65 70 75 80

Gly Val Pro Asn Arg Phe Ser Ala Ser Gly Ser Gly Thr Asp Phe Thr

85 90 95

Leu Lys Ile Ser Gly Ile Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys
100 105 110

Val Gln Ser Ser His Thr Pro Tyr Thr Phe Gly Thr Gly Thr Lys Leu
115 120 125

Glu Leu Lys
130

<210> 155
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 155
Met Asp Ile Arg Leu Ser Leu Val Phe Leu Val Leu Phe Met Lys Gly
1 5 10 15

Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
20 25 30

Pro Gly Arg Ser Leu Lys Leu Ser Cys Ala Ala Ser Arg Phe Thr Phe
35 40 45

Ser Asp Tyr Asn Met Ala Trp Val Arg Gln Ala Pro Lys Lys Gly Leu
50 55 60

Glu Trp Val Ala Thr Ile Tyr His Asp Asp Ser Gly Ser Tyr Tyr Arg
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asn Asn Ala Lys Ser
85 90 95

```
Thr Leu Tyr Leu Gln Met Asp Ser Leu Arg Ser Glu Asp Met Ala Thr
            100                 105                 110


Tyr Tyr Cys Ala Arg His Asn Asn Gly Phe Asp Tyr Trp Gly Gln Gly
        115                 120                 125


Val Met Val Thr Val Ala Ser
    130                 135


<210> 156
<211> 131
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 156
Met Lys Trp Pro Val Arg Leu Leu Val Leu Phe Phe Trp Ile Pro Ala
1               5                   10                  15


Ser Gly Gly Asp Val Val Met Thr Gln Thr Pro Val Ser Leu Pro Val
            20                  25                  30


Arg Leu Gly Gly Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
        35                  40                  45


Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro
    50                  55                  60


Gly Gln Ser Pro Gln Leu Leu Ile Asn Arg Val Ser Asn Arg Phe Ser
65                  70                  75                  80


Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
                85                  90                  95


Leu Lys Ile Asn Arg Val Glu Pro Glu Asp Leu Gly Asp Tyr Tyr Cys
            100                 105                 110
```

Leu Gln Ser Thr His Phe Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu
115 120 125

Glu Thr Lys
130

<210> 157
<211> 136
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 157
Met Asp Ile Arg Leu Ser Leu Gly Phe Leu Val Leu Phe Ile Lys Gly
1 5 10 15

Asp Gln Cys Ala Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
20 25 30

Pro Gly Arg Ser Leu Lys Leu Ser Cys Ala Ala Ser Arg Ile Thr Phe
35 40 45

Thr Asp Tyr Tyr Met Ala Trp Val Arg Gln Ala Pro Thr Lys Gly Leu
50 55 60

Glu Trp Val Ala Thr Ile Ser Ser Asp Gly Gly Asp Thr Phe Tyr Arg
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser
85 90 95

Thr Leu Tyr Leu Gln Met Val Ser Leu Arg Ser Glu Asp Thr Ala Thr
100 105 110

Tyr Tyr Cys Ser Thr Asp Arg Gly Ala Gln Phe Gly Tyr Trp Gly Gln
115 120 125

Gly Thr Leu Val Thr Val Ser Ser
    130   135

<210> 158
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 158
Met Ala Pro Val Gln Leu Leu Gly Leu Leu Leu Ile Trp Leu Pro Ala
1   5   10   15

Met Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Phe Leu Ser Ala
            20   25   30

Ser Val Gly Asp Arg Val Ser Ile Asn Cys Lys Ala Ser Gln Asn Val
        35   40   45

His Glu Asn Leu Asn Trp Tyr Gln Gln Lys Leu Gly Glu Ala Pro Lys
    50   55   60

Arg Leu Ile Tyr Asn Thr Asn Asn Leu Gln Thr Gly Ile Pro Ser Arg
65   70   75   80

Phe Ser Gly Ser Gly Ser Gly Ala Asp Tyr Thr Leu Thr Ile Ser Ser
                85   90   95

Leu Gln Pro Glu Asp Phe Ala Thr Tyr Phe Cys Leu Gln His Asn Ala
            100   105   110

Phe Pro Tyr Thr Phe Gly Pro Gly Thr Lys Leu Glu Leu Lys
        115   120   125

<210> 159

<211> 455
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 159
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Phe Lys Gly
1 5 10 15

Val Gln Cys Gln Glu Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys
20 25 30

Pro Gly Ala Ser Leu Thr Leu Thr Cys Thr Ala Ser Gly Phe Ser Phe
35 40 45

Asn Lys Asn Tyr Trp Met Cys Trp Val Arg Gln Ala Pro Gly Lys Gly
50 55 60

Leu Glu Trp Ile Gly Cys Ile Tyr Asn Gly Asp Gly Asn Thr Tyr Tyr
65 70 75 80

Ala Ser Trp Val Asn Gly Arg Phe Thr Ile Ser Lys Thr Ser Ser Thr
85 90 95

Thr Val Thr Leu Gln Met Thr Ser Leu Thr Val Ala Asp Thr Ala Ile
100 105 110

Tyr Phe Cys Ala Arg Leu Leu Asn Met Trp Gly Pro Gly Thr Leu Val
115 120 125

Thr Val Ser Ser Gly Gln Pro Lys Ala Pro Ser Val Phe Pro Leu Ala
130 135 140

Pro Cys Cys Gly Asp Thr Pro Ser Ser Thr Val Thr Leu Gly Cys Leu
145 150 155 160

```
Val Lys Gly Tyr Leu Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly
                165                 170                 175

Thr Leu Thr Asn Gly Val Arg Thr Phe Pro Ser Val Arg Gln Ser Ser
            180                 185                 190

Gly Leu Tyr Ser Leu Ser Ser Val Val Ser Val Thr Ser Ser Ser Gln
        195                 200                 205

Pro Val Thr Cys Asn Val Ala His Pro Ala Thr Asn Thr Lys Val Asp
    210                 215                 220

Lys Thr Val Ala Pro Ser Thr Cys Ser Lys Pro Met Cys Pro Pro Pro
225                 230                 235                 240

Glu Leu Pro Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys
                245                 250                 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
            260                 265                 270

Asp Val Ser Gln Asp Asp Pro Glu Val Gln Phe Thr Trp Tyr Ile Asn
        275                 280                 285

Asn Glu Gln Val Arg Thr Ala Arg Pro Pro Leu Arg Glu Gln Gln Phe
    290                 295                 300

Asn Ser Thr Ile Arg Val Val Ser Thr Leu Pro Ile Ala His Gln Asp
305                 310                 315                 320

Trp Leu Arg Gly Lys Glu Phe Lys Cys Lys Val His Asn Lys Ala Leu
                325                 330                 335

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Arg Gly Gln Pro Leu
            340                 345                 350

Glu Pro Lys Val Tyr Thr Met Gly Pro Pro Arg Glu Glu Leu Ser Ser
        355                 360                 365
```

```
Arg Ser Val Ser Leu Thr Cys Met Ile Asn Gly Phe Tyr Pro Ser Asp
    370                 375                 380

Ile Ser Val Glu Trp Glu Lys Asn Gly Lys Ala Glu Asp Asn Tyr Lys
385                 390                 395                 400

Thr Thr Pro Thr Val Leu Asp Ser Asp Gly Ser Tyr Phe Leu Tyr Ser
                405                 410                 415

Lys Leu Ser Val Pro Thr Ser Glu Trp Gln Arg Gly Asp Val Phe Thr
            420                 425                 430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
        435                 440                 445

Ile Ser Arg Ser Pro Gly Lys
    450                 455


<210> 160
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 160
Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
1               5                   10                  15

Leu Pro Gly Ala Arg Cys Ala Asp Ile Val Met Thr Gln Thr Pro Ala
            20                  25                  30

Ser Val Glu Ala Ala Val Gly Gly Thr Val Thr Ile Lys Cys Gln Ala
        35                  40                  45

Ser Glu Ser Ile Gly Asn Ala Leu Ala Trp Tyr Gln Gln Lys Pro Gly
```

```
    50                  55                  60

Gln Pro Pro Lys Leu Leu Ile Tyr Thr Ala Ala Thr Leu Ala Ser Gly
65                  70                  75                  80

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu
                85                  90                  95

Thr Ile Ser Gly Val Gln Cys Asp Asp Ala Ala Thr Tyr Tyr Cys Gln
            100                 105                 110

Ser Tyr Tyr Phe Thr Ser Val Ser Ser Tyr Gly Asn Ala Phe Gly Gly
        115                 120                 125

Gly Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu
    130                 135                 140

Ile Phe Pro Pro Ala Ala Asp Gln Val Ala Thr Gly Thr Val Thr Ile
145                 150                 155                 160

Val Cys Val Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu
                165                 170                 175

Val Asp Gly Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro
            180                 185                 190

Gln Asn Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu
        195                 200                 205

Thr Ser Thr Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr
    210                 215                 220

Gln Gly Thr Thr Ser Val Val Gln Ser Phe Asn Arg Gly Asp Cys
225                 230                 235

<210> 161
<211> 466
<212> PRT
```

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 161
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1 5 10 15

Val Gln Cys Gln Ser Leu Glu Glu Ser Gly Gly Asp Leu Val Lys Pro
20 25 30

Gly Ala Ser Leu Thr Leu Thr Cys Arg Val Ser Gly Phe Ser Phe Ser
35 40 45

Ser Ser Tyr Tyr Met Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Ile Ala Cys Ile Gly Thr Thr Arg Gly Ser Thr Tyr Tyr Ala
65 70 75 80

Thr Trp Ala Lys Gly Arg Phe Thr Ile Ser Lys Ile Ser Ser Thr Thr
85 90 95

Val Thr Leu Gln Met Thr Ser Leu Thr Asp Ala Asp Thr Ala Thr Tyr
100 105 110

Phe Cys Ala Arg Asp Ala Thr Gly Tyr Arg Ile Asn Thr Ile Gly Leu
115 120 125

Tyr Phe Asn Leu Trp Gly Pro Gly Thr Leu Val Thr Val Ser Ser Gly
130 135 140

Gln Pro Lys Ala Pro Ser Val Phe Pro Leu Ala Pro Cys Cys Gly Asp
145 150 155 160

Thr Pro Ser Ser Thr Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Leu
165 170 175

```
Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Thr Leu Thr Asn Gly
            180                 185                 190

Val Arg Thr Phe Pro Ser Val Arg Gln Ser Ser Gly Leu Tyr Ser Leu
        195                 200                 205

Ser Ser Val Val Ser Val Thr Ser Ser Ser Gln Pro Val Thr Cys Asn
    210                 215                 220

Val Ala His Pro Ala Thr Asn Thr Lys Val Asp Lys Thr Val Ala Pro
225                 230                 235                 240

Ser Thr Cys Ser Lys Pro Met Cys Pro Pro Pro Glu Leu Pro Gly Gly
                245                 250                 255

Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
            260                 265                 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Asp
        275                 280                 285

Asp Pro Glu Val Gln Phe Thr Trp Tyr Ile Asn Asn Glu Gln Val Arg
    290                 295                 300

Thr Ala Arg Pro Pro Leu Arg Glu Gln Gln Phe Asn Ser Thr Ile Arg
305                 310                 315                 320

Val Val Ser Thr Leu Pro Ile Ala His Gln Asp Trp Leu Arg Gly Lys
                325                 330                 335

Glu Phe Lys Cys Lys Val His Asn Lys Ala Leu Pro Ala Pro Ile Glu
            340                 345                 350

Lys Thr Ile Ser Lys Ala Arg Gly Gln Pro Leu Glu Pro Lys Val Tyr
        355                 360                 365
```

```
Thr Met Gly Pro Pro Arg Glu Glu Leu Ser Ser Arg Ser Val Ser Leu
    370                 375                 380

Thr Cys Met Ile Asn Gly Phe Tyr Pro Ser Asp Ile Ser Val Glu Trp
385                 390                 395                 400

Glu Lys Asn Gly Lys Ala Glu Asp Asn Tyr Lys Thr Thr Pro Thr Val
                405                 410                 415

Leu Asp Ser Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Pro
            420                 425                 430

Thr Ser Glu Trp Gln Arg Gly Asp Val Phe Thr Cys Ser Val Met His
        435                 440                 445

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Ile Ser Arg Ser Pro
    450                 455                 460

Gly Lys
465
```

<210> 162
<211> 237
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 162

```
Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
1               5                   10                  15

Leu Pro Gly Ala Arg Cys Ala Phe Glu Leu Thr Gln Thr Pro Ser Ser
            20                  25                  30

Val Glu Ala Ala Val Gly Gly Thr Pro Thr Ile Lys Cys Gln Ala Ser
        35                  40                  45
```

```
Gln Thr Ile Tyr Ser Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Gly Gln
    50                  55                  60

Pro Pro Lys Leu Leu Ile Tyr Glu Ala Ser Lys Leu Ala Ser Gly Val
65                  70                  75                  80

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr
                85                  90                  95

Ile Ser Asp Leu Glu Cys Ala Asp Ala Ala Thr Tyr Tyr Cys Gln Ser
            100                 105                 110

Tyr His Gly Thr Ala Ser Thr Glu Tyr Asn Thr Phe Gly Gly Gly Thr
        115                 120                 125

Glu Val Val Val Arg Gly Asp Pro Val Ala Pro Thr Val Leu Ile Phe
    130                 135                 140

Pro Pro Ala Ala Asp Gln Val Ala Thr Gly Thr Val Thr Ile Val Cys
145                 150                 155                 160

Val Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu Val Asp
                165                 170                 175

Gly Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro Gln Asn
            180                 185                 190

Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu Thr Ser
        195                 200                 205

Thr Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr Gln Gly
    210                 215                 220

Thr Thr Ser Val Val Gln Ser Phe Asn Arg Gly Asp Cys
225                 230                 235
```

<210> 163

<211> 466
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 163
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1 5 10 15

Val Gln Cys Gln Gln Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
20 25 30

Pro Gly Ala Ala Leu Thr Phe Thr Cys Thr Ala Ser Gly Phe Ser Phe
35 40 45

Ser Gly Asn Tyr Trp Ile Cys Trp Val Arg Gln Ala Pro Gly Lys Gly
50 55 60

Leu Glu Trp Ile Ala Cys Ile Gly Thr Ile Thr Ser Arg Thr Tyr Tyr
65 70 75 80

Ala Ser Trp Ala Lys Gly Arg Phe Thr Ile Ser Lys Thr Ser Ser Thr
85 90 95

Thr Val Thr Leu Gln Met Thr Ser Leu Thr Ala Ala Asp Thr Ala Thr
100 105 110

Tyr Phe Cys Ala Arg Gly Ala Val Val Ser Ser Gly Asn Ala Pro Tyr
115 120 125

Tyr Phe Thr Leu Trp Gly Pro Gly Thr Leu Val Thr Val Ser Ser Gly
130 135 140

Gln Pro Lys Ala Pro Ser Val Phe Pro Leu Ala Pro Cys Cys Gly Asp
145 150 155 160

```
Thr Pro Ser Ser Thr Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Leu
                165                 170                 175

Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Thr Leu Thr Asn Gly
            180                 185                 190

Val Arg Thr Phe Pro Ser Val Arg Gln Ser Ser Gly Leu Tyr Ser Leu
        195                 200                 205

Ser Ser Val Val Ser Val Thr Ser Ser Ser Gln Pro Val Thr Cys Asn
    210                 215                 220

Val Ala His Pro Ala Thr Asn Thr Lys Val Asp Lys Thr Val Ala Pro
225                 230                 235                 240

Ser Thr Cys Ser Lys Pro Met Cys Pro Pro Pro Glu Leu Pro Gly Gly
                245                 250                 255

Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
            260                 265                 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Asp
        275                 280                 285

Asp Pro Glu Val Gln Phe Thr Trp Tyr Ile Asn Asn Glu Gln Val Arg
    290                 295                 300

Thr Ala Arg Pro Pro Leu Arg Glu Gln Gln Phe Asn Ser Thr Ile Arg
305                 310                 315                 320

Val Val Ser Thr Leu Pro Ile Ala His Gln Asp Trp Leu Arg Gly Lys
                325                 330                 335

Glu Phe Lys Cys Lys Val His Asn Lys Ala Leu Pro Ala Pro Ile Glu
            340                 345                 350

Lys Thr Ile Ser Lys Ala Arg Gly Gln Pro Leu Glu Pro Lys Val Tyr
        355                 360                 365
```

Thr Met Gly Pro Pro Arg Glu Glu Leu Ser Ser Arg Ser Val Ser Leu
370 375 380

Thr Cys Met Ile Asn Gly Phe Tyr Pro Ser Asp Ile Ser Val Glu Trp
385 390 395 400

Glu Lys Asn Gly Lys Ala Glu Asp Asn Tyr Lys Thr Thr Pro Thr Val
405 410 415

Leu Asp Ser Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Pro
420 425 430

Thr Ser Glu Trp Gln Arg Gly Asp Val Phe Thr Cys Ser Val Met His
435 440 445

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Ile Ser Arg Ser Pro
450 455 460

Gly Lys
465

<210> 164
<211> 236
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 164
Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Pro Gly Ala Arg Cys Ala Phe Glu Leu Thr Gln Thr Pro Ser Ser
20 25 30

Val Glu Ala Ala Val Gly Gly Thr Val Thr Ile Lys Cys Gln Ala Ser

```
        35                  40                  45

Gln Ser Ile Ser Ser Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Gly Gln
    50                  55                  60

Pro Pro Lys Leu Leu Ile Tyr Arg Ala Ser Thr Leu Glu Ser Gly Val
65                  70                  75                  80

Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
                85                  90                  95

Ile Ser Asp Leu Glu Cys Ala Asp Ala Ala Thr Tyr Phe Cys Gln Ser
            100                 105                 110

Tyr Tyr Gly Val Thr Phe Ser Gly Phe Ala Phe Gly Gly Gly Thr Glu
        115                 120                 125

Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Ile Phe Pro
    130                 135                 140

Pro Ala Ala Asp Gln Val Ala Thr Gly Thr Val Thr Ile Val Cys Val
145                 150                 155                 160

Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu Val Asp Gly
                165                 170                 175

Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro Gln Asn Ser
            180                 185                 190

Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu Thr Ser Thr
        195                 200                 205

Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr Gln Gly Thr
    210                 215                 220

Thr Ser Val Val Gln Ser Phe Asn Arg Gly Asp Cys
225                 230                 235
```

<210> 165
<211> 460
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 165
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1 5 10 15

Val Gln Cys Gln Ser Leu Glu Glu Ser Gly Gly Asp Leu Val Lys Pro
20 25 30

Gly Ala Ser Leu Thr Leu Thr Cys Lys Ala Ser Gly Ile Asp Phe Asn
35 40 45

Asn Tyr Trp Ile Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
50 55 60

Trp Ile Ala Cys Ile Tyr Val Gly Ile Thr Gly Arg Thr Trp Tyr Ala
65 70 75 80

Asn Trp Ala Lys Gly Arg Phe Thr Ile Ser Lys Ala Ser Ser Thr Val
85 90 95

Asp Leu Lys Met Thr Ser Leu Thr Ala Ala Asp Thr Ala Thr Tyr Phe
100 105 110

Cys Ala Arg Asn Gly Asp Gly Gly Ile Tyr Ala Leu Asn Leu Trp Gly
115 120 125

Pro Gly Thr Leu Val Thr Val Ser Ser Gly Gln Pro Lys Ala Pro Ser
130 135 140

Val Phe Pro Leu Ala Pro Cys Cys Gly Asp Thr Pro Ser Ser Thr Val
145 150 155 160

```
Thr Leu Gly Cys Leu Val Lys Gly Tyr Leu Pro Glu Pro Val Thr Val
                165                 170                 175

Thr Trp Asn Ser Gly Thr Leu Thr Asn Gly Val Arg Thr Phe Pro Ser
            180                 185                 190

Val Arg Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Ser Val
        195                 200                 205

Thr Ser Ser Ser Gln Pro Val Thr Cys Asn Val Ala His Pro Ala Thr
    210                 215                 220

Asn Thr Lys Val Asp Lys Thr Val Ala Pro Ser Thr Cys Ser Lys Pro
225                 230                 235                 240

Met Cys Pro Pro Pro Glu Leu Pro Gly Gly Pro Ser Val Phe Ile Phe
                245                 250                 255

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
            260                 265                 270

Thr Cys Val Val Val Asp Val Ser Gln Asp Asp Pro Glu Val Gln Phe
        275                 280                 285

Thr Trp Tyr Ile Asn Asn Glu Gln Val Arg Thr Ala Arg Pro Pro Leu
    290                 295                 300

Arg Glu Gln Gln Phe Asn Ser Thr Ile Arg Val Val Ser Thr Leu Pro
305                 310                 315                 320

Ile Ala His Gln Asp Trp Leu Arg Gly Lys Glu Phe Lys Cys Lys Val
                325                 330                 335

His Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
            340                 345                 350
```

```
Arg Gly Gln Pro Leu Glu Pro Lys Val Tyr Thr Met Gly Pro Pro Arg
        355                 360                 365

Glu Glu Leu Ser Ser Arg Ser Val Ser Leu Thr Cys Met Ile Asn Gly
    370                 375                 380

Phe Tyr Pro Ser Asp Ile Ser Val Glu Trp Glu Lys Asn Gly Lys Ala
385                 390                 395                 400

Glu Asp Asn Tyr Lys Thr Thr Pro Thr Val Leu Asp Ser Asp Gly Ser
                405                 410                 415

Tyr Phe Leu Tyr Ser Lys Leu Ser Val Pro Thr Ser Glu Trp Gln Arg
            420                 425                 430

Gly Asp Val Phe Thr Cys Ser Val Met His Glu Ala Leu His Asn His
        435                 440                 445

Tyr Thr Gln Lys Ser Ile Ser Arg Ser Pro Gly Lys
    450                 455                 460
```

<210> 166
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 166

```
Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
1               5                   10                  15

Leu Pro Gly Ala Thr Phe Ala Gln Val Leu Thr Gln Thr Ala Ser Ser
            20                  25                  30

Val Ser Ala Ala Val Gly Gly Thr Val Thr Ile Ser Cys Gln Ser Ser
        35                  40                  45
```

```
Gln Ser Val Tyr Asn Asn Asn Trp Leu Ala Trp Tyr Gln Gln Lys Pro
    50                  55                  60

Gly Gln Pro Pro Lys Leu Leu Ile Tyr Arg Ala Ser Thr Leu Thr Ser
65                  70                  75                  80

Gly Val Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Gln Phe Thr
                85                  90                  95

Leu Thr Ile Ser Asp Leu Glu Cys Asp Asp Ala Ala Thr Tyr Tyr Cys
            100                 105                 110

Ala Gly Gly Tyr Ser Gly Asn Ile Tyr Val Asn Asp Phe Gly Gly Gly
        115                 120                 125

Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Ile
    130                 135                 140

Phe Pro Pro Ala Ala Asp Gln Val Ala Thr Gly Thr Val Thr Ile Val
145                 150                 155                 160

Cys Val Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu Val
                165                 170                 175

Asp Gly Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro Gln
            180                 185                 190

Asn Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu Thr
        195                 200                 205

Ser Thr Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr Gln
    210                 215                 220

Gly Thr Thr Ser Val Val Gln Ser Phe Asn Arg Gly Asp Cys
225                 230                 235
```

<210> 167

<211> 459
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 167
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1 5 10 15

Val Gln Cys Gln Glu Gln Leu Glu Glu Ser Gly Gly Asp Leu Val Lys
20 25 30

Pro Gly Gly Ser Leu Thr Leu Thr Cys Lys Ala Ser Gly Phe Ser Phe
35 40 45

Ser Asn Thr Tyr Trp Ala Cys Trp Val Arg Gln Ala Pro Gly Lys Gly
50 55 60

Leu Glu Trp Ile Ala Cys Met Asn Pro Ala Ser Ser Gly Ser Ser Tyr
65 70 75 80

Tyr Ala Ser Trp Ala Lys Gly Arg Phe Thr Ile Ser Lys Thr Ser Ser
85 90 95

Thr Thr Val Thr Leu His Met Pro Ser Leu Thr Ala Ala Asp Thr Ala
100 105 110

Thr Tyr Phe Cys Ala Lys Trp Asp Thr Ala Phe Asp Val Trp Gly Pro
115 120 125

Gly Thr Leu Val Thr Val Ser Ser Gly Gln Pro Lys Ala Pro Ser Val
130 135 140

Phe Pro Leu Ala Pro Cys Cys Gly Asp Thr Pro Ser Ser Thr Val Thr
145 150 155 160

```
Leu Gly Cys Leu Val Lys Gly Tyr Leu Pro Glu Pro Val Thr Val Thr
                165                 170                 175

Trp Asn Ser Gly Thr Leu Thr Asn Gly Val Arg Thr Phe Pro Ser Val
            180                 185                 190

Arg Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Ser Val Thr
        195                 200                 205

Ser Ser Ser Gln Pro Val Thr Cys Asn Val Ala His Pro Ala Thr Asn
    210                 215                 220

Thr Lys Val Asp Lys Thr Val Ala Pro Ser Thr Cys Ser Lys Pro Met
225                 230                 235                 240

Cys Pro Pro Pro Glu Leu Pro Gly Gly Pro Ser Val Phe Ile Phe Pro
                245                 250                 255

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
            260                 265                 270

Cys Val Val Val Asp Val Ser Gln Asp Asp Pro Glu Val Gln Phe Thr
        275                 280                 285

Trp Tyr Ile Asn Asn Glu Gln Val Arg Thr Ala Arg Pro Pro Leu Arg
    290                 295                 300

Glu Gln Gln Phe Asn Ser Thr Ile Arg Val Val Ser Thr Leu Pro Ile
305                 310                 315                 320

Ala His Gln Asp Trp Leu Arg Gly Lys Glu Phe Lys Cys Lys Val His
                325                 330                 335

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Arg
            340                 345                 350

Gly Gln Pro Leu Glu Pro Lys Val Tyr Thr Met Gly Pro Pro Arg Glu
        355                 360                 365
```

```
Glu Leu Ser Ser Arg Ser Val Ser Leu Thr Cys Met Ile Asn Gly Phe
    370                 375                 380

Tyr Pro Ser Asp Ile Ser Val Glu Trp Glu Lys Asn Gly Lys Ala Glu
385                 390                 395                 400

Asp Asn Tyr Lys Thr Thr Pro Thr Val Leu Asp Ser Asp Gly Ser Tyr
                405                 410                 415

Phe Leu Tyr Ser Lys Leu Ser Val Pro Thr Ser Glu Trp Gln Arg Gly
            420                 425                 430

Asp Val Phe Thr Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
        435                 440                 445

Thr Gln Lys Ser Ile Ser Arg Ser Pro Gly Lys
    450                 455


<210> 168
<211> 237
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 168
Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
1               5                   10                  15

Leu Pro Gly Ala Arg Cys Ala Asp Val Val Met Thr Gln Thr Pro Ser
            20                  25                  30

Ser Val Glu Ala Ala Val Gly Gly Thr Val Thr Ile Lys Cys Gln Ala
        35                  40                  45

Ser Gln Ser Ile Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
```

```
    50                  55                  60

Gln Pro Pro Lys Leu Leu Ile Tyr Gly Ala Ser Asn Leu Glu Ser Gly
65                  70                  75                  80

Val Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Glu Tyr Thr Leu
                85                  90                  95

Thr Ile Ser Gly Val Gln Cys Asp Asp Ala Ala Thr Tyr Tyr Cys Gln
            100                 105                 110

Asn Tyr Tyr Ala Ile Asp Thr Tyr Gly His Ala Phe Gly Gly Gly Thr
        115                 120                 125

Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Ile Phe
    130                 135                 140

Pro Pro Ala Ala Asp Gln Val Ala Thr Gly Thr Val Thr Ile Val Cys
145                 150                 155                 160

Val Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu Val Asp
                165                 170                 175

Gly Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro Gln Asn
            180                 185                 190

Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu Thr Ser
        195                 200                 205

Thr Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr Gln Gly
    210                 215                 220

Thr Thr Ser Val Val Gln Ser Phe Asn Arg Gly Asp Cys
225                 230                 235


<210> 169
<211> 455
<212> PRT
```

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 169
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1 5 10 15

Val Gln Cys Gln Glu Gln Leu Glu Glu Ser Gly Gly Asp Leu Val Lys
20 25 30

Pro Gly Ala Ser Leu Thr Leu Thr Cys Thr Ala Ser Gly Phe Ser Phe
35 40 45

Ser Ser Asn Tyr His Ile Cys Trp Val Arg Gln Ala Pro Gly Lys Gly
50 55 60

Leu Glu Leu Ile Ala Cys Ile Tyr Val Gly Asp Gly Ser Thr Tyr Tyr
65 70 75 80

Ala Ser Trp Ala Lys Gly Arg Phe Thr Ile Ser Lys Ser Ser Ser Thr
85 90 95

Thr Val Ala Leu Gln Met Thr Ser Leu Thr Ala Ala Asp Thr Ala Thr
100 105 110

Tyr Phe Cys Gly Arg Met Phe Asn Leu Trp Gly Pro Gly Thr Leu Val
115 120 125

Thr Val Ser Ser Gly Gln Pro Lys Ala Pro Ser Val Phe Pro Leu Ala
130 135 140

Pro Cys Cys Gly Asp Thr Pro Ser Ser Thr Val Thr Leu Gly Cys Leu
145 150 155 160

Val Lys Gly Tyr Leu Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly
165 170 175

```
Thr Leu Thr Asn Gly Val Arg Thr Phe Pro Ser Val Arg Gln Ser Ser
            180                 185                 190

Gly Leu Tyr Ser Leu Ser Ser Val Val Ser Val Thr Ser Ser Ser Gln
        195                 200                 205

Pro Val Thr Cys Asn Val Ala His Pro Ala Thr Asn Thr Lys Val Asp
    210                 215                 220

Lys Thr Val Ala Pro Ser Thr Cys Ser Lys Pro Met Cys Pro Pro Pro
225                 230                 235                 240

Glu Leu Pro Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys
                245                 250                 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
            260                 265                 270

Asp Val Ser Gln Asp Asp Pro Glu Val Gln Phe Thr Trp Tyr Ile Asn
        275                 280                 285

Asn Glu Gln Val Arg Thr Ala Arg Pro Pro Leu Arg Glu Gln Gln Phe
    290                 295                 300

Asn Ser Thr Ile Arg Val Val Ser Thr Leu Pro Ile Ala His Gln Asp
305                 310                 315                 320

Trp Leu Arg Gly Lys Glu Phe Lys Cys Lys Val His Asn Lys Ala Leu
                325                 330                 335

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Arg Gly Gln Pro Leu
            340                 345                 350

Glu Pro Lys Val Tyr Thr Met Gly Pro Pro Arg Glu Glu Leu Ser Ser
        355                 360                 365
```

```
Arg Ser Val Ser Leu Thr Cys Met Ile Asn Gly Phe Tyr Pro Ser Asp
    370                 375                 380

Ile Ser Val Glu Trp Glu Lys Asn Gly Lys Ala Glu Asp Asn Tyr Lys
385                 390                 395                 400

Thr Thr Pro Thr Val Leu Asp Ser Asp Gly Ser Tyr Phe Leu Tyr Ser
                405                 410                 415

Lys Leu Ser Val Pro Thr Ser Glu Trp Gln Arg Gly Asp Val Phe Thr
            420                 425                 430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
        435                 440                 445

Ile Ser Arg Ser Pro Gly Lys
    450                 455


<210> 170
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 170
Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
1               5                   10                  15

Leu Pro Gly Ala Ile Cys Asp Pro Val Leu Thr Gln Thr Pro Ser Ser
            20                  25                  30

Val Ser Ala Ala Val Gly Val Thr Val Thr Ile Asn Cys Gln Ser Ser
        35                  40                  45

Pro Ser Val Tyr Ser Asn Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Gly
    50                  55                  60
```

```
Gln Pro Pro Lys Leu Leu Ile Tyr Leu Ala Ser Thr Leu Ala Ser Gly
65                  70                  75                  80

Val Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Gln Phe Thr Leu
                85                  90                  95

Thr Ile Ser Asp Val Gln Cys Asp Asp Ala Ala Thr Tyr Tyr Cys Ala
            100                 105                 110

Gly Thr Tyr Ser Gly Asn Ile Trp Ser Phe Gly Gly Gly Thr Glu Val
        115                 120                 125

Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Ile Phe Pro Pro
    130                 135                 140

Ala Ala Asp Gln Val Ala Thr Gly Thr Val Thr Ile Val Cys Val Ala
145                 150                 155                 160

Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu Val Asp Gly Thr
                165                 170                 175

Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro Gln Asn Ser Ala
            180                 185                 190

Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu Thr Ser Thr Gln
        195                 200                 205

Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr Gln Gly Thr Thr
    210                 215                 220

Ser Val Val Gln Ser Phe Asn Arg Gly Asp Cys
225                 230                 235
```

<210> 171
<211> 460
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 171
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1   5   10   15

Val Gln Cys Gln Gln Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
            20   25   30

Pro Gly Ala Ser Leu Thr Leu Thr Cys Thr Ala Ser Gly Phe Ser Phe
        35   40   45

Ser Ser Gly Tyr His Met Cys Trp Val Arg Gln Ala Pro Gly Lys Gly
    50   55   60

Leu Glu Trp Ile Ala Cys Phe Gly Val Tyr Thr Gly Thr Thr Thr Tyr
65   70   75   80

Ala Ser Trp Ala Lys Gly Arg Phe Thr Ile Ser Lys Thr Ser Ser Thr
                85   90   95

Thr Val Thr Leu Gln Met Thr Ser Leu Thr Val Ala Asp Thr Ala Thr
            100   105   110

Tyr Phe Cys Ala Arg Ile Ser Ala Glu Asn Gly Gly Asp Leu Trp Gly
        115   120   125

Pro Gly Thr Leu Val Thr Val Ser Ser Gly Gln Pro Lys Ala Pro Ser
    130   135   140

Val Phe Pro Leu Ala Pro Cys Cys Gly Asp Thr Pro Ser Ser Thr Val
145   150   155   160

Thr Leu Gly Cys Leu Val Lys Gly Tyr Leu Pro Glu Pro Val Thr Val
                165   170   175

```
Thr Trp Asn Ser Gly Thr Leu Thr Asn Gly Val Arg Thr Phe Pro Ser
            180                 185                 190

Val Arg Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Ser Val
        195                 200                 205

Thr Ser Ser Ser Gln Pro Val Thr Cys Asn Val Ala His Pro Ala Thr
    210                 215                 220

Asn Thr Lys Val Asp Lys Thr Val Ala Pro Ser Thr Cys Ser Lys Pro
225                 230                 235                 240

Met Cys Pro Pro Pro Glu Leu Pro Gly Gly Pro Ser Val Phe Ile Phe
                245                 250                 255

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
            260                 265                 270

Thr Cys Val Val Val Asp Val Ser Gln Asp Asp Pro Glu Val Gln Phe
        275                 280                 285

Thr Trp Tyr Ile Asn Asn Glu Gln Val Arg Thr Ala Arg Pro Pro Leu
    290                 295                 300

Arg Glu Gln Gln Phe Asn Ser Thr Ile Arg Val Val Ser Thr Leu Pro
305                 310                 315                 320

Ile Ala His Gln Asp Trp Leu Arg Gly Lys Glu Phe Lys Cys Lys Val
                325                 330                 335

His Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
            340                 345                 350

Arg Gly Gln Pro Leu Glu Pro Lys Val Tyr Thr Met Gly Pro Pro Arg
        355                 360                 365

Glu Glu Leu Ser Ser Arg Ser Val Ser Leu Thr Cys Met Ile Asn Gly
    370                 375                 380
```

```
Phe Tyr Pro Ser Asp Ile Ser Val Glu Trp Glu Lys Asn Gly Lys Ala
385                 390                 395                 400


Glu Asp Asn Tyr Lys Thr Thr Pro Thr Val Leu Asp Ser Asp Gly Ser
                405                 410                 415


Tyr Phe Leu Tyr Ser Lys Leu Ser Val Pro Thr Ser Glu Trp Gln Arg
            420                 425                 430


Gly Asp Val Phe Thr Cys Ser Val Met His Glu Ala Leu His Asn His
        435                 440                 445


Tyr Thr Gln Lys Ser Ile Ser Arg Ser Pro Gly Lys
    450                 455                 460


<210> 172
<211> 236
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 172
Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
1               5                   10                  15


Leu Pro Gly Ala Arg Cys Asp Val Val Met Thr Gln Thr Pro Ala Ser
            20                  25                  30


Val Glu Ala Ala Val Gly Gly Thr Val Thr Ile Lys Cys Gln Ala Ser
        35                  40                  45


Gln Ser Ile Ser Asn Tyr Phe Ser Trp Tyr Gln Gln Lys Pro Gly Gln
    50                  55                  60


Pro Pro Lys Leu Leu Ile Tyr Arg Ala Ser Thr Leu Ala Ser Gly Val
```

65 70 75 80

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
85 90 95

Ile Ser Asp Leu Glu Cys Ala Asp Ser Ala Thr Tyr Tyr Cys Gln Cys
100 105 110

Thr Tyr Gly Ser Ser Ser Thr Gly Phe Gly Phe Gly Gly Gly Thr Glu
115 120 125

Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Pro Ile Phe Pro
130 135 140

Pro Ala Ala Asp Gln Val Ala Thr Gly Thr Val Thr Ile Val Cys Val
145 150 155 160

Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu Val Asp Gly
165 170 175

Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro Gln Asn Ser
180 185 190

Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu Thr Ser Thr
195 200 205

Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr Gln Gly Thr
210 215 220

Thr Ser Val Val Gln Ser Phe Asn Arg Gly Asp Cys
225 230 235

<210> 173
<211> 456
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 173

```
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1               5                  10                  15


Val Gln Cys Gln Ser Leu Glu Glu Ser Gly Gly Asp Leu Val Lys Pro
            20                  25                  30


Gly Ala Ser Leu Thr Leu Thr Cys Met Ala Ser Gly Ile Asp Phe Ser
        35                  40                  45


Ser Gly Tyr Gly Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60


Glu Tyr Ile Gly Tyr Ile Asp Thr Gly Asp Asp Asn Thr Tyr Tyr Ala
65                  70                  75                  80


Asn Trp Ala Lys Gly Arg Phe Thr Ile Ser Lys Thr Ser Ser Thr Thr
                85                  90                  95


Val Thr Leu Gln Met Thr Ser Leu Thr Val Ala Asp Thr Ala Thr Tyr
            100                 105                 110


Phe Cys Ala Lys Gly Gly Ala Ile Asp Leu Trp Gly Pro Gly Thr Leu
        115                 120                 125


Val Thr Val Ser Ser Gly Gln Pro Lys Ala Pro Ser Val Phe Pro Leu
    130                 135                 140


Ala Pro Cys Cys Gly Asp Thr Pro Ser Ser Thr Val Thr Leu Gly Cys
145                 150                 155                 160


Leu Val Lys Gly Tyr Leu Pro Glu Pro Val Thr Val Thr Trp Asn Ser
                165                 170                 175


Gly Thr Leu Thr Asn Gly Val Arg Thr Phe Pro Ser Val Arg Gln Ser
            180                 185                 190
```

```
Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Ser Val Thr Ser Ser Ser
        195                 200                 205

Gln Pro Val Thr Cys Asn Val Ala His Pro Ala Thr Asn Thr Lys Val
    210                 215                 220

Asp Lys Thr Val Ala Pro Ser Thr Cys Ser Lys Pro Met Cys Pro Pro
225                 230                 235                 240

Pro Glu Leu Pro Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro
                245                 250                 255

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
            260                 265                 270

Val Asp Val Ser Gln Asp Asp Pro Glu Val Gln Phe Thr Trp Tyr Ile
        275                 280                 285

Asn Asn Glu Gln Val Arg Thr Ala Arg Pro Pro Leu Arg Glu Gln Gln
    290                 295                 300

Phe Asn Ser Thr Ile Arg Val Val Ser Thr Leu Pro Ile Ala His Gln
305                 310                 315                 320

Asp Trp Leu Arg Gly Lys Glu Phe Lys Cys Lys Val His Asn Lys Ala
                325                 330                 335

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Arg Gly Gln Pro
            340                 345                 350

Leu Glu Pro Lys Val Tyr Thr Met Gly Pro Pro Arg Glu Glu Leu Ser
        355                 360                 365

Ser Arg Ser Val Ser Leu Thr Cys Met Ile Asn Gly Phe Tyr Pro Ser
    370                 375                 380
```

```
Asp Ile Ser Val Glu Trp Glu Lys Asn Gly Lys Ala Glu Asp Asn Tyr
385                 390                 395                 400


Lys Thr Thr Pro Thr Val Leu Asp Ser Asp Gly Ser Tyr Phe Leu Tyr
                405                 410                 415


Ser Lys Leu Ser Val Pro Thr Ser Glu Trp Gln Arg Gly Asp Val Phe
            420                 425                 430


Thr Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
        435                 440                 445


Ser Ile Ser Arg Ser Pro Gly Lys
    450                 455


<210> 174
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 174
Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
1               5                   10                  15


Leu Pro Gly Ala Arg Cys Ala Asp Ile Val Met Thr Gln Thr Pro Ala
            20                  25                  30


Ser Val Glu Ala Ala Val Gly Gly Thr Val Thr Ile Lys Cys Gln Ala
        35                  40                  45


Ser Gln Ser Ile Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
    50                  55                  60


Gln Arg Pro Lys Leu Leu Ile Tyr Arg Ala Ser Thr Leu Lys Ser Gly
65                  70                  75                  80
```

```
Val Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Glu Tyr Thr Leu
                85                  90                  95

Thr Ile Ser Asp Leu Glu Cys Ala Asp Ala Ala Thr Tyr Tyr Cys Gln
            100                 105                 110

Ala Tyr Tyr Leu Ser Ser Ser Ile Ser Tyr Gly Asn Thr Phe Gly Gly
        115                 120                 125

Gly Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu
    130                 135                 140

Ile Phe Pro Pro Ala Ala Asp Gln Val Ala Thr Gly Thr Val Thr Ile
145                 150                 155                 160

Val Cys Val Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu
                165                 170                 175

Val Asp Gly Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro
            180                 185                 190

Gln Asn Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu
        195                 200                 205

Thr Ser Thr Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr
    210                 215                 220

Gln Gly Thr Thr Ser Val Val Gln Ser Phe Asn Arg Gly Asp Cys
225                 230                 235
```

<210> 175
<211> 456
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 175

```
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1               5                  10                  15

Val Gln Cys Gln Ser Leu Glu Glu Ser Gly Gly Asp Leu Val Lys Pro
            20                  25                  30

Gly Ala Ser Leu Thr Leu Thr Cys Thr Ala Ser Gly Phe Ser Leu Ser
        35                  40                  45

Ser Gly Tyr Gly Met Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60

Glu Trp Ile Gly Tyr Thr Asp Thr Ala Thr Gly Thr Ile His Tyr Ala
65                  70                  75                  80

Ser Trp Ala Lys Gly Arg Phe Thr Ile Ser Lys Thr Ser Ser Thr Thr
                85                  90                  95

Val Thr Leu Gln Met Thr Ser Leu Thr Ala Ala Asp Thr Ala Thr Tyr
            100                 105                 110

Phe Cys Ala Lys Gly Gly Ala Met Asp Leu Trp Gly Pro Gly Thr Leu
        115                 120                 125

Val Thr Val Ser Ser Gly Gln Pro Lys Ala Pro Ser Val Phe Pro Leu
    130                 135                 140

Ala Pro Cys Cys Gly Asp Thr Pro Ser Ser Thr Val Thr Leu Gly Cys
145                 150                 155                 160

Leu Val Lys Gly Tyr Leu Pro Glu Pro Val Thr Val Thr Trp Asn Ser
                165                 170                 175

Gly Thr Leu Thr Asn Gly Val Arg Thr Phe Pro Ser Val Arg Gln Ser
            180                 185                 190
```

```
Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Ser Val Thr Ser Ser Ser
        195                 200                 205

Gln Pro Val Thr Cys Asn Val Ala His Pro Ala Thr Asn Thr Lys Val
    210                 215                 220

Asp Lys Thr Val Ala Pro Ser Thr Cys Ser Lys Pro Met Cys Pro Pro
225                 230                 235                 240

Pro Glu Leu Pro Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro
                245                 250                 255

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
            260                 265                 270

Val Asp Val Ser Gln Asp Asp Pro Glu Val Gln Phe Thr Trp Tyr Ile
        275                 280                 285

Asn Asn Glu Gln Val Arg Thr Ala Arg Pro Pro Leu Arg Glu Gln Gln
    290                 295                 300

Phe Asn Ser Thr Ile Arg Val Val Ser Thr Leu Pro Ile Ala His Gln
305                 310                 315                 320

Asp Trp Leu Arg Gly Lys Glu Phe Lys Cys Lys Val His Asn Lys Ala
                325                 330                 335

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Arg Gly Gln Pro
            340                 345                 350

Leu Glu Pro Lys Val Tyr Thr Met Gly Pro Pro Arg Glu Glu Leu Ser
        355                 360                 365

Ser Arg Ser Val Ser Leu Thr Cys Met Ile Asn Gly Phe Tyr Pro Ser
    370                 375                 380

Asp Ile Ser Val Glu Trp Glu Lys Asn Gly Lys Ala Glu Asp Asn Tyr
385                 390                 395                 400
```

Lys Thr Thr Pro Thr Val Leu Asp Ser Asp Gly Ser Tyr Phe Leu Tyr
405 410 415

Ser Lys Leu Ser Val Pro Thr Ser Glu Trp Gln Arg Gly Asp Val Phe
420 425 430

Thr Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
435 440 445

Ser Ile Ser Arg Ser Pro Gly Lys
450 455

<210> 176
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 176
Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Pro Gly Ala Arg Cys Ala Asp Ile Val Met Thr Gln Thr Pro Ala
20 25 30

Ser Val Glu Ala Ala Val Gly Gly Thr Val Thr Ile Lys Cys Gln Ala
35 40 45

Ser Gln Ser Ile Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
50 55 60

Gln Pro Pro Lys Leu Leu Ile Tyr Arg Thr Ser Thr Leu Ala Ser Gly
65 70 75 80

Val Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Glu Tyr Thr Leu

```
                85                  90                  95

Thr Ile Ser Asp Leu Glu Cys Ala Asp Ala Ala Thr Tyr Tyr Cys Gln
            100                 105                 110

Ser Tyr Ala Tyr Ser Ser Ser Ser Ser Tyr Gly Asn Ala Phe Gly Gly
        115                 120                 125

Gly Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu
    130                 135                 140

Ile Phe Pro Pro Ala Ala Asp Gln Val Ala Thr Gly Thr Val Thr Ile
145                 150                 155                 160

Val Cys Val Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu
                165                 170                 175

Val Asp Gly Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro
            180                 185                 190

Gln Asn Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu
        195                 200                 205

Thr Ser Thr Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr
    210                 215                 220

Gln Gly Thr Thr Ser Val Val Gln Ser Phe Asn Arg Gly Asp Cys
225                 230                 235


<210> 177
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 177
```

```
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1               5                  10                  15

Val Gln Cys Gln Ser Leu Glu Glu Ser Gly Gly Asp Leu Val Lys Pro
            20                  25                  30

Gly Ala Ser Leu Thr Leu Thr Cys Thr Gly Ser Gly Ile Asp Phe Ser
        35                  40                  45

Ser Ser Tyr Trp Ile Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60

Glu Trp Ile Ala Cys Ile Asp Gly Ser Asp Gly Asn Thr Tyr Tyr Ala
65                  70                  75                  80

Ser Trp Ala Arg Gly Arg Phe Thr Ile Ser Lys Thr Ser Ser Thr Thr
                85                  90                  95

Val Thr Leu Gln Met Ala Ser Leu Thr Ala Ala Asp Thr Ala Thr Tyr
            100                 105                 110

Phe Cys Thr Arg Asp Leu Arg Leu Trp Gly Pro Gly Thr Leu Val Thr
        115                 120                 125

Val Ser Ser Gly Gln Pro Lys Ala Pro Ser Val Phe Pro Leu Ala Pro
    130                 135                 140

Cys Cys Gly Asp Thr Pro Ser Ser Thr Val Thr Leu Gly Cys Leu Val
145                 150                 155                 160

Lys Gly Tyr Leu Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Thr
                165                 170                 175

Leu Thr Asn Gly Val Arg Thr Phe Pro Ser Val Arg Gln Ser Ser Gly
            180                 185                 190

Leu Tyr Ser Leu Ser Ser Val Val Ser Val Thr Ser Ser Ser Gln Pro
        195                 200                 205
```

```
Val Thr Cys Asn Val Ala His Pro Ala Thr Asn Thr Lys Val Asp Lys
    210                 215                 220

Thr Val Ala Pro Ser Thr Cys Ser Lys Pro Met Cys Pro Pro Pro Glu
225                 230                 235                 240

Leu Pro Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp
                245                 250                 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
            260                 265                 270

Val Ser Gln Asp Asp Pro Glu Val Gln Phe Thr Trp Tyr Ile Asn Asn
        275                 280                 285

Glu Gln Val Arg Thr Ala Arg Pro Pro Leu Arg Glu Gln Gln Phe Asn
    290                 295                 300

Ser Thr Ile Arg Val Val Ser Thr Leu Pro Ile Ala His Gln Asp Trp
305                 310                 315                 320

Leu Arg Gly Lys Glu Phe Lys Cys Lys Val His Asn Lys Ala Leu Pro
                325                 330                 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Arg Gly Gln Pro Leu Glu
            340                 345                 350

Pro Lys Val Tyr Thr Met Gly Pro Pro Arg Glu Glu Leu Ser Ser Arg
        355                 360                 365

Ser Val Ser Leu Thr Cys Met Ile Asn Gly Phe Tyr Pro Ser Asp Ile
    370                 375                 380

Ser Val Glu Trp Glu Lys Asn Gly Lys Ala Glu Asp Asn Tyr Lys Thr
385                 390                 395                 400
```

Thr Pro Thr Val Leu Asp Ser Asp Gly Ser Tyr Phe Leu Tyr Ser Lys
405 410 415

Leu Ser Val Pro Thr Ser Glu Trp Gln Arg Gly Asp Val Phe Thr Cys
420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Ile
435 440 445

Ser Arg Ser Pro Gly Lys
450

<210> 178
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 178
Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Pro Gly Ala Arg Cys Ala Asp Ile Val Leu Thr Gln Thr Pro Ala
20 25 30

Ser Val Ser Ala Ala Val Gly Gly Thr Val Thr Ile Asn Cys Gln Ala
35 40 45

Ser Gln Asn Val Tyr Ser Asn Asn Ala Leu Ala Trp His Gln Gln Lys
50 55 60

Pro Gly Gln Arg Pro Asn Leu Leu Ile Tyr Lys Ala Ser Thr Leu Ala
65 70 75 80

Ser Gly Val Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Gln Phe
85 90 95

```
Thr Leu Thr Ile Ser Asp Val Gln Cys Asp Asp Ala Ala Thr Tyr Tyr
            100                 105                 110


Cys Leu Gly Glu Phe Ser Cys Ser Ser Gly Asp Cys Phe Val Phe Gly
        115                 120                 125


Gly Gly Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val
    130                 135                 140


Leu Ile Phe Pro Pro Ala Ala Asp Gln Val Ala Thr Gly Thr Val Thr
145                 150                 155                 160


Ile Val Cys Val Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp
                165                 170                 175


Glu Val Asp Gly Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr
            180                 185                 190


Pro Gln Asn Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr
        195                 200                 205


Leu Thr Ser Thr Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val
    210                 215                 220


Thr Gln Gly Thr Thr Ser Val Val Gln Ser Phe Asn Arg Gly Asp Cys
225                 230                 235                 240


<210> 179
<211> 456
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 179
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1               5                   10                  15
```

```
Val Gln Cys Gln Ser Leu Glu Glu Ser Gly Gly Asp Leu Val Lys Pro
            20                  25                  30

Gly Ala Ser Leu Thr Leu Thr Cys Met Ala Ser Gly Ile Asp Phe Ser
        35                  40                  45

Ser Gly Tyr Gly Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60

Glu Tyr Ile Gly Tyr Ile Asp Thr Gly Asp Asp Asn Thr Tyr Tyr Ala
65                  70                  75                  80

Asn Trp Ala Lys Gly Arg Phe Thr Ile Ser Lys Thr Ser Ser Thr Thr
                85                  90                  95

Val Thr Leu Gln Met Thr Ser Leu Thr Val Ala Asp Thr Ala Thr Tyr
            100                 105                 110

Phe Cys Ala Lys Gly Gly Ala Ile Asp Leu Trp Gly Pro Gly Thr Leu
        115                 120                 125

Val Thr Val Ser Ser Gly Gln Pro Lys Ala Pro Ser Val Phe Pro Leu
    130                 135                 140

Ala Pro Cys Cys Gly Asp Thr Pro Ser Ser Thr Val Thr Leu Gly Cys
145                 150                 155                 160

Leu Val Lys Gly Tyr Leu Pro Glu Pro Val Thr Val Thr Trp Asn Ser
                165                 170                 175

Gly Thr Leu Thr Asn Gly Val Arg Thr Phe Pro Ser Val Arg Gln Ser
            180                 185                 190

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Ser Val Thr Ser Ser Ser
        195                 200                 205
```

```
Gln Pro Val Thr Cys Asn Val Ala His Pro Ala Thr Asn Thr Lys Val
    210                 215                 220

Asp Lys Thr Val Ala Pro Ser Thr Cys Ser Lys Pro Met Cys Pro Pro
225                 230                 235                 240

Pro Glu Leu Pro Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro
                245                 250                 255

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
            260                 265                 270

Val Asp Val Ser Gln Asp Asp Pro Glu Val Gln Phe Thr Trp Tyr Ile
        275                 280                 285

Asn Asn Glu Gln Val Arg Thr Ala Arg Pro Pro Leu Arg Glu Gln Gln
    290                 295                 300

Phe Asn Ser Thr Ile Arg Val Val Ser Thr Leu Pro Ile Ala His Gln
305                 310                 315                 320

Asp Trp Leu Arg Gly Lys Glu Phe Lys Cys Lys Val His Asn Lys Ala
                325                 330                 335

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Arg Gly Gln Pro
            340                 345                 350

Leu Glu Pro Lys Val Tyr Thr Met Gly Pro Pro Arg Glu Glu Leu Ser
        355                 360                 365

Ser Arg Ser Val Ser Leu Thr Cys Met Ile Asn Gly Phe Tyr Pro Ser
    370                 375                 380

Asp Ile Ser Val Glu Trp Glu Lys Asn Gly Lys Ala Glu Asp Asn Tyr
385                 390                 395                 400

Lys Thr Thr Pro Thr Val Leu Asp Ser Asp Gly Ser Tyr Phe Leu Tyr
                405                 410                 415
```

```
Ser Lys Leu Ser Val Pro Thr Ser Glu Trp Gln Arg Gly Asp Val Phe
            420                 425                 430


Thr Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
        435                 440                 445


Ser Ile Ser Arg Ser Pro Gly Lys
    450                 455


<210> 180
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 180
Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
1               5                   10                  15


Leu Pro Gly Ala Arg Cys Ala Asp Ile Val Met Thr Gln Thr Pro Ala
            20                  25                  30


Ser Val Glu Ala Ala Val Gly Gly Thr Val Thr Ile Lys Cys Gln Ala
        35                  40                  45


Ser Gln Ser Ile Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
    50                  55                  60


Gln Arg Pro Lys Leu Leu Ile Tyr Arg Ala Ser Thr Leu Lys Ser Gly
65                  70                  75                  80


Val Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Glu Tyr Thr Leu
                85                  90                  95


Thr Ile Ser Asp Leu Glu Cys Ala Asp Ala Ala Thr Tyr Tyr Cys Gln
```

```
            100                 105                 110

Ala Tyr Tyr Leu Ser Ser Ser Ile Ser Tyr Gly Asn Thr Phe Gly Gly
        115                 120                 125

Gly Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu
    130                 135                 140

Ile Phe Pro Pro Ala Ala Asp Gln Val Ala Thr Gly Thr Val Thr Ile
145                 150                 155                 160

Val Cys Val Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu
                165                 170                 175

Val Asp Gly Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro
            180                 185                 190

Gln Asn Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu
        195                 200                 205

Thr Ser Thr Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr
    210                 215                 220

Gln Gly Thr Thr Ser Val Val Gln Ser Phe Asn Arg Gly Asp Cys
225                 230                 235


<210> 181
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 181
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1               5                   10                  15
```

```
Val Gln Cys Gln Gln Gln Leu Glu Glu Ser Gly Gly Gly Leu Val Lys
            20                  25                  30

Pro Gly Gly Thr Leu Thr Leu Thr Cys Lys Ala Ser Gly Val Ala Leu
        35                  40                  45

Asn Pro Tyr Tyr Tyr Met Cys Trp Val Arg Gln Ala Pro Gly Lys Gly
    50                  55                  60

Leu Glu Trp Ile Ala Cys Val Asp Ala Asp Ser Ser Gly Ser Thr Tyr
65                  70                  75                  80

Tyr Ala Ser Trp Ala Lys Gly Arg Phe Thr Ile Ser Lys Thr Ser Ser
                85                  90                  95

Thr Thr Val Thr Leu Lys Met Thr Ser Leu Thr Ala Ala Asp Thr Ala
            100                 105                 110

Thr Tyr Phe Cys Ala Arg Glu Ser Val Asp Tyr Ser Ser Val Gly Ile
        115                 120                 125

Gly Tyr Val His Gly Thr Asp Gly Leu Trp Gly Pro Gly Thr Leu Val
    130                 135                 140

Thr Val Ser Ser Gly Gln Pro Lys Ala Pro Ser Val Phe Pro Leu Ala
145                 150                 155                 160

Pro Cys Cys Gly Asp Thr Pro Ser Ser Thr Val Thr Leu Gly Cys Leu
                165                 170                 175

Val Lys Gly Tyr Leu Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly
            180                 185                 190

Thr Leu Thr Asn Gly Val Arg Thr Phe Pro Ser Val Arg Gln Ser Ser
        195                 200                 205

Gly Leu Tyr Ser Leu Ser Ser Val Val Ser Val Thr Ser Ser Ser Gln
    210                 215                 220
```

```
Pro Val Thr Cys Asn Val Ala His Pro Ala Thr Asn Thr Lys Val Asp
225                 230                 235                 240

Lys Thr Val Ala Pro Ser Thr Cys Ser Lys Pro Met Cys Pro Pro Pro
                245                 250                 255

Glu Leu Pro Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys
            260                 265                 270

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285

Asp Val Ser Gln Asp Asp Pro Glu Val Gln Phe Thr Trp Tyr Ile Asn
    290                 295                 300

Asn Glu Gln Val Arg Thr Ala Arg Pro Pro Leu Arg Glu Gln Gln Phe
305                 310                 315                 320

Asn Ser Thr Ile Arg Val Val Ser Thr Leu Pro Ile Ala His Gln Asp
                325                 330                 335

Trp Leu Arg Gly Lys Glu Phe Lys Cys Lys Val His Asn Lys Ala Leu
            340                 345                 350

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Arg Gly Gln Pro Leu
        355                 360                 365

Glu Pro Lys Val Tyr Thr Met Gly Pro Pro Arg Glu Glu Leu Ser Ser
    370                 375                 380

Arg Ser Val Ser Leu Thr Cys Met Ile Asn Gly Phe Tyr Pro Ser Asp
385                 390                 395                 400

Ile Ser Val Glu Trp Glu Lys Asn Gly Lys Ala Glu Asp Asn Tyr Lys
                405                 410                 415
```

Thr Thr Pro Thr Val Leu Asp Ser Asp Gly Ser Tyr Phe Leu Tyr Ser
420 425 430

Lys Leu Ser Val Pro Thr Ser Glu Trp Gln Arg Gly Asp Val Phe Thr
435 440 445

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
450 455 460

Ile Ser Arg Ser Pro Gly Lys
465 470

<210> 182
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 182
Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Pro Gly Ala Arg Cys Ala Asp Ile Val Val Thr Gln Thr Pro Ser
20 25 30

Ser Val Ser Ala Ala Val Gly Gly Thr Val Thr Ile Lys Cys Gln Ala
35 40 45

Ser Gln Ser Ile Ser Asn Tyr Phe Ser Trp Tyr Gln Gln Lys Pro Gly
50 55 60

Gln Pro Pro Lys Leu Leu Ile Tyr Arg Ala Ser Thr Leu Ala Ser Gly
65 70 75 80

Val Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu
85 90 95

```
Thr Ile Ser Asp Leu Glu Cys Ala Asp Ala Ala Thr Tyr Tyr Cys Gln
            100                 105                 110


Cys Thr Tyr Gly Arg Ser Asn Ser Asn Phe Phe Tyr Gly Phe Gly Gly
        115                 120                 125


Gly Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu
    130                 135                 140


Ile Phe Pro Pro Ala Ala Asp Gln Val Ala Thr Gly Thr Val Thr Ile
145                 150                 155                 160


Val Cys Val Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu
                165                 170                 175


Val Asp Gly Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro
            180                 185                 190


Gln Asn Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu
        195                 200                 205


Thr Ser Thr Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr
    210                 215                 220


Gln Gly Thr Thr Ser Val Val Gln Ser Phe Asn Arg Gly Asp Cys
225                 230                 235


<210> 183
<211> 464
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 183
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1               5                   10                  15
```

```
Val Gln Cys Gln Ser Leu Glu Glu Ser Gly Gly Asp Leu Val Lys Pro
            20                  25                  30

Gly Ala Ser Leu Thr Leu Thr Cys Thr Ala Ser Gly Ser Ser Phe Ser
        35                  40                  45

Ser Thr Tyr Trp Asn Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60

Glu Trp Ile Ala Cys Ile Asn Ala Gly Ser Gly Thr Thr Tyr Tyr Ala
65                  70                  75                  80

Ser Trp Ala Lys Gly Arg Phe Thr Val Ser Lys Thr Ser Ser Thr Thr
                85                  90                  95

Val Thr Leu Gln Met Thr Ser Leu Thr Ala Ala Asp Thr Ala Thr Tyr
            100                 105                 110

Phe Cys Thr Arg Asp Ser Asp Gly Arg Phe Ser Ser Gly Tyr Tyr Phe
        115                 120                 125

Asn Leu Trp Gly Pro Gly Thr Leu Val Thr Val Ser Ser Gly Gln Pro
    130                 135                 140

Lys Ala Pro Ser Val Phe Pro Leu Ala Pro Cys Cys Gly Asp Thr Pro
145                 150                 155                 160

Ser Ser Thr Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Leu Pro Glu
                165                 170                 175

Pro Val Thr Val Thr Trp Asn Ser Gly Thr Leu Thr Asn Gly Val Arg
            180                 185                 190

Thr Phe Pro Ser Val Arg Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
        195                 200                 205
```

```
Val Val Ser Val Thr Ser Ser Ser Gln Pro Val Thr Cys Asn Val Ala
    210                 215                 220

His Pro Ala Thr Asn Thr Lys Val Asp Lys Thr Val Ala Pro Ser Thr
225                 230                 235                 240

Cys Ser Lys Pro Met Cys Pro Pro Pro Glu Leu Pro Gly Gly Pro Ser
                245                 250                 255

Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
            260                 265                 270

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Asp Asp Pro
        275                 280                 285

Glu Val Gln Phe Thr Trp Tyr Ile Asn Asn Glu Gln Val Arg Thr Ala
    290                 295                 300

Arg Pro Pro Leu Arg Glu Gln Gln Phe Asn Ser Thr Ile Arg Val Val
305                 310                 315                 320

Ser Thr Leu Pro Ile Ala His Gln Asp Trp Leu Arg Gly Lys Glu Phe
                325                 330                 335

Lys Cys Lys Val His Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
            340                 345                 350

Ile Ser Lys Ala Arg Gly Gln Pro Leu Glu Pro Lys Val Tyr Thr Met
        355                 360                 365

Gly Pro Pro Arg Glu Glu Leu Ser Ser Arg Ser Val Ser Leu Thr Cys
    370                 375                 380

Met Ile Asn Gly Phe Tyr Pro Ser Asp Ile Ser Val Glu Trp Glu Lys
385                 390                 395                 400

Asn Gly Lys Ala Glu Asp Asn Tyr Lys Thr Thr Pro Thr Val Leu Asp
                405                 410                 415
```

```
Ser Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Pro Thr Ser
            420                 425                 430


Glu Trp Gln Arg Gly Asp Val Phe Thr Cys Ser Val Met His Glu Ala
        435                 440                 445


Leu His Asn His Tyr Thr Gln Lys Ser Ile Ser Arg Ser Pro Gly Lys
    450                 455                 460


<210> 184
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 184
Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
1               5                   10                  15


Leu Pro Gly Ala Thr Phe Ala Gln Val Leu Thr Gln Thr Ala Ser Pro
            20                  25                  30


Val Ser Ala Ala Val Gly Gly Thr Val Thr Ile Asn Cys Gln Ser Ser
        35                  40                  45


Gln Ser Val Tyr Asp Asn Asn Trp Leu Ala Trp Tyr Gln Gln Lys Pro
    50                  55                  60


Gly Gln Pro Pro Lys Leu Leu Ile Asp Asp Ala Ser Lys Leu Thr Ser
65                  70                  75                  80


Gly Val Ser Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Gln Phe Thr
                85                  90                  95


Leu Thr Ile Ser Gly Val Gln Cys Asp Asp Ala Ala Thr Tyr Tyr Cys
```

```
            100                 105                 110

Gln Gly Ala Tyr Tyr Ser Ser Gly Trp Tyr Trp Ala Phe Gly Gly Gly
        115                 120                 125

Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Ile
    130                 135                 140

Phe Pro Pro Ala Ala Asp Gln Val Ala Thr Gly Thr Val Thr Ile Val
145                 150                 155                 160

Cys Val Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu Val
                165                 170                 175

Asp Gly Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro Gln
            180                 185                 190

Asn Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu Thr
        195                 200                 205

Ser Thr Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr Gln
    210                 215                 220

Gly Thr Thr Ser Val Val Gln Ser Phe Asn Arg Gly Asp Cys
225                 230                 235


<210> 185
<211> 467
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 185
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1               5                   10                  15
```

```
Val Gln Cys Gln Gln Gln Leu Glu Glu Ser Gly Gly Gly Leu Val Lys
            20                  25                  30

Pro Gly Gly Thr Leu Thr Leu Thr Cys Lys Ala Ser Gly Ile Asp Phe
        35                  40                  45

Ser Ser Tyr Tyr Tyr Met Cys Trp Val Arg Gln Ala Pro Gly Lys Gly
    50                  55                  60

Leu Glu Leu Ile Val Cys Ile Tyr Thr Ser Ser Gly Gly Thr Trp Tyr
65                  70                  75                  80

Ala Ser Trp Val Asn Gly Arg Leu Thr Ile Ser Arg Ser Thr Ser Leu
                85                  90                  95

Asn Thr Val Asp Leu Lys Met Thr Ser Leu Thr Ala Ala Asp Thr Ala
            100                 105                 110

Thr Tyr Phe Cys Ala Arg Gly Val Tyr Ser Gly Ser Ser Asp Tyr Pro
        115                 120                 125

Thr Arg Leu Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Leu
    130                 135                 140

Gly Gln Pro Lys Ala Pro Ser Val Phe Pro Leu Ala Pro Cys Cys Gly
145                 150                 155                 160

Asp Thr Pro Ser Ser Thr Val Thr Leu Gly Cys Leu Val Lys Gly Tyr
                165                 170                 175

Leu Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Thr Leu Thr Asn
            180                 185                 190

Gly Val Arg Thr Phe Pro Ser Val Arg Gln Ser Ser Gly Leu Tyr Ser
        195                 200                 205

Leu Ser Ser Val Val Ser Val Thr Ser Ser Ser Gln Pro Val Thr Cys
    210                 215                 220
```

```
Asn Val Ala His Pro Ala Thr Asn Thr Lys Val Asp Lys Thr Val Ala
225                 230                 235                 240

Pro Ser Thr Cys Ser Lys Pro Met Cys Pro Pro Pro Glu Leu Pro Gly
                245                 250                 255

Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln
        275                 280                 285

Asp Asp Pro Glu Val Gln Phe Thr Trp Tyr Ile Asn Asn Glu Gln Val
    290                 295                 300

Arg Thr Ala Arg Pro Pro Leu Arg Glu Gln Gln Phe Asn Ser Thr Ile
305                 310                 315                 320

Arg Val Val Ser Thr Leu Pro Ile Ala His Gln Asp Trp Leu Arg Gly
                325                 330                 335

Lys Glu Phe Lys Cys Lys Val His Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

Glu Lys Thr Ile Ser Lys Ala Arg Gly Gln Pro Leu Glu Pro Lys Val
        355                 360                 365

Tyr Thr Met Gly Pro Pro Arg Glu Glu Leu Ser Ser Arg Ser Val Ser
    370                 375                 380

Leu Thr Cys Met Ile Asn Gly Phe Tyr Pro Ser Asp Ile Ser Val Glu
385                 390                 395                 400

Trp Glu Lys Asn Gly Lys Ala Glu Asp Asn Tyr Lys Thr Thr Pro Thr
                405                 410                 415
```

Val Leu Asp Ser Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val
420 425 430

Pro Thr Ser Glu Trp Gln Arg Gly Asp Val Phe Thr Cys Ser Val Met
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Ile Ser Arg Ser
450 455 460

Pro Gly Lys
465

<210> 186
<211> 236
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 186
Met Asp Thr Ser Thr Ser Thr Ala Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Thr Gly Ala Arg Cys Ala Ile Glu Met Thr Gln Ser Pro Pro Ser
20 25 30

Leu Ser Ala Ser Val Gly Glu Thr Val Arg Ile Arg Cys Leu Ala Ser
35 40 45

Glu Asp Ile Tyr Ser Gly Ile Ser Trp Tyr Gln Gln Lys Pro Glu Lys
50 55 60

Pro Pro Thr Leu Leu Ile Ser Gly Ala Ser Asn Leu Glu Ser Gly Val
65 70 75 80

Pro Pro Arg Phe Ser Gly Gly Gly Ser Gly Thr Asp Tyr Thr Leu Thr
85 90 95

```
Ile Gly Gly Val Gln Ala Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly
            100                 105                 110


Gly Tyr Ser Phe Ser Ser Thr Gly Leu Thr Phe Gly Ala Gly Thr Lys
        115                 120                 125


Val Glu Ile Lys Arg Asp Pro Val Ala Pro Ser Val Leu Leu Phe Pro
    130                 135                 140


Pro Ser Lys Glu Glu Leu Thr Thr Gly Thr Ala Thr Ile Val Cys Val
145                 150                 155                 160


Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu Val Asp Gly
                165                 170                 175


Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro Gln Asn Ser
            180                 185                 190


Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu Thr Ser Thr
        195                 200                 205


Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr Gln Gly Thr
    210                 215                 220


Thr Ser Val Val Gln Ser Phe Asn Arg Gly Asp Cys
225                 230                 235


<210> 187
<211> 460
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 187
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1               5                   10                  15
```

```
Val Gln Cys Gln Gln His Leu Val Glu Ser Gly Gly Gly Leu Val Lys
            20                  25                  30

Pro Gly Ala Ser Leu Thr Leu Thr Cys Thr Ala Ser Gly Phe Ser Phe
        35                  40                  45

Thr Thr Gly Tyr His Met Cys Trp Val Arg Gln Ala Pro Gly Lys Gly
    50                  55                  60

Leu Glu Trp Ile Ala Cys Phe Gly Val Tyr Thr Ser Thr Thr Thr Tyr
65                  70                  75                  80

Ala Ser Trp Ala Lys Gly Arg Phe Thr Ile Ser Lys Thr Ser Ser Thr
                85                  90                  95

Thr Val Thr Leu Gln Met Thr Ser Leu Thr Val Ala Asp Thr Ala Thr
            100                 105                 110

Tyr Phe Cys Ala Arg Ile Ser Ala Glu Asp Gly Gly Asp Leu Trp Gly
        115                 120                 125

Pro Gly Thr Leu Val Thr Val Ser Ser Gly Gln Pro Lys Ala Pro Ser
    130                 135                 140

Val Phe Pro Leu Ala Pro Cys Cys Gly Asp Thr Pro Ser Ser Thr Val
145                 150                 155                 160

Thr Leu Gly Cys Leu Val Lys Gly Tyr Leu Pro Glu Pro Val Thr Val
                165                 170                 175

Thr Trp Asn Ser Gly Thr Leu Thr Asn Gly Val Arg Thr Phe Pro Ser
            180                 185                 190

Val Arg Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Ser Val
        195                 200                 205
```

```
Thr Ser Ser Ser Gln Pro Val Thr Cys Asn Val Ala His Pro Ala Thr
    210                 215                 220

Asn Thr Lys Val Asp Lys Thr Val Ala Pro Ser Thr Cys Ser Lys Pro
225                 230                 235                 240

Met Cys Pro Pro Pro Glu Leu Pro Gly Gly Pro Ser Val Phe Ile Phe
                245                 250                 255

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
            260                 265                 270

Thr Cys Val Val Val Asp Val Ser Gln Asp Asp Pro Glu Val Gln Phe
        275                 280                 285

Thr Trp Tyr Ile Asn Asn Glu Gln Val Arg Thr Ala Arg Pro Pro Leu
    290                 295                 300

Arg Glu Gln Gln Phe Asn Ser Thr Ile Arg Val Val Ser Thr Leu Pro
305                 310                 315                 320

Ile Ala His Gln Asp Trp Leu Arg Gly Lys Glu Phe Lys Cys Lys Val
                325                 330                 335

His Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
            340                 345                 350

Arg Gly Gln Pro Leu Glu Pro Lys Val Tyr Thr Met Gly Pro Pro Arg
        355                 360                 365

Glu Glu Leu Ser Ser Arg Ser Val Ser Leu Thr Cys Met Ile Asn Gly
    370                 375                 380

Phe Tyr Pro Ser Asp Ile Ser Val Glu Trp Glu Lys Asn Gly Lys Ala
385                 390                 395                 400

Glu Asp Asn Tyr Lys Thr Thr Pro Thr Val Leu Asp Ser Asp Gly Ser
                405                 410                 415
```

```
Tyr Phe Leu Tyr Ser Lys Leu Ser Val Pro Thr Ser Glu Trp Gln Arg
            420                 425                 430


Gly Asp Val Phe Thr Cys Ser Val Met His Glu Ala Leu His Asn His
        435                 440                 445


Tyr Thr Gln Lys Ser Ile Ser Arg Ser Pro Gly Lys
    450                 455                 460


<210> 188
<211> 236
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 188
Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
1               5                   10                  15


Leu Pro Gly Ala Arg Cys Asp Val Val Met Thr Gln Thr Pro Ala Ser
            20                  25                  30


Val Glu Ala Ala Val Gly Gly Thr Val Thr Ile Thr Cys Gln Ala Ser
        35                  40                  45


Gln Ser Ile Ser Asn Tyr Phe Ser Trp Tyr Gln Gln Lys Pro Gly Gln
    50                  55                  60


Pro Pro Lys Leu Leu Ile Tyr Arg Ala Ser Thr Leu Ala Ser Gly Val
65                  70                  75                  80


Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Phe Thr Leu Thr
                85                  90                  95


Ile Ser Asp Leu Glu Cys Ala Asp Ser Ala Thr Tyr Ala Cys Gln Cys
```

```
            100                 105                 110

Thr Tyr Gly Ser Ser Ser Thr Gly Phe Gly Phe Gly Gly Gly Thr Glu
        115                 120                 125

Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Ile Phe Pro
    130                 135                 140

Pro Ala Ala Asp Gln Val Ala Thr Gly Thr Val Thr Ile Val Cys Val
145                 150                 155                 160

Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu Val Asp Gly
                165                 170                 175

Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro Gln Asn Ser
            180                 185                 190

Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu Thr Ser Thr
        195                 200                 205

Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr Gln Gly Thr
    210                 215                 220

Thr Ser Val Val Gln Ser Phe Asn Arg Gly Asp Cys
225                 230                 235


<210> 189
<211> 462
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 189
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1               5                   10                  15
```

```
Val Gln Cys Gln Ser Leu Glu Glu Ser Gly Gly Asp Leu Val Lys Pro
            20                  25                  30

Gly Ala Ser Leu Thr Leu Thr Cys Lys Ala Ser Gly Phe Ser Phe Ser
        35                  40                  45

Ser Tyr Phe Trp Ile Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60

Glu Trp Ser Ala Cys Ile Tyr Gly Asp Ser Ser Gly Ser Ser Tyr Tyr
65                  70                  75                  80

Ala Ser Trp Ala Lys Gly Arg Phe Thr Ile Ser Lys Thr Ser Ser Thr
                85                  90                  95

Thr Val Thr Leu Gln Met Thr Ser Leu Thr Ala Ala Asp Thr Ala Thr
            100                 105                 110

Tyr Phe Cys Ala Ser Tyr Gly Ser Ser Ser Tyr Tyr Tyr Ser Asn Leu
        115                 120                 125

Trp Gly Pro Gly Thr Leu Val Thr Val Ser Ser Gly Gln Pro Lys Ala
    130                 135                 140

Pro Ser Val Phe Pro Leu Ala Pro Cys Cys Gly Asp Thr Pro Ser Ser
145                 150                 155                 160

Thr Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Leu Pro Glu Pro Val
                165                 170                 175

Thr Val Thr Trp Asn Ser Gly Thr Leu Thr Asn Gly Val Arg Thr Phe
            180                 185                 190

Pro Ser Val Arg Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
        195                 200                 205

Ser Val Thr Ser Ser Ser Gln Pro Val Thr Cys Asn Val Ala His Pro
    210                 215                 220
```

```
Ala Thr Asn Thr Lys Val Asp Lys Thr Val Ala Pro Ser Thr Cys Ser
225                 230                 235                 240

Lys Pro Met Cys Pro Pro Pro Glu Leu Pro Gly Gly Pro Ser Val Phe
                245                 250                 255

Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
            260                 265                 270

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Asp Asp Pro Glu Val
        275                 280                 285

Gln Phe Thr Trp Tyr Ile Asn Asn Glu Gln Val Arg Thr Ala Arg Pro
    290                 295                 300

Pro Leu Arg Glu Gln Gln Phe Asn Ser Thr Ile Arg Val Val Ser Thr
305                 310                 315                 320

Leu Pro Ile Ala His Gln Asp Trp Leu Arg Gly Lys Glu Phe Lys Cys
                325                 330                 335

Lys Val His Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
            340                 345                 350

Lys Ala Arg Gly Gln Pro Leu Glu Pro Lys Val Tyr Thr Met Gly Pro
        355                 360                 365

Pro Arg Glu Glu Leu Ser Ser Arg Ser Val Ser Leu Thr Cys Met Ile
    370                 375                 380

Asn Gly Phe Tyr Pro Ser Asp Ile Ser Val Glu Trp Glu Lys Asn Gly
385                 390                 395                 400

Lys Ala Glu Asp Asn Tyr Lys Thr Thr Pro Thr Val Leu Asp Ser Asp
                405                 410                 415
```

Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Pro Thr Ser Glu Trp
420 425 430

Gln Arg Gly Asp Val Phe Thr Cys Ser Val Met His Glu Ala Leu His
435 440 445

Asn His Tyr Thr Gln Lys Ser Ile Ser Arg Ser Pro Gly Lys
450 455 460

<210> 190
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 190
Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Pro Gly Ala Ile Cys Asp Pro Val Met Thr Gln Thr Pro Ser Ser
20 25 30

Thr Ser Ala Ala Val Gly Gly Thr Val Thr Ile Ser Cys Gln Ser Ser
35 40 45

Gln Ser Val Tyr Asn Asn Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
50 55 60

Gly Gln Pro Pro Lys Arg Leu Ile Tyr Glu Ser Ser Lys Leu Ala Ser
65 70 75 80

Gly Val Pro Ser Arg Phe Arg Gly Ser Gly Ser Gly Ala Gln Phe Thr
85 90 95

Leu Thr Ile Ser Asp Leu Glu Cys Asp Asp Ala Ala Thr Tyr Tyr Cys
100 105 110

```
Leu Gly Ala Tyr Tyr Thr Thr Leu Asp Phe Gly Gly Gly Thr Glu Val
        115                 120                 125


Val Val Arg Gly Asp Pro Val Ala Pro Thr Val Leu Ile Phe Pro Pro
    130                 135                 140


Ala Ala Asp Gln Val Ala Thr Gly Thr Val Thr Ile Val Cys Val Ala
145                 150                 155                 160


Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu Val Asp Gly Thr
                165                 170                 175


Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro Gln Asn Ser Ala
            180                 185                 190


Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu Thr Ser Thr Gln
        195                 200                 205


Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr Gln Gly Thr Thr
    210                 215                 220


Ser Val Val Gln Ser Phe Asn Arg Gly Asp Cys
225                 230                 235


<210> 191
<211> 460
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 191
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1               5                   10                  15


Val Gln Cys Gln Glu Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
            20                  25                  30
```

```
Pro Glu Gly Ser Leu Thr Leu Thr Cys Lys Ala Ser Gly Phe Asp Phe
        35                  40                  45

Ser Ser Asn Ala Met Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60

Glu Trp Ile Ala Cys Ile Tyr Asn Gly Asp Gly Ser Thr Tyr Tyr Ala
65                  70                  75                  80

Ser Trp Val Asn Gly Arg Phe Thr Ile Ser Lys Thr Ser Ser Thr Thr
                85                  90                  95

Val Thr Leu Gln Met Thr Ser Leu Thr Ala Ala Asp Thr Ala Thr Tyr
            100                 105                 110

Phe Cys Ala Arg Gly Leu Ser Asn Trp Asn Arg Asp Asn Leu Trp Gly
        115                 120                 125

Pro Gly Thr Leu Val Thr Val Ser Ser Gly Gln Pro Lys Ala Pro Ser
    130                 135                 140

Val Phe Pro Leu Ala Pro Cys Cys Gly Asp Thr Pro Ser Ser Thr Val
145                 150                 155                 160

Thr Leu Gly Cys Leu Val Lys Gly Tyr Leu Pro Glu Pro Val Thr Val
                165                 170                 175

Thr Trp Asn Ser Gly Thr Leu Thr Asn Gly Val Arg Thr Phe Pro Ser
            180                 185                 190

Val Arg Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Ser Val
        195                 200                 205

Thr Ser Ser Ser Gln Pro Val Thr Cys Asn Val Ala His Pro Ala Thr
    210                 215                 220
```

```
Asn Thr Lys Val Asp Lys Thr Val Ala Pro Ser Thr Cys Ser Lys Pro
225                 230                 235                 240

Met Cys Pro Pro Pro Glu Leu Pro Gly Gly Pro Ser Val Phe Ile Phe
                245                 250                 255

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
            260                 265                 270

Thr Cys Val Val Val Asp Val Ser Gln Asp Asp Pro Glu Val Gln Phe
        275                 280                 285

Thr Trp Tyr Ile Asn Asn Glu Gln Val Arg Thr Ala Arg Pro Pro Leu
    290                 295                 300

Arg Glu Gln Gln Phe Asn Ser Thr Ile Arg Val Val Ser Thr Leu Pro
305                 310                 315                 320

Ile Ala His Gln Asp Trp Leu Arg Gly Lys Glu Phe Lys Cys Lys Val
                325                 330                 335

His Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
            340                 345                 350

Arg Gly Gln Pro Leu Glu Pro Lys Val Tyr Thr Met Gly Pro Pro Arg
        355                 360                 365

Glu Glu Leu Ser Ser Arg Ser Val Ser Leu Thr Cys Met Ile Asn Gly
    370                 375                 380

Phe Tyr Pro Ser Asp Ile Ser Val Glu Trp Glu Lys Asn Gly Lys Ala
385                 390                 395                 400

Glu Asp Asn Tyr Lys Thr Thr Pro Thr Val Leu Asp Ser Asp Gly Ser
                405                 410                 415

Tyr Phe Leu Tyr Ser Lys Leu Ser Val Pro Thr Ser Glu Trp Gln Arg
            420                 425                 430
```

```
Gly Asp Val Phe Thr Cys Ser Val Met His Glu Ala Leu His Asn His
        435                 440                 445


Tyr Thr Gln Lys Ser Ile Ser Arg Ser Pro Gly Lys
    450                 455                 460


<210> 192
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 192
Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
1               5                   10                  15


Leu Pro Gly Ala Thr Phe Ala Gln Val Leu Thr Gln Thr Pro Ser Ser
            20                  25                  30


Val Ser Ala Ala Val Gly Gly Thr Ala Thr Ile Asn Cys Gln Ala Ser
        35                  40                  45


Gln Ser Leu Tyr Ser Pro Lys Asn Leu Ala Trp Tyr Gln Gln Thr Pro
    50                  55                  60


Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ser Ala Ser Lys Leu Ala Ser
65                  70                  75                  80


Gly Val Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Gln Phe Thr
                85                  90                  95


Leu Thr Ile Ser Gly Val Gln Cys Asp Asp Ala Ala Ile Tyr Tyr Cys
            100                 105                 110


Gln Gly Glu Phe Ser Cys Thr Thr Ala Ala Cys Phe Ala Phe Gly Gly
```

115 120 125

Gly Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu
130 135 140

Ile Phe Pro Pro Ala Ala Asp Gln Val Ala Thr Gly Thr Val Thr Ile
145 150 155 160

Val Cys Val Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu
165 170 175

Val Asp Gly Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro
180 185 190

Gln Asn Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu
195 200 205

Thr Ser Thr Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr
210 215 220

Gln Gly Thr Thr Ser Val Val Gln Ser Phe Asn Arg Gly Asp Cys
225 230 235

<210> 193
<211> 461
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 193
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1 5 10 15

Val Gln Cys Gln Ser Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro
20 25 30

```
Glu Gly Ser Leu Thr Leu Ala Cys Thr Ala Ser Gly Phe Ser Phe Ser
        35                  40                  45

Ser Tyr Tyr Tyr Ile Cys Trp Val Arg Gln Ala Pro Gly Thr Gly Leu
    50                  55                  60

Glu Trp Ile Gly Cys Ile Asn Thr Gly Ser Asp Asp Thr His Tyr Ala
65                  70                  75                  80

Ser Trp Leu Lys Gly Arg Phe Thr Phe Ser Lys Ala Ser Ser Thr Thr
                85                  90                  95

Leu Thr Leu Gln Met Thr Ser Leu Thr Ala Ala Asp Thr Ala Thr Tyr
            100                 105                 110

Phe Cys Ala Arg Ser Ser Gly Ser Ser Asp Asp Ala Tyr Asp Leu Trp
        115                 120                 125

Gly Pro Gly Thr Leu Val Thr Val Ser Ser Gly Gln Pro Lys Ala Pro
    130                 135                 140

Ser Val Phe Pro Leu Ala Pro Cys Cys Gly Asp Thr Pro Ser Ser Thr
145                 150                 155                 160

Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Leu Pro Glu Pro Val Thr
                165                 170                 175

Val Thr Trp Asn Ser Gly Thr Leu Thr Asn Gly Val Arg Thr Phe Pro
            180                 185                 190

Ser Val Arg Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Ser
        195                 200                 205

Val Thr Ser Ser Ser Gln Pro Val Thr Cys Asn Val Ala His Pro Ala
    210                 215                 220

Thr Asn Thr Lys Val Asp Lys Thr Val Ala Pro Ser Thr Cys Ser Lys
225                 230                 235                 240
```

```
Pro Met Cys Pro Pro Pro Glu Leu Pro Gly Gly Pro Ser Val Phe Ile
                245                 250                 255

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
            260                 265                 270

Val Thr Cys Val Val Val Asp Val Ser Gln Asp Asp Pro Glu Val Gln
        275                 280                 285

Phe Thr Trp Tyr Ile Asn Asn Glu Gln Val Arg Thr Ala Arg Pro Pro
    290                 295                 300

Leu Arg Glu Gln Gln Phe Asn Ser Thr Ile Arg Val Val Ser Thr Leu
305                 310                 315                 320

Pro Ile Ala His Gln Asp Trp Leu Arg Gly Lys Glu Phe Lys Cys Lys
                325                 330                 335

Val His Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
            340                 345                 350

Ala Arg Gly Gln Pro Leu Glu Pro Lys Val Tyr Thr Met Gly Pro Pro
        355                 360                 365

Arg Glu Glu Leu Ser Ser Arg Ser Val Ser Leu Thr Cys Met Ile Asn
    370                 375                 380

Gly Phe Tyr Pro Ser Asp Ile Ser Val Glu Trp Glu Lys Asn Gly Lys
385                 390                 395                 400

Ala Glu Asp Asn Tyr Lys Thr Thr Pro Thr Val Leu Asp Ser Asp Gly
                405                 410                 415

Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Pro Thr Ser Glu Trp Gln
            420                 425                 430
```

Arg Gly Asp Val Phe Thr Cys Ser Val Met His Glu Ala Leu His Asn
435 440 445

His Tyr Thr Gln Lys Ser Ile Ser Arg Ser Pro Gly Lys
450 455 460

<210> 194
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 194
Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Pro Gly Ala Arg Cys Asp Val Val Met Thr Gln Thr Pro Ala Ser
20 25 30

Val Ser Glu Pro Val Gly Gly Ala Val Thr Ile Lys Cys Gln Ala Ser
35 40 45

Gln Ser Ile Gly Ser Asn Leu Ala Trp Tyr Gln His Lys Pro Gly Gln
50 55 60

Pro Pro Lys Leu Leu Ile Tyr Phe Ala Ser Ser Leu Ala Ser Gly Val
65 70 75 80

Ser Ser Arg Phe Lys Gly Gly Arg Ser Gly Thr Gln Phe Thr Leu Thr
85 90 95

Ile Ser Asp Leu Glu Cys Ala Asp Ala Ala Thr Tyr Tyr Cys His Cys
100 105 110

Thr Tyr Tyr Pro Leu Ser Tyr Val Thr Phe Gly Gly Gly Thr Glu Val
115 120 125

```
Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Ile Phe Pro Pro
    130                 135                 140

Ala Ala Asp Gln Val Ala Thr Gly Thr Val Thr Ile Val Cys Val Ala
145                 150                 155                 160

Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu Val Asp Gly Thr
                165                 170                 175

Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro Gln Asn Ser Ala
            180                 185                 190

Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu Thr Ser Thr Gln
        195                 200                 205

Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr Gln Gly Thr Thr
    210                 215                 220

Ser Val Val Gln Ser Phe Asn Arg Gly Asp Cys
225                 230                 235


<210> 195
<211> 464
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 195
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1               5                   10                  15

Val Gln Cys Gln Ser Leu Glu Glu Ser Gly Gly Asp Leu Val Lys Pro
            20                  25                  30

Gly Thr Ser Leu Thr Leu Ser Cys Thr Ala Ser Gly Phe Ser Phe Gly
        35                  40                  45
```

```
Ser Tyr Tyr Tyr Met Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60

Glu Trp Ile Ala Cys Ile Asp Val Gly Ser Ser Gly Asp Thr Tyr Tyr
65                  70                  75                  80

Ala Ser Trp Val Asn Gly Arg Phe Thr Ile Ser Lys Thr Ser Ser Thr
                85                  90                  95

Thr Val Thr Leu Gln Met Thr Ser Leu Thr Ala Ala Asp Thr Ala Thr
            100                 105                 110

Tyr Phe Cys Ala Arg Asp Asp Thr Ala Ala Gly Gly Phe Gly Asn Leu
        115                 120                 125

Glu Leu Trp Gly Pro Gly Thr Leu Val Thr Val Ser Ser Gly Gln Pro
    130                 135                 140

Lys Ala Pro Ser Val Phe Pro Leu Ala Pro Cys Cys Gly Asp Thr Pro
145                 150                 155                 160

Ser Ser Thr Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Leu Pro Glu
                165                 170                 175

Pro Val Thr Val Thr Trp Asn Ser Gly Thr Leu Thr Asn Gly Val Arg
            180                 185                 190

Thr Phe Pro Ser Val Arg Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
        195                 200                 205

Val Val Ser Val Thr Ser Ser Ser Gln Pro Val Thr Cys Asn Val Ala
    210                 215                 220

His Pro Ala Thr Asn Thr Lys Val Asp Lys Thr Val Ala Pro Ser Thr
225                 230                 235                 240
```

```
Cys Ser Lys Pro Met Cys Pro Pro Pro Glu Leu Pro Gly Gly Pro Ser
                245                 250                 255

Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
            260                 265                 270

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Asp Asp Pro
        275                 280                 285

Glu Val Gln Phe Thr Trp Tyr Ile Asn Asn Glu Gln Val Arg Thr Ala
    290                 295                 300

Arg Pro Pro Leu Arg Glu Gln Gln Phe Asn Ser Thr Ile Arg Val Val
305                 310                 315                 320

Ser Thr Leu Pro Ile Ala His Gln Asp Trp Leu Arg Gly Lys Glu Phe
                325                 330                 335

Lys Cys Lys Val His Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
            340                 345                 350

Ile Ser Lys Ala Arg Gly Gln Pro Leu Glu Pro Lys Val Tyr Thr Met
        355                 360                 365

Gly Pro Pro Arg Glu Glu Leu Ser Ser Arg Ser Val Ser Leu Thr Cys
    370                 375                 380

Met Ile Asn Gly Phe Tyr Pro Ser Asp Ile Ser Val Glu Trp Glu Lys
385                 390                 395                 400

Asn Gly Lys Ala Glu Asp Asn Tyr Lys Thr Thr Pro Thr Val Leu Asp
                405                 410                 415

Ser Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Pro Thr Ser
            420                 425                 430

Glu Trp Gln Arg Gly Asp Val Phe Thr Cys Ser Val Met His Glu Ala
        435                 440                 445
```

```
Leu His Asn His Tyr Thr Gln Lys Ser Ile Ser Arg Ser Pro Gly Lys
    450                 455                 460


<210> 196
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 196
Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
1               5                   10                  15


Leu Pro Gly Ala Arg Cys Ala Phe Glu Leu Thr Gln Thr Pro Ser Ser
            20                  25                  30


Val Ser Glu Pro Val Gly Gly Thr Val Thr Ile Lys Cys Gln Ala Ser
        35                  40                  45


Gln Ser Ile Tyr Ser Tyr Phe Ser Trp Tyr Gln Gln Lys Pro Gly Gln
    50                  55                  60


Pro Pro Lys Arg Leu Ile Tyr Gln Ala Ser Thr Leu Ala Ser Gly Val
65                  70                  75                  80


Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
                85                  90                  95


Ile Ser Asp Leu Glu Cys Ala Asp Ala Ala Thr Tyr Tyr Cys Gln Asn
            100                 105                 110


Asn Tyr Gly Arg Gly Ser Gly Ser Tyr Phe Phe Gly Phe Gly Gly Gly
        115                 120                 125


Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Ile
```

```
    130                 135                 140

Phe Pro Pro Ala Ala Asp Gln Val Ala Thr Gly Thr Val Thr Ile Val
145                 150                 155                 160

Cys Val Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu Val
                165                 170                 175

Asp Gly Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro Gln
            180                 185                 190

Asn Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu Thr
        195                 200                 205

Ser Thr Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr Gln
    210                 215                 220

Gly Thr Thr Ser Val Val Gln Ser Phe Asn Arg Gly Asp Cys
225                 230                 235


<210> 197
<211> 456
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 197
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1               5                   10                  15

Val Gln Cys Gln Ser Leu Glu Glu Ser Gly Gly Asp Leu Val Lys Pro
            20                  25                  30

Gly Ala Ser Leu Thr Leu Thr Cys Lys Ala Ser Gly Ile Asp Phe Ser
        35                  40                  45
```

```
Ser Gly Tyr Gly Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60

Glu Tyr Ile Gly Tyr Ile Asp Thr Gly Ser Gly Ser Thr Tyr Tyr Ala
65                  70                  75                  80

Asn Trp Ala Lys Gly Arg Phe Thr Ile Ser Lys Thr Ser Ser Thr Met
                85                  90                  95

Val Thr Leu Gln Met Thr Ser Leu Thr Val Ala Asp Thr Ala Thr Tyr
            100                 105                 110

Phe Cys Ala Lys Gly Gly Ala Ile Asp Leu Trp Gly Pro Gly Thr Leu
        115                 120                 125

Val Thr Val Ser Ser Gly Gln Pro Lys Ala Pro Ser Val Phe Pro Leu
    130                 135                 140

Ala Pro Cys Cys Gly Asp Thr Pro Ser Ser Thr Val Thr Leu Gly Cys
145                 150                 155                 160

Leu Val Lys Gly Tyr Leu Pro Glu Pro Val Thr Val Thr Trp Asn Ser
                165                 170                 175

Gly Thr Leu Thr Asn Gly Val Arg Thr Phe Pro Ser Val Arg Gln Ser
            180                 185                 190

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Ser Val Thr Ser Ser Ser
        195                 200                 205

Gln Pro Val Thr Cys Asn Val Ala His Pro Ala Thr Asn Thr Lys Val
    210                 215                 220

Asp Lys Thr Val Ala Pro Ser Thr Cys Ser Lys Pro Met Cys Pro Pro
225                 230                 235                 240

Pro Glu Leu Pro Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro
                245                 250                 255
```

```
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
            260                 265                 270

Val Asp Val Ser Gln Asp Asp Pro Glu Val Gln Phe Thr Trp Tyr Ile
        275                 280                 285

Asn Asn Glu Gln Val Arg Thr Ala Arg Pro Pro Leu Arg Glu Gln Gln
    290                 295                 300

Phe Asn Ser Thr Ile Arg Val Val Ser Thr Leu Pro Ile Ala His Gln
305                 310                 315                 320

Asp Trp Leu Arg Gly Lys Glu Phe Lys Cys Lys Val His Asn Lys Ala
                325                 330                 335

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Arg Gly Gln Pro
            340                 345                 350

Leu Glu Pro Lys Val Tyr Thr Met Gly Pro Pro Arg Glu Glu Leu Ser
        355                 360                 365

Ser Arg Ser Val Ser Leu Thr Cys Met Ile Asn Gly Phe Tyr Pro Ser
    370                 375                 380

Asp Ile Ser Val Glu Trp Glu Lys Asn Gly Lys Ala Glu Asp Asn Tyr
385                 390                 395                 400

Lys Thr Thr Pro Thr Val Leu Asp Ser Asp Gly Ser Tyr Phe Leu Tyr
                405                 410                 415

Ser Lys Leu Ser Val Pro Thr Ser Glu Trp Gln Arg Gly Asp Val Phe
            420                 425                 430

Thr Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
        435                 440                 445
```

Ser Ile Ser Arg Ser Pro Gly Lys
450 455

<210> 198
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 198
Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Pro Gly Ala Arg Cys Ala Asp Ile Val Met Thr Gln Thr Pro Ala
20 25 30

Ser Val Glu Ala Ala Val Gly Gly Thr Val Thr Ile Lys Cys Gln Ala
35 40 45

Ser Gln Ser Ile Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
50 55 60

Gln Arg Pro Lys Leu Leu Ile Tyr Arg Ala Ser Thr Leu Ala Ser Gly
65 70 75 80

Val Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu
85 90 95

Thr Ile Ser Asp Leu Glu Cys Ala Asp Ala Ala Thr Tyr Tyr Cys His
100 105 110

Thr Tyr Tyr Leu Ser Ser Ser Ile Ser Tyr Gly Asn Thr Phe Gly Gly
115 120 125

Gly Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu
130 135 140

```
Ile Phe Pro Pro Ala Ala Asp Gln Val Ala Thr Gly Thr Val Thr Ile
145                 150                 155                 160


Val Cys Val Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu
                165                 170                 175


Val Asp Gly Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro
            180                 185                 190


Gln Asn Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu
        195                 200                 205


Thr Ser Thr Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr
    210                 215                 220


Gln Gly Thr Thr Ser Val Val Gln Ser Phe Asn Arg Gly Asp Cys
225                 230                 235


<210> 199
<211> 465
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 199
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1               5                   10                  15


Val Gln Cys Gln Glu Gln Leu Glu Glu Ser Gly Gly Asp Leu Val Lys
            20                  25                  30


Pro Glu Gly Ser Leu Thr Leu Thr Cys Lys Ala Ser Gly Phe Ser Phe
        35                  40                  45


Ser Ser Ile Tyr Trp Ile Cys Trp Val Arg Gln Ala Pro Gly Lys Gly
    50                  55                  60
```

```
Leu Glu Trp Ile Ala Cys Thr Thr Val Val Lys Ser Gly Arg Thr Tyr
65                  70                  75                  80

Tyr Ala Asn Trp Ala Lys Gly Arg Phe Thr Ile Ser Lys Thr Ser Ser
                85                  90                  95

Thr Thr Val Thr Leu Gln Met Thr Ser Leu Thr Ala Ala Asp Thr Ala
            100                 105                 110

Thr Tyr Phe Cys Ala Arg Glu Phe Val Asp Gly Gly Gly Ser Ser Gly
        115                 120                 125

Arg Asp Leu Trp Gly Pro Gly Thr Leu Val Thr Val Ser Ser Gly Gln
    130                 135                 140

Pro Lys Ala Pro Ser Val Phe Pro Leu Ala Pro Cys Cys Gly Asp Thr
145                 150                 155                 160

Pro Ser Ser Thr Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Leu Pro
                165                 170                 175

Glu Pro Val Thr Val Thr Trp Asn Ser Gly Thr Leu Thr Asn Gly Val
            180                 185                 190

Arg Thr Phe Pro Ser Val Arg Gln Ser Ser Gly Leu Tyr Ser Leu Ser
        195                 200                 205

Ser Val Val Ser Val Thr Ser Ser Ser Gln Pro Val Thr Cys Asn Val
    210                 215                 220

Ala His Pro Ala Thr Asn Thr Lys Val Asp Lys Thr Val Ala Pro Ser
225                 230                 235                 240

Thr Cys Ser Lys Pro Met Cys Pro Pro Pro Glu Leu Pro Gly Gly Pro
                245                 250                 255
```

```
Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
            260                 265                 270

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Asp Asp
        275                 280                 285

Pro Glu Val Gln Phe Thr Trp Tyr Ile Asn Asn Glu Gln Val Arg Thr
    290                 295                 300

Ala Arg Pro Pro Leu Arg Glu Gln Gln Phe Asn Ser Thr Ile Arg Val
305                 310                 315                 320

Val Ser Thr Leu Pro Ile Ala His Gln Asp Trp Leu Arg Gly Lys Glu
                325                 330                 335

Phe Lys Cys Lys Val His Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
            340                 345                 350

Thr Ile Ser Lys Ala Arg Gly Gln Pro Leu Glu Pro Lys Val Tyr Thr
        355                 360                 365

Met Gly Pro Pro Arg Glu Glu Leu Ser Ser Arg Ser Val Ser Leu Thr
    370                 375                 380

Cys Met Ile Asn Gly Phe Tyr Pro Ser Asp Ile Ser Val Glu Trp Glu
385                 390                 395                 400

Lys Asn Gly Lys Ala Glu Asp Asn Tyr Lys Thr Thr Pro Thr Val Leu
                405                 410                 415

Asp Ser Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Pro Thr
            420                 425                 430

Ser Glu Trp Gln Arg Gly Asp Val Phe Thr Cys Ser Val Met His Glu
        435                 440                 445

Ala Leu His Asn His Tyr Thr Gln Lys Ser Ile Ser Arg Ser Pro Gly
    450                 455                 460
```

Lys
465

<210> 200
<211> 236
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 200
Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Pro Gly Ala Arg Cys Ala Tyr Asp Met Thr Gln Thr Pro Ala Ser
20 25 30

Val Glu Ala Ala Val Gly Gly Thr Val Thr Ile Lys Cys Gln Ala Ser
35 40 45

Gln Ser Ile Ser Arg Asp Leu Ser Trp Tyr Gln Gln Lys Pro Gly Gln
50 55 60

Pro Pro Lys Arg Leu Ile Tyr Lys Ala Ser Thr Leu Ala Ser Gly Val
65 70 75 80

Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
85 90 95

Ile Ser Asp Leu Glu Cys Ala Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
100 105 110

Gly Tyr Ser Ser Ile Asp Val Asp Asn Asp Phe Gly Gly Gly Thr Glu
115 120 125

Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Ile Phe Pro

```
    130                 135                 140

Pro Ala Ala Asp Gln Val Ala Thr Gly Thr Val Thr Ile Val Cys Val
145                 150                 155                 160

Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu Val Asp Gly
                165                 170                 175

Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro Gln Asn Ser
            180                 185                 190

Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu Thr Ser Thr
        195                 200                 205

Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr Gln Gly Thr
    210                 215                 220

Thr Ser Val Val Gln Ser Phe Asn Arg Gly Asp Cys
225                 230                 235


<210> 201
<211> 467
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 201
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1               5                   10                  15

Val Gln Cys Gln Glu Gln Leu Glu Glu Ser Gly Gly Gly Leu Val Lys
            20                  25                  30

Pro Glu Gly Ser Leu Thr Leu Thr Cys Lys Ala Ser Gly Phe Asp Leu
        35                  40                  45
```

```
Ser Ser Gly Tyr Asp Met Cys Trp Val Arg Gln Ala Pro Gly Lys Gly
    50                  55                  60

Leu Glu Trp Ile Ala Cys Ile Tyr Ala Asp Tyr Ser Gly Ser Thr Tyr
65                  70                  75                  80

Tyr Ala Ser Trp Val Asn Gly Arg Phe Thr Ile Ser Ser Ser Thr Ser
                85                  90                  95

Leu Asn Thr Val Asp Leu Lys Met Thr Ser Leu Thr Ala Ala Asp Thr
            100                 105                 110

Ala Thr Tyr Phe Cys Ala Arg Gly Ala Thr Gly Asn Gly Gly Tyr Gly
        115                 120                 125

Tyr Tyr Phe Asn Leu Trp Gly Pro Gly Thr Leu Val Thr Val Ser Ser
    130                 135                 140

Gly Gln Pro Lys Ala Pro Ser Val Phe Pro Leu Ala Pro Cys Cys Gly
145                 150                 155                 160

Asp Thr Pro Ser Ser Thr Val Thr Leu Gly Cys Leu Val Lys Gly Tyr
                165                 170                 175

Leu Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Thr Leu Thr Asn
            180                 185                 190

Gly Val Arg Thr Phe Pro Ser Val Arg Gln Ser Ser Gly Leu Tyr Ser
        195                 200                 205

Leu Ser Ser Val Val Ser Val Thr Ser Ser Ser Gln Pro Val Thr Cys
    210                 215                 220

Asn Val Ala His Pro Ala Thr Asn Thr Lys Val Asp Lys Thr Val Ala
225                 230                 235                 240

Pro Ser Thr Cys Ser Lys Pro Met Cys Pro Pro Pro Glu Leu Pro Gly
                245                 250                 255
```

```
Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln
        275                 280                 285

Asp Asp Pro Glu Val Gln Phe Thr Trp Tyr Ile Asn Asn Glu Gln Val
    290                 295                 300

Arg Thr Ala Arg Pro Pro Leu Arg Glu Gln Gln Phe Asn Ser Thr Ile
305                 310                 315                 320

Arg Val Val Ser Thr Leu Pro Ile Ala His Gln Asp Trp Leu Arg Gly
                325                 330                 335

Lys Glu Phe Lys Cys Lys Val His Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

Glu Lys Thr Ile Ser Lys Ala Arg Gly Gln Pro Leu Glu Pro Lys Val
        355                 360                 365

Tyr Thr Met Gly Pro Pro Arg Glu Glu Leu Ser Ser Arg Ser Val Ser
    370                 375                 380

Leu Thr Cys Met Ile Asn Gly Phe Tyr Pro Ser Asp Ile Ser Val Glu
385                 390                 395                 400

Trp Glu Lys Asn Gly Lys Ala Glu Asp Asn Tyr Lys Thr Thr Pro Thr
                405                 410                 415

Val Leu Asp Ser Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val
            420                 425                 430

Pro Thr Ser Glu Trp Gln Arg Gly Asp Val Phe Thr Cys Ser Val Met
        435                 440                 445
```

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Ile Ser Arg Ser
    450   455   460

Pro Gly Lys
465

<210> 202
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 202
Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
1   5   10   15

Leu Pro Gly Ala Arg Cys Ala Asp Ile Val Met Thr Gln Thr Pro Ala
            20   25   30

Ser Val Ser Glu Pro Val Gly Gly Thr Val Thr Ile Lys Cys Gln Ala
        35   40   45

Ser Gln Asn Ile Asn Ser Gly Leu Ala Trp Tyr Gln Gln Lys Pro Gly
    50   55   60

Gln Pro Pro Lys Leu Leu Ile Tyr Lys Ala Ser Thr Leu Ala Ser Gly
65   70   75   80

Val Ser Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu
                85   90   95

Thr Ile Ser Asp Leu Glu Cys Ala Asp Ala Ala Thr Tyr Tyr Cys Gln
            100   105   110

Thr Tyr Tyr Tyr Ser Ser Ser Ser Ser Asp Asn Ala Phe Gly Gly Gly
        115   120   125

```
Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Ile
    130                 135                 140


Phe Pro Pro Ala Ala Asp Gln Val Ala Thr Gly Thr Val Thr Ile Val
145                 150                 155                 160


Cys Val Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu Val
                165                 170                 175


Asp Gly Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro Gln
            180                 185                 190


Asn Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu Thr
        195                 200                 205


Ser Thr Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr Gln
    210                 215                 220


Gly Thr Thr Ser Val Val Gln Ser Phe Asn Arg Gly Asp Cys
225                 230                 235


<210> 203
<211> 462
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 203
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1               5                   10                  15


Val Gln Cys Gln Ser Leu Glu Glu Ser Gly Gly Asp Leu Val Lys Pro
            20                  25                  30


Gly Ala Ser Leu Thr Leu Thr Cys Thr Ala Ser Gly Phe Ser Phe Ser
        35                  40                  45
```

```
Ser Ser Tyr Trp Ile Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60

Glu Trp Ile Ala Cys Ile Tyr Gly Gly Ser Ser Gly Asn Ile Ala Tyr
65                  70                  75                  80

Ala Ser Trp Ala Lys Gly Arg Phe Thr Ile Ser Lys Thr Ser Ser Thr
                85                  90                  95

Thr Val Thr Leu Gln Met Thr Ser Leu Thr Ala Ala Asp Thr Ala Thr
            100                 105                 110

Tyr Phe Cys Ala Arg Asp Ile Pro Ser Asp Ala Phe Thr Leu Asp Leu
        115                 120                 125

Trp Gly Pro Gly Thr Leu Val Thr Val Ser Ser Gly Gln Pro Lys Ala
    130                 135                 140

Pro Ser Val Phe Pro Leu Ala Pro Cys Cys Gly Asp Thr Pro Ser Ser
145                 150                 155                 160

Thr Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Leu Pro Glu Pro Val
                165                 170                 175

Thr Val Thr Trp Asn Ser Gly Thr Leu Thr Asn Gly Val Arg Thr Phe
            180                 185                 190

Pro Ser Val Arg Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
        195                 200                 205

Ser Val Thr Ser Ser Ser Gln Pro Val Thr Cys Asn Val Ala His Pro
    210                 215                 220

Ala Thr Asn Thr Lys Val Asp Lys Thr Val Ala Pro Ser Thr Cys Ser
225                 230                 235                 240
```

```
Lys Pro Met Cys Pro Pro Pro Glu Leu Pro Gly Gly Pro Ser Val Phe
                245                 250                 255

Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
            260                 265                 270

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Asp Asp Pro Glu Val
        275                 280                 285

Gln Phe Thr Trp Tyr Ile Asn Asn Glu Gln Val Arg Thr Ala Arg Pro
    290                 295                 300

Pro Leu Arg Glu Gln Gln Phe Asn Ser Thr Ile Arg Val Val Ser Thr
305                 310                 315                 320

Leu Pro Ile Ala His Gln Asp Trp Leu Arg Gly Lys Glu Phe Lys Cys
                325                 330                 335

Lys Val His Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
            340                 345                 350

Lys Ala Arg Gly Gln Pro Leu Glu Pro Lys Val Tyr Thr Met Gly Pro
        355                 360                 365

Pro Arg Glu Glu Leu Ser Ser Arg Ser Val Ser Leu Thr Cys Met Ile
    370                 375                 380

Asn Gly Phe Tyr Pro Ser Asp Ile Ser Val Glu Trp Glu Lys Asn Gly
385                 390                 395                 400

Lys Ala Glu Asp Asn Tyr Lys Thr Thr Pro Thr Val Leu Asp Ser Asp
                405                 410                 415

Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Pro Thr Ser Glu Trp
            420                 425                 430

Gln Arg Gly Asp Val Phe Thr Cys Ser Val Met His Glu Ala Leu His
        435                 440                 445
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Asn His Tyr Thr Gln Lys Ser Ile Ser Arg Ser Pro Gly Lys
    450   455   460

<210> 204
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 204
Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
1   5   10   15

Leu Pro Gly Ala Thr Phe Ala Gln Val Leu Thr Gln Thr Pro Ser Ser
            20   25   30

Val Ser Ala Ala Val Gly Ser Thr Val Thr Ile Asn Cys Gln Ala Ser
        35   40   45

Gln Ser Val Tyr Lys Asp Asn Asn Leu Ala Trp Tyr Gln Gln Lys Pro
    50   55   60

Gly Gln Pro Pro Lys Leu Leu Ile Tyr Lys Ala Ser Thr Leu Ala Ser
65   70   75   80

Gly Val Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Gln Phe Thr
                85   90   95

Leu Thr Ile Ser Gly Val Gln Cys Glu Asp Ala Ala Thr Tyr Tyr Cys
            100   105   110

Gln Gly Glu Phe Ser Cys Gly Ser Ala Asp Cys Ile Ala Phe Gly Gly
        115   120   125

Gly Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu

130 135 140

Ile Phe Pro Pro Ala Ala Asp Gln Val Ala Thr Gly Thr Val Thr Ile
145 150 155 160

Val Cys Val Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu
165 170 175

Val Asp Gly Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro
180 185 190

Gln Asn Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu
195 200 205

Thr Ser Thr Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr
210 215 220

Gln Gly Thr Thr Ser Val Val Gln Ser Phe Asn Arg Gly Asp Cys
225 230 235

<210> 205
<211> 456
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 205
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1 5 10 15

Val Gln Cys Gln Ser Leu Glu Glu Ser Gly Gly Asp Leu Val Lys Pro
20 25 30

Gly Ala Ser Leu Thr Leu Thr Cys Lys Gly Ser Gly Ile Asp Phe Ser
35 40 45

```
Ser Gly Tyr Gly Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60

Glu Tyr Ile Gly Tyr Ile Asp Thr Gly Tyr Gly Ser Thr Tyr Tyr Ala
65                  70                  75                  80

Ser Trp Ala Lys Gly Arg Phe Thr Ile Ser Lys Thr Ser Ser Thr Thr
                85                  90                  95

Val Thr Leu Gln Met Thr Ser Leu Thr Val Ala Asp Thr Ala Thr Tyr
            100                 105                 110

Phe Cys Ala Lys Gly Gly Ala Ile Asp Leu Trp Gly Pro Gly Thr Leu
        115                 120                 125

Val Thr Val Ser Ser Gly Gln Pro Lys Ala Pro Ser Val Phe Pro Leu
    130                 135                 140

Ala Pro Cys Cys Gly Asp Thr Pro Ser Ser Thr Val Thr Leu Gly Cys
145                 150                 155                 160

Leu Val Lys Gly Tyr Leu Pro Glu Pro Val Thr Val Thr Trp Asn Ser
                165                 170                 175

Gly Thr Leu Thr Asn Gly Val Arg Thr Phe Pro Ser Val Arg Gln Ser
            180                 185                 190

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Ser Val Thr Ser Ser Ser
        195                 200                 205

Gln Pro Val Thr Cys Asn Val Ala His Pro Ala Thr Asn Thr Lys Val
    210                 215                 220

Asp Lys Thr Val Ala Pro Ser Thr Cys Ser Lys Pro Met Cys Pro Pro
225                 230                 235                 240

Pro Glu Leu Pro Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro
                245                 250                 255
```

```
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
            260                 265                 270

Val Asp Val Ser Gln Asp Asp Pro Glu Val Gln Phe Thr Trp Tyr Ile
        275                 280                 285

Asn Asn Glu Gln Val Arg Thr Ala Arg Pro Pro Leu Arg Glu Gln Gln
    290                 295                 300

Phe Asn Ser Thr Ile Arg Val Val Ser Thr Leu Pro Ile Ala His Gln
305                 310                 315                 320

Asp Trp Leu Arg Gly Lys Glu Phe Lys Cys Lys Val His Asn Lys Ala
                325                 330                 335

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Arg Gly Gln Pro
            340                 345                 350

Leu Glu Pro Lys Val Tyr Thr Met Gly Pro Pro Arg Glu Glu Leu Ser
        355                 360                 365

Ser Arg Ser Val Ser Leu Thr Cys Met Ile Asn Gly Phe Tyr Pro Ser
    370                 375                 380

Asp Ile Ser Val Glu Trp Glu Lys Asn Gly Lys Ala Glu Asp Asn Tyr
385                 390                 395                 400

Lys Thr Thr Pro Thr Val Leu Asp Ser Asp Gly Ser Tyr Phe Leu Tyr
                405                 410                 415

Ser Lys Leu Ser Val Pro Thr Ser Glu Trp Gln Arg Gly Asp Val Phe
            420                 425                 430

Thr Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
        435                 440                 445
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Ser Ile Ser Arg Ser Pro Gly Lys
    450   455

<210> 206
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 206
Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
1   5   10   15

Leu Pro Gly Ala Thr Phe Ala Ala Val Leu Thr Gln Thr Pro Ala Ser
            20   25   30

Thr Ser Ala Ala Val Gly Gly Thr Val Thr Ile Asn Cys Gln Ser Ser
        35   40   45

Gln Ser Val Tyr Arg Ser Asn Trp Leu Ala Trp Tyr Gln Gln Lys Pro
    50   55   60

Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Val Phe Asn Leu Ala Ser
65   70   75   80

Gly Val Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Gln Phe Thr
                85   90   95

Leu Thr Ile Ser Gly Val Gln Cys Ala Asp Ala Ala Thr Tyr Tyr Cys
            100   105   110

Gln Gly Ser Tyr Tyr Ser Gly Asn Trp Tyr Ser Ala Phe Gly Gly Gly
        115   120   125

Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Ile
    130   135   140

```
Phe Pro Pro Ala Ala Asp Gln Val Ala Thr Gly Thr Val Thr Ile Val
145                 150                 155                 160


Cys Val Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu Val
                165                 170                 175


Asp Gly Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro Gln
            180                 185                 190


Asn Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu Thr
        195                 200                 205


Ser Thr Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr Gln
    210                 215                 220


Gly Thr Thr Ser Val Val Gln Ser Phe Asn Arg Gly Asp Cys
225                 230                 235


<210> 207
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 207
Ala Ala Trp Asp Asp Ser Leu Asn Gly Leu Asn Trp Val
1               5                   10


<210> 208
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"
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<400> 208
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser
            20   25

<210> 209
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 209
Gly Phe Thr Phe Ser Asn Tyr Gly
1   5

<210> 210
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 210
Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
1   5   10   15

Tyr

<210> 211
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 211
Ile Ser Ser Ser Gly Ser Thr Val
1 5

<210> 212
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 212
Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
1 5 10 15

Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Asp Glu Asp
20 25 30

Thr Ala Val Tyr Tyr Cys Ala Ser
35 40

<210> 213
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 213
Gly Gln Leu Asp Thr Ser Asp Ala Phe Asp Ile
1 5 10

<210> 214
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 214
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 215
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 215
Asp Ile Glu Met Thr Gln Ser Pro Ser Ser Pro Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
20 25

<210> 216
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 216
Gln Ser Ile Ser Ser Tyr
1 5

<210> 217
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 217
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
1   5   10   15

Tyr

<210> 218
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 218
Ala Ala Ser
1

<210> 219
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 219
Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
1   5   10   15

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
            20   25   30

Thr Tyr Tyr Cys
        35

<210> 220
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 220
Gln Gln Ser Tyr Ser Thr Pro Leu Thr
1 5

<210> 221
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 221
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> 222
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 222
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Ser Gly Arg
1 5 10 15

Ser Leu Arg Val Ser Cys Ala Ala Ser
20 25

<210> 223
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 223
Gly Phe Ser Phe Ser Ser Tyr Gly
1 5

<210> 224
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 224
Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
1 5 10 15

Tyr

<210> 225
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 225
Ile Ser Ser Ser Gly Ser Thr Ile
1 5

<210> 226
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 226
Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
1 5 10 15

Ala Glu Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
20 25 30

Thr Ala Val Tyr Tyr Cys Ala Arg
35 40

<210> 227
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 227
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
20 25

<210> 228
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

peptide"

<400> 228
Gln Gly Ile Ser Asn Tyr
1 5

<210> 229
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 229
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile
1 5 10 15

Tyr

<210> 230
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 230
Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
20 25 30

Thr Tyr Tyr Cys
35

<210> 231

<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 231
Phe Gly Gly Gly Thr Lys Val Glu Val Lys
1 5 10

<210> 232
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 232
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 233
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 233
Ile Ser Ser Ser Ser Ser Thr Ile
1 5

<210> 234
<211> 11

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<220>
<221> MOD_RES
<222> (3)..(3)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Any amino acid

<400> 234
Gly Gln Xaa Asp Xaa Ser Asp Ala Phe Asp Ile
1 5 10

<210> 235
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<220>
<221> MOD_RES
<222> (3)..(3)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (16)..(16)
<223> Any amino acid

<400> 235
Leu Asn Xaa Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Xaa
1 5 10 15

Tyr

<210> 236
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<400> 236
Xaa Ala Ser
1

<210> 237
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> MOD_RES
<222> (31)..(31)
<223> Any amino acid

<400> 237
Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
1   5   10   15

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Xaa Ala
            20   25   30

Thr Tyr Tyr Cys
35

<210> 238
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Any amino acid

<400> 238
Phe Gly Gly Gly Xaa Lys Xaa Glu Ile Lys
1 5 10

<210> 239
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 239
Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn
1 5 10 15

Ala Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
20 25 30

Thr Ala Leu Tyr Tyr Cys Ala Lys

35 40

<210> 240
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 240
Ala Thr Arg Tyr Asp Ile Leu Thr Gly Tyr Ser Asp Gly Val Asp Tyr
1 5 10 15

Phe Asp Tyr

<210> 241
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 241
His Gln Ser Tyr Ser Thr Pro Tyr Thr
1 5

<210> 242
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 242
Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
1 5 10

<210> 243
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 243
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 244
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 244
Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
1 5 10 15

Asn

<210> 245
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 245
Ile Lys Gln Asp Gly Ser Glu Lys
1   5

<210> 246
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 246
Tyr Tyr Val Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
1   5   10   15

Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
            20   25   30

Thr Ala Val Tyr Tyr Cys Ala Arg
        35   40

<210> 247
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 247
Val Thr Ser Pro His Ala Phe Asp Ile
1   5

<210> 248
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 248
Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 249
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 249
Asp Ile Gln Met Thr Gln Ser Pro Ser Ala Met Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
20 25

<210> 250
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 250
Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Val Pro Lys Arg Leu Ile
1 5 10 15

Tyr

<210> 251
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 251
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 252
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 252
Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
1 5 10 15

Gly

<210> 253
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 253
Ile Asn Trp Asn Gly Gly Ser Thr
1 5

<210> 254

<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 254
Gly Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
1 5 10 15

Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Gly Glu Asp
20 25 30

Thr Ala Val Tyr Tyr Cys Val Thr
35 40

<210> 255
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 255
Gln Gly Ser Ala Phe Asp Ile
1 5

<210> 256
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 256
Ser Tyr Glu Leu Thr Gln Pro Pro Ser Leu Ser Val Ser Pro Gly Gln
1 5 10 15

Thr Ala Arg Ile Thr Cys Ser Gly Asp
            20   25

<210> 257
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 257
Ala Leu Ala Lys Gln Tyr
1   5

<210> 258
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 258
Ala Tyr Trp Tyr Gln Gln Thr Pro Gly Gln Ala Pro Val Leu Val Ile
1   5   10   15

Tyr

<210> 259
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 259
Lys Asp Thr
1

<210> 260
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 260
Glu Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Ser Ser Gly
1 5 10 15

Thr Thr Val Thr Leu Thr Ile Ser Gly Val Gln Ala Glu Asp Glu Val
20 25 30

Asp Tyr Tyr Cys
35

<210> 261
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 261
Gln Ser Thr Asp Ser Ser Gly Thr Tyr Gln Val
1 5 10

<210> 262
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 262
Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
1 5 10

<210> 263
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 263
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser
20 25

<210> 264
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 264
Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
1 5 10 15

Trp

<210> 265
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 265
Ile Ser Ala Tyr Asn Gly Asn Thr
1 5

<210> 266
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 266
Asn Tyr Ala Gln Lys Leu Gln Gly Arg Val Thr Met Thr Thr Asp Thr
1 5 10 15

Ser Thr Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp
20 25 30

Thr Ala Ala Tyr Tyr Cys Ala Arg
35 40

<210> 267
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 267
Val Thr Gly Ile Thr Gly Thr Thr Ile Asp Pro
1 5 10

<210> 268

<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 268
Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
1 5 10

<210> 269
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 269
Asp Ala Ser
1

<210> 270
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 270
Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala
20 25 30

Val Tyr Tyr Cys
35

<210> 271
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 271
Gln Gln Tyr Asn Asn Trp Pro Gln Thr
1 5

<210> 272
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 272
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> 273
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 273
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 274
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 274
Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
1 5 10 15

Ala

<210> 275
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 275
Ile Ser Gly Ser Gly Gly Ser Thr
1 5

<210> 276
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 276
Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
1 5 10 15

Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
            20   25   30

Thr Ala Val Tyr Tyr Cys Ala Arg
        35   40

<210> 277
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 277
Asp Tyr Gly Gly Tyr Asp Gly Val Tyr Phe Asp Tyr
1   5   10

<210> 278
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 278
Ser Tyr Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln
1   5   10   15

Thr Val Arg Ile Thr Cys Gln Gly Asp
            20   25

<210> 279
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

peptide"

<400> 279
Ser Leu Arg Ser Tyr Tyr
1 5

<210> 280
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 280
Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile
1 5 10 15

Tyr

<210> 281
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 281
Gly Lys Asn
1

<210> 282
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 282
Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly
1   5   10   15

Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala
            20   25   30

Asp Tyr Tyr Cys
        35

<210> 283
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 283
Asn Ser Arg Asp Ser Ser Gly Asn His Val Val
1   5   10

<210> 284
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 284
Phe Gly Gly Gly Thr Lys Val Thr Val Leu
1   5   10

<210> 285
<211> 25
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 285
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 286
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 286
Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
1 5 10 15

Val

<210> 287
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 287
Ile Ser Tyr Asp Gly Ser Asn Lys
1 5

<210> 288
<211> 40
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 288
Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn
1 5 10 15

Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
20 25 30

Thr Ala Val Tyr Tyr Cys Ala Arg
35 40

<210> 289
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 289
Asp Arg Asp Val Gly Pro Thr Tyr Tyr Tyr Tyr Gly Met Asp Val
1 5 10 15

<210> 290
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 290
Ser Tyr Glu Leu Thr Gln Pro Pro Ser Leu Ser Val Ser Pro Gly Gln
1 5 10 15

Thr Ala Arg Ile Thr Cys Ser Gly His
            20   25

<210> 291
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 291
Ala Leu Pro Lys Gln Tyr
1   5

<210> 292
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 292
Glu Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Ser Ser Gly
1   5   10   15

Thr Thr Val Thr Leu Thr Ile Ser Gly Val Gln Ala Glu Asp Glu Ala
            20   25   30

Asp Tyr Tyr Cys
        35

<210> 293
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

peptide"

<400> 293
Gln Ser Ala Asp Ser Ser Gly Pro Tyr Gln Val
1 5 10

<210> 294
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 294
Phe Gly Gly Gly Thr Gln Leu Thr Val Leu
1 5 10

<210> 295
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 295
Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
1 5 10 15

Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
20 25 30

Thr Ala Val Tyr Tyr Cys Ala Lys
35 40

<210> 296
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 296
Asp Arg Glu Tyr Ile Ala Val Ala Ala Asp Tyr
1 5 10

<210> 297
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 297
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
1 5 10

<210> 298
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 298
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Thr Ile Ser Ile Thr Cys Arg Ala Ser
20 25

<210> 299
<211> 36
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 299
Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Arg
1 5 10 15

Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Pro Glu Asp Phe Ala
20 25 30

Thr Tyr Tyr Cys
35

<210> 300
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 300
Gln Gln Ser Tyr Ser Thr Pro Phe Thr
1 5

<210> 301
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 301
Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> 302
<211> 25
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 302
Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser
20 25

<210> 303
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 303
Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
1 5 10 15

Ile

<210> 304
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 304
Ile Asn Pro Ser Gly Gly Ser Thr
1 5

<210> 305
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 305
Ile Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr
1 5 10 15

Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp
20 25 30

Thr Ala Val Tyr Tyr Cys Ala Arg
35 40

<210> 306
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 306
Ser Leu Arg Asp Gly Tyr Asn Tyr Ile Gly Ser Leu Gly Tyr
1 5 10

<210> 307
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 307
Gln Ser Glu Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln

1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser
20 25

<210> 308
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 308
Ser Ser Asn Ile Gly Ser Asn Tyr
1 5

<210> 309
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 309
Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile
1 5 10 15

Tyr

<210> 310
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 310
Arg Asn Asn
1

<210> 311
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 311
Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
1 5 10 15

Thr Ser Ala Ser Leu Ala Ile Arg Gly Leu Gln Ser Glu Asp Glu Ala
20 25 30

Gly Tyr Tyr Cys
35

<210> 312
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 312
Gly Phe Thr Phe Asp Asp Tyr Ala
1 5

<210> 313
<211> 17
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 313
Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
1 5 10 15

Gly

<210> 314
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 314
Ile Ser Trp Asn Ser Gly Ser Thr
1 5

<210> 315
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 315
Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
1 5 10 15

Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
20 25 30

Thr Ala Val Tyr Tyr Cys Ala Gly
35 40

<210> 316
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 316
Gly Ser Arg Arg Tyr Asp Ser Ser Gly Tyr Tyr Tyr Glu Ser Phe Asp
1 5 10 15

Tyr

<210> 317
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 317
Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
20 25 30

Thr Tyr Tyr Cys
35

<210> 318
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 318
Gln Gln Ser Tyr His Thr Pro Tyr Thr
1 5

<210> 319
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 319
Gln Met Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser
20 25

<210> 320
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 320
Gly Gly Thr Phe Ser Ser Tyr Ala
1 5

<210> 321
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

peptide"

<400> 321
Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
1 5 10 15

Arg

<210> 322
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 322
Ile Ile Pro Ile Leu Gly Ile Ala
1 5

<210> 323
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 323
Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Lys
1 5 10 15

Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp
20 25 30

Thr Ala Val Tyr Tyr Cys Ala Arg
35 40

<210> 324

<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 324
Asp Ile Asn Arg Tyr Asn Trp Asn Phe Arg Ala Phe Asp Ile
1 5 10

<210> 325
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 325
Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr
1 5 10

<210> 326
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 326
Leu Ala Trp Tyr Gln Gln Lys Pro Arg Gln Pro Pro Lys Leu Leu Ile
1 5 10 15

Tyr

<210> 327
<211> 3

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 327
Trp Ala Ser
1

<210> 328
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 328
Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Asn Gly Ser Gly
1 5 10 15

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala
20 25 30

Ala Tyr Tyr Cys
35

<210> 329
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 329
Gln Gln His Tyr Ser Thr Pro Leu Thr
1 5

<210> 330
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 330
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser
20 25

<210> 331
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 331
Asn Tyr Ala Gln Lys Leu Gln Gly Arg Val Thr Met Thr Thr Asn Thr
1 5 10 15

Ser Thr Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp
20 25 30

Thr Ala Val Tyr Tyr Cys Ala Arg
35 40

<210> 332
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 332
Leu Asn Trp Tyr Arg Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
1 5 10 15

Tyr

<210> 333
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 333
Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Ala Ala
20 25 30

Thr Tyr Tyr Cys
35

<210> 334
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 334
Gln Gln Tyr Asp Ser Gln Ser Gly Thr
1 5

<210> 335
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 335
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 336
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 336
Ile Ser Tyr Asp Gly Val Lys Lys
1 5

<210> 337
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 337
Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
1 5 10 15

Ser Lys Ser Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Val Asp Asp

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            20                  25                  30

Thr Ala Val Tyr Tyr Cys Ala Lys
        35                  40


<210> 338
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 338
Asp Leu Gly Trp Gln Asn Asp Tyr
1               5


<210> 339
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 339
Gln Ser Val Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1               5                   10                  15


Ser Ile Thr Ile Ser Cys Thr Gly Thr Asp Leu Gly Trp Gln Asn Asp
            20                  25                  30


Tyr



<210> 340
<211> 9
<212> PRT
<213> Artificial Sequence
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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 340
Ser Ser Asp Val Gly Gly His Asn Tyr
1 5

<210> 341
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 341
Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu Met Ile
1 5 10 15

Tyr

<210> 342
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 342
Asp Val Ser
1

<210> 343
<211> 36
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 343
Asn Arg Pro Ser Gly Val Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly
1 5 10 15

Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala
20 25 30

Asp Tyr Tyr Cys
35

<210> 344
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 344
Ser Ser Tyr Thr Ser Ser Ser Pro Trp Val
1 5 10

<210> 345
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 345
Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
1 5 10

<210> 346
<211> 25
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 346
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser
            20   25

<210> 347
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 347
Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
1   5   10   15

Ser Lys Asn Ala Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
            20   25   30

Thr Ala Val Tyr Tyr Cys Arg Gly
        35   40

<210> 348
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 348

Tyr Cys Ser Ser Thr Ser Cys Tyr Gly Arg Arg Gly Ala Phe Asp Ile
1   5   10   15

<210> 349
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 349
Ser Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1   5   10

<210> 350
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 350
Gln Ala Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1   5   10   15

Arg Val Thr Ile Ser Cys Ser Gly Arg
            20   25

<210> 351
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 351
Asn Ser Asn Ile Gly Ser Asn Asn

1 5

<210> 352
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 352
Val Asn Trp Tyr Gln His Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile
1 5 10 15

Tyr

<210> 353
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 353
Ser Asn Asn
1

<210> 354
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 354
Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Ala Ser Lys Ser Gly
1 5 10 15

Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala
            20   25   30

Asp Tyr Tyr Cys
        35

<210> 355
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 355
Ala Ala Trp Asp Asp Arg Met Asn Gly Pro Val
1   5   10

<210> 356
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 356
Ile Gly Gly Gly Thr Lys Val Thr Val Leu Gly
1   5   10

<210> 357
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 357
Met His Trp Val Arg Gln Ala Pro Ala Lys Gly Leu Val Trp Val Ser
1   5   10   15

Arg

<210> 358
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 358
Ile Asn Ser Asp Gly Ser Ser Thr
1   5

<210> 359
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 359
Ser Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
1   5   10   15

Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
            20   25   30

Thr Ala Val Tyr Tyr Cys Ala Arg
        35   40

<210> 360
<211> 14
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 360
Asp Phe Trp Ser Gly Arg Pro Tyr Tyr Tyr Tyr Met Asp Val
1 5 10

<210> 361
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 361
Gln Asp Ile Gly Asp Asp
1 5

<210> 362
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 362
Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
1 5 10 15

Tyr

<210> 363
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 363
Thr Leu Gln Gly Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
20 25 30

Thr Tyr Tyr Cys
35

<210> 364
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 364
Gln Gln Ser Tyr Ser Thr Pro Arg Thr
1 5

<210> 365
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 365
Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
1 5 10 15

Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Arg Arg Ala Glu Asp

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            20                  25                  30

Thr Ala Val Tyr Tyr Cys Ala Arg
        35                  40


<210> 366
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 366
Trp Gly Ile Val Ala Ala Arg Pro Asn Tyr Tyr Tyr Gly Met Asp Val
1               5                   10                  15


<210> 367
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 367
Gln Ser Ala Leu Thr Gln Pro Arg Ser Val Ser Gly Ser Pro Gly Gln
1               5                   10                  15


Ser Val Thr Ile Ser Cys Thr Gly Thr
            20                  25


<210> 368
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"
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<400> 368
Ser Ser Asp Val Gly Gly Tyr Asn Tyr
1   5

<210> 369
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 369
Ser Ser Tyr Ala Asn Asn Ser Pro Trp Val
1   5   10

<210> 370
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 370
Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly
1   5   10

<210> 371
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 371
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Arg Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser
            20   25

<210> 372
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 372
Asn Tyr Ala Gln Lys Leu Gln Gly Arg Val Thr Met Thr Thr Asp Thr
1   5   10   15

Ser Thr Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp
            20   25   30

Thr Ala Val Tyr Tyr Cys Ala Arg
        35   40

<210> 373
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 373
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser
            20   25

<210> 374
<211> 6
<212> PRT

<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 374
Gln Asp Ile Ser Asn Tyr
1 5

<210> 375
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 375
Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala
20 25 30

Thr Tyr Tyr Cys
35

<210> 376
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 376
Gln Gln Tyr Ala Asn Leu Pro Leu Thr
1 5

<210> 377
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 377
Gly Phe Thr Val Ser Ser Asn Tyr
1 5

<210> 378
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 378
Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
1 5 10 15

Val

<210> 379
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 379
Ile Tyr Ser Gly Gly Ser Thr
1 5

<210> 380

<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 380
Gly Gly Leu Thr Gly Asp Asp Ala Phe Asp Ile
1 5 10

<210> 381
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 381
Gln Ser Ile Ser Ser Phe
1 5

<210> 382
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 382
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile
1 5 10 15

Tyr

<210> 383
<211> 3

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 383
Thr Thr Ser
1

<210> 384
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 384
Gln Gln Gly Asn Ser Leu Pro Leu Thr
1 5

<210> 385
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 385
Asp Lys Glu Leu Ser Tyr
1 5

<210> 386
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 386
Gln Ser Gly Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

Ser Ile Thr Ile Ser Cys Thr Gly Thr
20 25

<210> 387
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 387
Glu Val Ser
1

<210> 388
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 388
Asn Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
1 5 10 15

Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala
20 25 30

Asp Tyr Tyr Cys
35

<210> 389
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 389
Lys Thr Ser
1

<210> 390
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 390
Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
1 5 10 15

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
20 25 30

Thr Tyr Tyr Cys
35

<210> 391
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 391
Met Ser Trp Val Arg Gln Ala Pro Ala Lys Gly Leu Glu Trp Val Ser

1 5 10 15

Ala

<210> 392
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 392
Asp Arg Pro Tyr Ser Tyr Gly Lys Asn Asp Ala Phe Asp Ile
1 5 10

<210> 393
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 393
Gln Asp Val Ser Asn Tyr
1 5

<210> 394
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 394
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
1 5 10

<210> 395
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 395
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser
20 25

<210> 396
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 396
Gly Tyr Thr Phe Thr Ser Tyr Tyr
1 5

<210> 397
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 397
Ser Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr
1 5 10 15

Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp
            20   25   30

Thr Ala Val Tyr Tyr Cys Ala Arg
        35   40

<210> 398
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 398
Ala Gly Gly Tyr Tyr Tyr Tyr Tyr Met Asp Val
1   5   10

<210> 399
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 399
Gln Ser Gly Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1   5   10   15

Arg Val Thr Ile Ser Cys Ser Gly Ser
            20   25

<210> 400
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 400
Gly Pro Asn Ile Gly Asn Asn Tyr
1 5

<210> 401
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 401
Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Met
1 5 10 15

Tyr

<210> 402
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 402
Ser Pro Trp Leu Ile Thr Phe Gly Gly Val Ile Ala Met Gly Tyr
1 5 10 15

<210> 403
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

peptide"

<400> 403
Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser
20 25

<210> 404
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 404
Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
1 5 10 15

Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg Ser Glu Asp Glu Ala
20 25 30

Asp Tyr Tyr Cys
35

<210> 405
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 405
Ala Ala Trp Asp Asp Ser Leu Ser Gly Val Val
1 5 10

<210> 406

<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 406
Phe Gly Gly Gly Thr Gln Leu Thr Val Leu Gly
1 5 10

<210> 407
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 407
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
20 25

<210> 408
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 408
Gln Gln Phe Asn Asn Tyr Pro Leu Thr
1 5

<210> 409
<211> 25

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 409
Gln Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser
20 25

<210> 410
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 410
Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
1 5 10 15

Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala
20 25 30

Asp Tyr Tyr Cys
35

<210> 411
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 411
Ala Ala Trp Asp Asp Ser Leu Asn Gly Tyr Val
1   5   10

<210> 412
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<400> 412
Phe Gly Thr Gly Thr Lys Leu Thr Val Leu Gly
1   5   10

<210> 413
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 413
Gln Ile Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1   5   10   15

Ser Leu Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20   25   30

Ala Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
        35   40   45

Gly Ile Ile Asn Thr Gln Thr Gly Lys Pro Lys Tyr Ser Pro Ser Phe
    50   55   60

Gln Gly Gln Phe Ile Phe Ser Leu Asp Thr Ser Ile Asn Thr Thr Tyr
65   70   75   80

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Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Ile Tyr Phe Cys
                85                  90                  95


Thr Arg Leu Gly Thr Gly Asn Thr Lys Gly Phe Ala Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 414
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 414
Asp Ile Gln Ile Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1               5                   10                  15


Asp Lys Val Thr Ile Thr Cys Arg Ser Ser Gln Ser Leu Leu Tyr Ser
            20                  25                  30


Glu Asn Asn Gln Asp Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
        35                  40                  45


Ala Pro Lys Leu Leu Ile Tyr Gly Ala Ser Asn Leu Gln Ser Gly Val
    50                  55                  60


Pro Ser Arg Phe Ser Gly Arg Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80


Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Glu Gln
                85                  90                  95


Thr Tyr Arg Tyr Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile
            100                 105                 110
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Lys Arg

<210> 415
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 415
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1   5   10   15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20   25   30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35   40   45

Pro Asp Tyr Asn Met Asp Trp Val Arg Gln Ala Pro Gly Gln Arg Leu
    50   55   60

Glu Trp Met Gly Tyr Ile Asn Pro Asp Asn Gly Gly Thr Ile Tyr Asn
65   70   75   80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Thr Ser Ala Ser
                85   90   95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100   105   110

Tyr Tyr Cys Ala Arg Leu Asp Ser Ser Gly Tyr Gly Tyr Tyr Ala Met
        115   120   125

Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr

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    130                 135                 140

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145                 150                 155                 160

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
                165                 170                 175

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
        195                 200                 205

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
225                 230                 235                 240

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            260                 265                 270

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    290                 295                 300

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305                 310                 315                 320

Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                325                 330                 335
```

```
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
            340                 345                 350


Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        355                 360                 365


Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
    370                 375                 380


Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385                 390                 395                 400


Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                405                 410                 415


Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
            420                 425                 430


Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
        435                 440                 445


Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
    450                 455                 460


Leu Ser Leu Ser Pro Gly Lys
465                 470


<210> 416
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 416
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1               5                   10                  15
```

```
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45

Pro Asp Tyr Asn Met Asp Trp Val Arg Gln Ala Pro Gly Gln Arg Leu
    50                  55                  60

Glu Trp Ile Gly Tyr Ile Asn Pro Asp Asn Gly Gly Thr Ile Tyr Asn
65                  70                  75                  80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Thr Ser Ala Ser
                85                  90                  95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Arg Leu Asp Ser Ser Gly Tyr Gly Tyr Tyr Ala Met
        115                 120                 125

Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr
    130                 135                 140

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145                 150                 155                 160

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
                165                 170                 175

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
        195                 200                 205
```

```
Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
225                 230                 235                 240

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            260                 265                 270

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    290                 295                 300

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305                 310                 315                 320

Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                325                 330                 335

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
            340                 345                 350

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        355                 360                 365

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
    370                 375                 380

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385                 390                 395                 400

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                405                 410                 415
```

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
420 425 430

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
435 440 445

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
450 455 460

Leu Ser Leu Ser Pro Gly Lys
465 470

<210> 417
<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 417
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Pro Asp Tyr Asn Met Asp Trp Val Arg Gln Ala Pro Gly Gln Arg Leu
50 55 60

Glu Trp Met Gly Tyr Ile Asn Pro Asp Asn Gly Gly Thr Ile Tyr Asn
65 70 75 80

Gln Lys Phe Lys Gly Arg Ala Thr Leu Thr Val Asp Thr Ser Ala Ser

```
                85                  90                  95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Arg Leu Asp Ser Ser Gly Tyr Gly Tyr Tyr Ala Met
        115                 120                 125

Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr
    130                 135                 140

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145                 150                 155                 160

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
                165                 170                 175

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
        195                 200                 205

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
225                 230                 235                 240

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            260                 265                 270

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285
```

```
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    290                 295                 300

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305                 310                 315                 320

Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                325                 330                 335

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
            340                 345                 350

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        355                 360                 365

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
    370                 375                 380

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385                 390                 395                 400

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                405                 410                 415

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
            420                 425                 430

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
        435                 440                 445

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
    450                 455                 460

Leu Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 418

<211> 471
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 418
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Pro Asp Tyr Asn Met Asp Trp Val Arg Gln Ala Pro Gly Gln Ser Leu
50 55 60

Glu Trp Ile Gly Tyr Ile Asn Pro Asp Asn Gly Gly Thr Ile Tyr Asn
65 70 75 80

Gln Lys Phe Lys Gly Arg Ala Thr Leu Thr Val Asp Thr Ser Ala Ser
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Leu Asp Ser Ser Gly Tyr Gly Tyr Tyr Ala Met
115 120 125

Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr
130 135 140

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145 150 155 160

```
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
                165                 170                 175

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
        195                 200                 205

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
225                 230                 235                 240

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            260                 265                 270

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    290                 295                 300

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305                 310                 315                 320

Ala Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                325                 330                 335

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
            340                 345                 350

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
        355                 360                 365
```

```
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
    370                 375                 380

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385                 390                 395                 400

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
                405                 410                 415

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
            420                 425                 430

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
        435                 440                 445

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
    450                 455                 460

Leu Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 419
<211> 237
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 419

```
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1               5                   10                  15

Val His Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val
            20                  25                  30

Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Glu Ser Val
```

```
        35                  40                  45

Asp Asn Tyr Gly Ile Ser Phe Met His Trp Tyr Gln Gln Lys Pro Gly
    50                  55                  60

Gln Pro Pro Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Asp Ser Gly
65                  70                  75                  80

Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
                85                  90                  95

Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Thr Tyr Tyr Cys Gln
            100                 105                 110

Gln Ser Tyr Lys Asp Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu
        115                 120                 125

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
    130                 135                 140

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
145                 150                 155                 160

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
                165                 170                 175

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
            180                 185                 190

Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
        195                 200                 205

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
    210                 215                 220

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235
```

<210> 420
<211> 237
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 420
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val
20 25 30

Ser Pro Gly Gln Arg Ala Thr Ile Thr Cys Arg Ala Ser Glu Ser Val
35 40 45

Asp Asn Tyr Gly Ile Ser Phe Met His Trp Tyr Gln Gln Lys Pro Gly
50 55 60

Gln Pro Pro Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Asp Ser Glu
65 70 75 80

Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu
85 90 95

Thr Ile Asn Pro Val Glu Ala Asn Asp Thr Ala Thr Tyr Tyr Cys Gln
100 105 110

Gln Ser Tyr Lys Asp Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu
115 120 125

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
130 135 140

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
145 150 155 160

```
Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
                165                 170                 175


Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
            180                 185                 190


Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
        195                 200                 205


Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
    210                 215                 220


Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235


<210> 421
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 421
Gln Ser Leu Glu Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Ala Ser
1               5                   10                  15


Leu Thr Leu Thr Cys Arg Val Ser Gly Phe Ser Phe Ser Ser Ser Tyr
            20                  25                  30


Tyr Met Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45


Ala Cys Ile Gly Thr Thr Arg Gly Ser Thr Tyr Tyr Ala Thr Trp Ala
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Lys Ile Ser Ser Thr Thr Val Thr Leu
```

65 70 75 80

Gln Met Thr Ser Leu Thr Asp Ala Asp Thr Ala Thr Tyr Phe Cys Ala
85 90 95

Arg Asp Ala Thr Gly Tyr Arg Ile Asn Thr Ile Gly Leu Tyr Phe Asn
100 105 110

Leu Trp Gly Pro Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 422
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 422
Gln Ser Leu Leu Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser
1 5 10 15

Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ser Phe Ser Ser Ser Tyr
20 25 30

Tyr Met Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Cys Ile Gly Thr Thr Arg Gly Ser Thr Tyr Tyr Ala Asp Ser Ala
50 55 60

Lys Gly Arg Phe Thr Ile Ser Lys Ile Ser Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Thr Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys Ala
85 90 95

Arg Asp Ala Thr Gly Tyr Arg Ile Asn Thr Ile Gly Leu Tyr Phe Asn
100 105 110

Leu Trp Gly Pro Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 423
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 423
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ser Phe Ser Ser Ser
20 25 30

Tyr Tyr Met Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
35 40 45

Val Ser Cys Ile Gly Thr Thr Arg Gly Ser Thr Tyr Tyr Ala Asp Ser
50 55 60

Ala Lys Gly Arg Phe Thr Ile Ser Lys Asp Asn Ser Lys Asn Thr Val
65 70 75 80

Tyr Leu Gln Met Thr Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe
85 90 95

Cys Ala Arg Asp Ala Thr Gly Tyr Arg Ile Asn Thr Ile Gly Leu Tyr
100 105 110

Phe Asn Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 424
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 424
Gln Ser Leu Leu Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser
1 5 10 15

Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ser Phe Ser Ser Ser Tyr
20 25 30

Tyr Met Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Cys Ile Gly Thr Thr Arg Gly Ser Thr Tyr Tyr Ala Asp Ser Ala
50 55 60

Lys Gly Arg Phe Thr Ile Ser Lys Glu Ser Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Ser Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys Ala
85 90 95

Arg Asp Ala Thr Gly Tyr Arg Ile Asn Thr Ile Gly Leu Tyr Phe Asn
100 105 110

Leu Trp Gly Pro Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 425
<211> 126
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 425
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ser Phe Ser Ser Ser
20 25 30

Tyr Tyr Met Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
35 40 45

Val Ser Cys Ile Gly Thr Thr Arg Gly Ser Thr Tyr Tyr Ala Asp Ser
50 55 60

Ala Lys Gly Arg Phe Thr Ile Ser Lys Asp Asn Ser Lys Asn Thr Val
65 70 75 80

Tyr Leu Gln Met Ser Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe
85 90 95

Cys Ala Arg Asp Ala Thr Gly Tyr Arg Ile Asn Thr Ile Gly Leu Tyr
100 105 110

Phe Asn Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 426
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 426
Gln Ser Leu Leu Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser
1 5 10 15

```
Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ser Phe Ser Ser Ser Tyr
            20                  25                  30


Tyr Met Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Cys Ile Gly Thr Thr Arg Gly Ser Thr Tyr Tyr Ala Asp Ser Ala
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Lys Glu Ser Lys Asn Thr Val Tyr Leu
65                  70                  75                  80


Gln Met Ser Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys Ala
                85                  90                  95


Arg Asp Ala Thr Gly Tyr Arg Ile Gln Thr Ile Gly Leu Tyr Phe Asn
            100                 105                 110


Leu Trp Gly Pro Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 427
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 427
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Ser Phe Ser Ser Ser
            20                  25                  30


Tyr Tyr Met Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
```

```
        35                  40                  45

Val Ser Cys Ile Gly Thr Thr Arg Gly Ser Thr Tyr Tyr Ala Asp Ser
    50                  55                  60

Ala Lys Gly Arg Phe Thr Ile Ser Lys Asp Asn Ser Lys Asn Thr Val
65                  70                  75                  80

Tyr Leu Gln Met Ser Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe
                85                  90                  95

Cys Ala Arg Asp Ala Thr Gly Tyr Arg Ile Gln Thr Ile Gly Leu Tyr
            100                 105                 110

Phe Asn Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125


<210> 428
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 428
Glu Leu Thr Gln Thr Pro Ser Ser Val Glu Ala Ala Val Gly Gly Thr
1               5                   10                  15

Pro Thr Ile Lys Cys Gln Ala Ser Gln Thr Ile Tyr Ser Tyr Leu Ser
            20                  25                  30

Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Glu
        35                  40                  45

Ala Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
    50                  55                  60
```

```
Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Asp Leu Glu Cys Ala Asp
65                  70                  75                  80


Ala Ala Thr Tyr Tyr Cys Gln Ser Tyr His Gly Thr Ala Ser Thr Glu
                85                  90                  95


Tyr Asn Thr Phe Gly Gly Gly Thr Glu Val Val Val Lys
            100                 105


<210> 429
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 429
Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
1               5                   10                  15


Val Thr Ile Thr Cys Gln Ala Ser Gln Thr Ile Tyr Ser Tyr Leu Ser
            20                  25                  30


Trp Tyr Gln Gln Lys Pro Gly Lys Pro Pro Lys Leu Leu Ile Tyr Glu
        35                  40                  45


Ala Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
    50                  55                  60


Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65                  70                  75                  80


Phe Ala Thr Tyr Tyr Cys Gln Ser Tyr His Gly Thr Ala Ser Thr Glu
                85                  90                  95


Tyr Asn Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105
```

<210> 430
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 430
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Thr Ile Tyr Ser Tyr
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Pro Pro Lys Leu Leu Ile
35 40 45

Tyr Glu Ala Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Ser Tyr His Gly Thr Ala Ser
85 90 95

Thr Glu Tyr Asn Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 431
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 431
Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
1   5   10   15

Val Thr Ile Thr Cys Gln Ala Ser Gln Thr Ile Tyr Ser Tyr Leu Ser
            20   25   30

Trp Tyr Gln Gln Lys Pro Gly Lys Pro Pro Lys Leu Leu Ile Tyr Glu
        35   40   45

Ala Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
    50   55   60

Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65   70   75   80

Thr Ala Thr Tyr Tyr Cys Gln Ser Tyr His Gly Thr Ala Ser Thr Glu
                85   90   95

Tyr Asn Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 432
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 432
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Thr Ile Tyr Ser Tyr
            20   25   30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Pro Pro Lys Leu Leu Ile
        35   40   45

```
Tyr Glu Ala Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Thr Ala Thr Tyr Tyr Cys Gln Ser Tyr His Gly Thr Ala Ser
                85                  90                  95


Thr Glu Tyr Asn Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


<210> 433
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 433
Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
1               5                   10                  15


Val Thr Ile Thr Cys Gln Ala Ser Gln Thr Ile Tyr Ser Tyr Leu Ser
            20                  25                  30


Trp Tyr Gln Gln Lys Pro Gly Lys Pro Pro Lys Leu Leu Ile Tyr Glu
        35                  40                  45


Ala Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
    50                  55                  60


Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65                  70                  75                  80


Thr Ala Thr Tyr Tyr Cys Gln Ser Tyr His Gly Thr Ala Ser Thr Glu
```

```
                85                  90                  95


Tyr Gln Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105


<210> 434
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<400> 434
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Thr Ile Tyr Ser Tyr
            20                  25                  30


Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Pro Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Glu Ala Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Thr Ala Thr Tyr Tyr Cys Gln Ser Tyr His Gly Thr Ala Ser
                85                  90                  95


Thr Glu Tyr Gln Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


<210> 435
<211> 26
<212> PRT
<213> Artificial Sequence
```

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 435
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
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Asp Tyr His Cys
        35