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

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
3 June 2004 (03.06.2004)

PCT

(10) International Publication Number
WO 2004/045542 A2

(51) International Patent Classification[7]: A61K

(21) International Application Number:
PCT/US2003/036763

(22) International Filing Date:
17 November 2003 (17.11.2003)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
10/295,734 15 November 2002 (15.11.2002) US

(71) Applicant: **ARIZONA BOARD OF REGENTS ARIZONA STATE UNIVERSITY** [US/US]; P.O. Box 879209, Tempe, AZ 85287 (US).

(72) Inventors: **MASSIA, Stephen, P.**; 2313 East Englewood Street, Mesa, AZ 85213 (US). **EHTESHAMI, Ghola, Reza**; 7735 East Adele Court, Scouttsdale, AZ 85255 (US).

(74) Agent: **BARBARA, J., Luther**; Quarles & Brady Streich Lang LLP, One Renaissance Square, Two North Central Avenue, Phoenix, AZ 85004 (US).

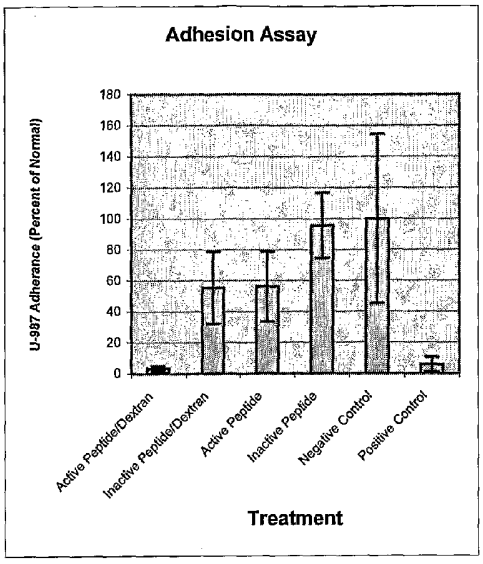
(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States *(regional)*: ARIPO patent (BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:
— *without international search report and to be republished upon receipt of that report*

[Continued on next page]

(54) Title: THERAPEUTIC BIOCONJUGATES



Monocyte adhesion to bovine endothelial cells. All but the positive control were activated with TNF-α to induce ICAM expression. SM1 is the CD11b/CD18 agonist and SM2 is the scrambled, inactive peptide.

(57) Abstract: A therapeutic bioconjugate is composed of a hydrophilic polymer covalently bound to one or more peptides capable of binding specifically to a ligand expressed on a cell surface and thereby forming a biofilm to prevent attachment of cells with the binding partner of the ligand.

WO 2004/045542 A2

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

THERAPEUTIC BIOCONJUGATES

CROSS REFERENCE

[0001] This application is a continuation in part of pending U.S. Utility Application, Serial No. 10/295,734, filed November 15, 2002, the disclosure of which is hereby incorporated by reference in its entirety.

FIELD OF THE INVENTION

[0002] The present invention relates generally to biomaterials and, more specifically, to therapeutic conjugates of polymers and peptides capable of binding selectively to ligands expressed on certain cells in target tissues.

SEQUENCE LISTING

[0003] This application also includes a Sequence Listing (158 pages) on paper and on one diskette and two Addenda, all of which are hereby incorporated by reference.

BACKGROUND

[0004] Integrins are cell-bound molecules that aid cell-to-cell interactions by providing binding sites for other cells. The integrins are receptors that recognize specific ligands in a variety of physiological and pathological processes. Cellular interactions mediated by the integrins include adhesion, migration, release of soluble factors (cytokines, free radical species, degradative enzymes, etc.), and extracellular matrix (ECM) deposition. These cellular interactions affect pathological processes by reversing them or by sustaining, enhancing or amplifying them.

[0005] The integrin superfamily is an important and well characterized group of cell-surface receptors for both cell-substrate and cell-cell adhesion. Integrins are characteristically membrane-spanning heterodimeric protein complexes consisting of a α subunit and a β subunit. Eighteen distinct α subunits and eight distinct β subunits have currently been isolated and identified. While 144 combinations are theoretically possible, 24 $\alpha\beta$ combinations have been observed. Integrin complexes containing the β_1 and β_3 subunits generally are involved in cell adhesion to the extracellular matrix, while the β_2 integrins are involved in cell-cell adhesion.

The complement of integrins expressed by different cell types varies greatly. Depending on the cell type, mammalian cells express from two to ten different integrins, which are the means by which the cell senses its local environment and responds to changes in extracellular matrix composition and topography. Integrins were initially identified as cell-surface adhesion receptors mechanically linking the cell's cytoskeleton to the extracellular matrix or to other cells. Now integrins are also recognized as cell signaling receptors implicated in the regulation of cellular adhesion, migration, tumor metastasis, proliferation, angiogenesis, bone resorption, apoptosis, and gene expression.

[0006] The pivotal importance of integrins in health and disease has lead to a search for therapeutic strategies that target specific receptor-ligand interactions. Research efforts have generally focused on developing antibodies, peptides, and small molecules as therapeutic agents that selectively inhibit these specific receptor/ligand interactions and suppress pathological immune responses. Strategies for pharmacological modulation include blockade of receptors (the application of mAb, soluble ligands, and synthetic ligands); inhibition of expression of adhesion receptors (immunosuppressive and anti-inflammatory drugs, phosphodiesterase and proteosome inhibitors, antisense oligonucleotides); and inhibition of activation of integrins (antagonists of chemokines; anti-inflammatory drugs).

[0007] A threatening pathological condition involving specific receptor-ligand interactions is an excessive inflammatory response. Receptor-ligand interactions are critical for every step of an inflammatory response including neutrophil, monocyte, lymphocyte, and macrophage adhesion to vascular endothelial cells, transvascular migration into inflamed tissues, and phagocytosis of foreign bodies, injured tissues, pathogens, etc. During the inflammatory response, cell signaling releases degradative enzymes and oxidative free radicals to facilitate pathogen and injured tissue removal. Excessive inflammatory response results in the release of these degradative agents at abnormally high levels, damaging healthy tissue.

[0008] One therapeutic approach involves antibodies that are effective in immunomodulation. Researchers have evaluated the effects of post-injury treatment with antibody inhibitors of CD11b/CD18 on pathogenic immune responses. Post-injury treatment with monoclonal antibodies directed against CD11b (integrin α_M subunit) has reduced intestinal ischemia/reperfusion-mediated lung and liver injury without affecting levels of circulating and sequestered PMNs. Monoclonal antibody directed against CD18 (integrin β_2 subunit) has

effectively reduced intestinal ischemia/reperfusion-mediated tissue injury *in vivo*. Preclinical studies have also shown that anti-ICAM-1 and anti-CD11b/CD18 therapies can increase tolerance (decrease rejection) in several transplantation models including cardiac, cornea, skin, pancreatic islet, and peripheral nerve allografts.

[0009] In another approach, antisense oligonucleotides, blocking ICAM-1 expression in donor and host tissues, are being developed to limit reperfusion injury and decrease allograft rejection rates for heart and kidney transplant.

[0010] However, the current therapeutic regimens against CD11b/CD18 are limited to local delivery because systemic delivery would lead to a globally impaired immune system. Delivery systems and reagents that selectively target and block cell adhesion to prevent pathological inflammation have been sought.

[0011] The repertoire of leukocyte types and receptor-ligand interaction described for inflammatory responses are also involved in autoimmune diseases [rheumatoid arthritis (RA), multiple sclerosis (MS), Graves disease, Crohn's disease (CD), AIDS, diabetes, graft-versus-host disease (GVHD), inflammatory bowel disease (IBD)] and rejection of allograft tissues/organs.

[0012] Autoimmune and allograft rejection responses are distinguished by the recruitment of T-cells and the development of a specific/adaptive immune response. Integrin interactions with ligands play a key role in recruiting circulating T-cells to extravascular sites where autoimmune and allograft rejection occurs. In the case of T-cells, extravascular infiltration is critical for antigen recognition, clonal expansion of specific antigen-responsive T-cells, and the destructive attack of cytotoxic T-cells on antigen-bearing tissues. These specific receptor-ligand interactions represent therapeutic targets for suppressing pathologic adaptive immune responses, and therapeutic strategies have been sought to modify receptor-ligand interactions in therapy of autoimmune diseases and allograft rejection.

[0013] New reagents and methods for treating and preventing excessive inflammation, autoimmune diseases, tissue rejection, cancer metastasis and other pathological conditions preceded by the binding of an integrin receptor with its ligand are being sought.

BRIEF DESCRIPTION OF THE FIGURES

[0014] FIG 1 schematically represents the anti-inflammatory/immunosuppressant action of the bioconjugates of the present invention. The normal immune response to vascular injury

and the response of the injured site in the presence of the biospecific bioconjugates are illustrated. The diagram shows the biointerface formed by the bioconjugates of the present invention creating a physical barrier against subsequent inflammatory cell adhesion.

[0015] FIG 2 is a reaction scheme for the preparation of a preferred embodiment of the present invention, a dextran-peptide bioconjugate.

[0016] FIG 3 is a nuclear magnetic resonance representation of dextran.

[0017] FIG 4 illustrates the results of an adhesion assay of a bioconjugate of the present invention with bovine endothelial cells stimulated to express the integrin ligand ICAM-1. In this assay, the bioconjugate effectively bound to endothelial cells, reducing monocyte adhesion to levels observed in control, non-stimulated cells.

SUMMARY

[0018] Bioconjugates capable of preventing cellular interactions mediated by integrin/ligand binding have been discovered. When administered to an individual, the bioconjugates form a cell adhesion barrier in a target tissue that prevents and treats the pathological conditions preceded by cellular interactions. The bioconjugates comprise a hydrophilic polymer and a peptide wherein the peptide preferably comprises at least the binding site of an integrin for a ligand expressed on a cell. When applied to a living tissue, the bioconjugates bind specifically to cells expressing the ligand and form a blockade or biofilm that prevents subsequent cell binding at the blocked tissue. Pathological consequences of cellular interactions, which include inflammation, autoimmune diseases, tissue rejection, cancer metastasis and other pathological conditions preceded by cellular interactions, are thus prevented.

[0019] The therapeutic bioconjugate includes a hydrophilic polymer; and one or more peptides capable of binding specifically to a ligand expressed on a cell surface. The bioconjugate blocks interactions between cells in a living tissue when the ligand is expressed on the surface of at least one of said cells. Moreover, the bioconjugate can block interaction between a cell and an extracellular matrix wherein said ligand is capable of binding to a component of said matrix. The bioconjugate is intended to block pathological reactions triggered by cellular interactions in a living tissue.

[0020] In some embodiments, the bioconjugate has a peptide that includes the amino acid sequence of the binding portion of an integrin for a tissue-bound ligand. The bioconjugate may have blocking cell signaling receptors implicated in the regulation of cellular adhesion, migration, tumor metastasis, proliferation, angiogenesis, bone resorption, apoptosis, or gene expression. Among these are the binding portion of an integrin α subunit or an integrin β subunit. These binding portions of the integrin subunits include SEQ ID NOS 1-202. The bioconjugate's binding portion can be, for example, a portion of the integrin α_2 subunit (CD49b, VLA-2, platelet gpla) I domain, integrin α_4 (CD49b, VLA-4), integrin α_5 (CD49e, VLA-5), integrin α_L (CD11a) I domain, integrin α_M subunit (CD11b) I domain, integrin α_{IIb} I domain, integrin α_{IIb} (CD41) heavy chain, integrin α_{11b} (CD41) light chain, integrin β_1 (CD29) subunit, the integrin β_2 (CD18) subunit, integrin β_3 (CD61) subunit, or integrin β_7 (LPAM-1) subunit.

[0021] In one embodiment, the bioconjugate's peptide includes the portion of the integrin α_2 subunit (CD49b, VLA-2, platelet gpla) I domain that binds specifically to ligands CN I, CN II, CN III, CN IV, LN and/or the echovirus-1 receptor. In another embodiment, the bioconjugate's peptide is a portion of the integrin α_4 (CD49b, VLA-4) subunit that binds specifically to the ligands VCAM-1, FN, MAdCAM-1, TSP and/or invasin. In yet another embodiment, the bioconjugate's peptide is a portion of the integrin α_5 (CD49e, VLA-5) that binds specifically to ligands FN, L1 or invasin. In other embodiments, the bioconjugate's peptide is a portion of the integrin α_1 (CD11a) I domain that binds specifically to the ligands ICAM-1, ICAM-2, ICAM-3 or LPS. In other embodiments, the bioconjugate's peptide is a portion of the integrin α_M subunit (CD11b) I domain that binds specifically to the ligands iC3b, ICAM-1, ICAM-2, ICAM-4, Fb, Factor X, CD23, NIF, heparin, beta glucan, or LPS. In other embodiments, the bioconjugate's peptide is a portion of the integrin α_{IIb} (CD41) heavy chain that binds specifically to the ligands Fb, FN, VN, TSP or vWF. In other embodiments, the bioconjugate's peptide is a portion of the integrin α_{11b} (CD41) light chain that binds specifically to the ligands Fb, FN, VN, TSP and vWF. In another embodiment, the bioconjugate's peptide is a portion of the integrin β_1 (CD29) subunit that binds specifically to the ligands FN, LN, CN, VCAM-1, FN, MAdCAM-1, TSP or invasin. Moreover, the bioconjugate's peptide can be a portion of the integrin β_2 (CD18) subunit that binds specifically to the ligands ICAM-1, ICAM-2, ICAM-3, ICAM-4, LPS, iC3b, Fb, Factor X, CD23, NIF, heparin, and/or betaglucan. In another embodiment, the bioconjugate's

peptide is a portion of the integrin β_3 (CD61) subunit that binds specifically to ligands fibrinogen, fibronectin, vitronectin, thrombospondin, von Willebrand factor, osteopontin, bone sialoprotein, laminins, collagens, and/or neural cell adhesion molecule L1.

[0022] In another embodiment, the bioconjugate's peptide is a portion of the integrin β_7 (LPAM-1) subunit that binds specifically to the ligands VCAM-1, fibronectin, MAdCAM-1, or E-cadherin (cadherin-1).

[0023] This invention also includes the nucleic acids coding for peptides of the peptide portion of the bioconjugates. The nucleic acid sequences are provided in SEQ ID NOS 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 86, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 186, 185, 187, 189, 191, 193, 195, 1197, 199 and 201.

[0024] This invention also includes the peptides for preparation of bioconjugate having their sequence set out in P-2, P-49 and SEQ ID NOS 1-218 and modified with an additional N-terminal or C-terminal cysteine residue. In another embodiment, the above nucleic acid sequences are modified to accommodate the additional cysteine residue(s).

[0025] The bioconjugates also include a polymer, that can be a polysaccharide or an oligosaccharide. In another embodiment, the polymer is derived from a polysaccharide or an oligosaccharide by the addition of chemical groups capable of reacting with a peptide to form said bioconjugate.

[0026] In another embodiment, the bioconjugate has the formula XY_b wherein X is a low cell-adhesive, hydrophilic polymer, Y is a peptide comprising a portion of the binding site of an integrin for a ligand expressed on a cell surface, and b is greater than 0. In another embodiment, the polymer X is a polysaccharide or an oligosaccharide. In another embodiment X is a derivative of a polysaccharide or of an oligosaccharide in which the derivative saccharide has reactive groups such that the derivative saccharide reacts with peptides to form the bioconjugate. The reactive group can be a hydroxyl group. In other embodiments, the polysaccharide or oligosaccharide can be agarose, dextran, heparin, chondroitin sulfate, hydroxyethyl starch, and hyaluronic acid. More preferably, the polymer is a dextran and thed peptide is the binding portion of an integrin. In other embodiments, the polymer is polyvalent and is, for example,

poly(ethylene glycol), poly(ethylene oxide), poly(vinyl alcohol), poly(acrylic acid), poly(ethylene-co-vinyl alcohol), poly(vinyl pyrrolidone), poly(ethyloxazoline), and/or poly(ethylene oxide)-co-poly(propylene oxide) block copolymers. In other embodiments, the polymer can be copolymers, block copolymers, graft copolymers, alternating copolymers, or random copolymers. Preferably, the polymer is essentially inert. Preferably, the polymer is degradable by hydrolytic or enzymatic means. Examples of degradable polymer are one or more blocks consisting of lactic acid, glycolic acid, ε-caprolactone, lactic-co-glycolic acid oligomers, trimethylene carbonate, anhydrides, and amino acids. In one embodiment, the polymer is a serum protein, such as albumin

[0027] In other embodiments, the bioconjugate is in a pharmaceutically acceptable carrier. Alternatively, the bioconjugate is immobilized on a solid substrate. Preferably, the bioconjugate is immobilized on an implantable medical device. The bioconjugate could be immobilized on a drug delivery device or an *in vitro* diagnostic device.

[0028] In other embodiments, there is provided a kit including one or more bioconjugates as well as reagents and apparatus suitable for administering the bioconjugate to an individual. Alternatively, the bioconjugate can be in a pharmaceutically acceptable carrier.

[0029] In one embodiment, there is formed on a mammalian tissue a biointerface such that the biointerface includes a plurality of bioconjugates bound to a plurality of ligands on the tissue.

[0030] There also is provided a method of preparing a bioconjugate including the steps of providing a hydrophilic polymer having one or more reactive groups, providing a bioselective peptide comprising a chemical group capable of reacting with the reactive groups, and contacting the polymer and the peptide under conditions such that the reactive and chemical groups react to form the bioconjugate. In another embodiment, the reactive groups of the polymer are hydroxyl groups and the chemical group of the peptide is a sulfhydryl group. In preferred embodiments, the polymer is a polysaccharide, such as activated dextran or hydroxyl starch.

[0031] In other embodiments the peptide of the bioconjugate is selected from the group consisting of SEQ ID NOS 7-14, 25-32, 35-38, 43-48, 55-56, 65, 66, 93, 94, 97, 98, 107-110, 119-124, 133-136,141, 142, 153, 154, 157-164, 171-174, 179-200, 203-212, 215 and 216, the peptide comprising a cysteine residue. In other embodiments, the peptide is selected from the

group consisting of SEQ ID NOS 1-218, the peptide including additionally an N-terminal or a C-terminal cysteine residue.

[0032] In other embodiments, there is provided a method of preparing a bioconjugate including the steps of providing a peptide selected from the group consisting of SEQ ID NOS 1-218, modifying the peptide by addition of an N-terminal or C-terminal cysteine residue, providing an amount of activated dextran, and contacting the activated dextran and the modified peptide under conditions, whereby the dextran and the modified peptide react to form the bioconjugate.

[0033] There is also provided a method for preventing adhesion of a mobile cell to a cell immobilized on a substrate including the step of applying a bioconjugate specific for the immobilized cell under such conditions that the bioconjugate forms a cell adhesion barrier on the immobilized cell and prevents adhesion of the mobile cell.

[0034] There also is provided a method of blocking pathological reactions triggered by cellular interactions in a living tissue. This method has the step of administering to the living tissue a bioconjugate selective for a target tissue, whereby the bioconjugate forms a cell adhesion barrier at a targeted tissue site. In other embodiments, the bioconjugate is the binding portion of an integrin for its ligand expressed on the target tissue. In other embodiments, the bioconjugate is administered intravascularly, orally, intramuscularly, intraperitoneally, subcutaneously, cerebrospinally, endovascularly, rectally or topically. When the bioconjugate is administered intravascularly in a biologically compatible solution, it is administered at a concentration of between about 1 μg/L and 100 g/L. Preferably the bioconjugate is administered to an individual in a pharmaceutically acceptable composition. Preferably, the amount of administered bioconjugate is between about 1-1000 mg/kg body weight.

[0035] In another method of preventing and treating thrombosis, an anti-coagulating amount of a bioconjugate having one or more peptides capable of binding selectively to integrin ligands expressed on inflamed endovascular cells is administered to tissue containing the inflamed endovascular cells. In other embodiments, the integrin ligands are CN I-IV, LN, or the Echovirus-1 receptor. In other embodiments, the bioconjugate's peptide is selected from the group consisting of P-2, P-49, and SEQ ID NOS 1, 2, 3-8, 91-106, 129-192, 203 and 204.

[0036] Also provided is a method of preventing and treating atherosclerosis. An anti-atherosclerotic-effective amount of the bioconjugate including one or more peptides capable of

binding selectively to integrin ligands expressed on or around atherosclerotic cells is administered to tissue containing the atherosclerotic cells. In other embodiments, the integrin ligands are VCAM-1, FN, MAdCAM-1, TSP, invasin or a combination thereof. In other embodiments, the bioconjugate's peptide is selected from the group consisting of P-49 and SEQ ID NOS 9-38, 59-106, 129-202 and 207-210.

[0037] Also provided is a method of Claim 57 for preventing and treating systemic inflammatory response syndrome. An effective amount of the bioconjugate comprising one or more peptides capable of binding selectively to integrin ligands expressed on cells in such inflamed tissue is administered to the tissue. In other embodiments, the integrin ligands are FN, L1 or invasin. The bioconjugate's peptide(s) is selected from the group consisting of P-49 and SEQ ID NOS 9-38, 59-106, 129-202 and 207-210.

[0038] In the method of preventing and treating multiple organ failure (MOF), a MOF-effective amount of the bioconjugate having one or more peptides capable of binding selectively to integrin ligands expressed on cells in affected tissue is administered to the tissue. In other embodiments, the integrin ligands are ICAM-1, ICAM-2, ICAM-3, LPS or a combination thereof. The bioconjugate's peptide(s) is selected from the group consisting of P-49 and SEQ ID NOS 39-58, 107-128 and 211-218.

[0039] In the method of preventing and treating autoimmune disease, an effective amount of a bioconjugate including one or more peptides capable of binding selectively to integrin ligands expressed on cells implicated in the autoimmune disease is administered to tissue containing the cells. In other embodiments, the integrin ligand is VCAM-1, FN, MAdCAM-1, TSP, invasin, ICAM-1, ICAM-2, ICAM-3, LPS, iC3b, ICAM-1, ICAM-2, ICAM-4, Fb, Factor X, CD23, NIF, heparin, β-glucan, LPS, FN, Fb, CN I, VN, FN, LN, CN, Fb, Factor X, CD23, NIF, heparin, β-glucan or a combination thereof. The bioconjugate's peptide(s) are selected from the group consisting of P-2, P-49 and SEQ ID NOS 1-218.

[0040] In the method of preventing and treating inflammatory diseases, an effective amount of a bioconjugate comprising one or more peptides capable of binding selectively to integrin ligands expressed on cells of inflamed tissue is administered to a tissue containing the inflamed cells. The integrin ligand may be CN I-IV, LN, Echovirus-1 receptor, VCAM-1, FN, MAdCAM-1, TSP, Invasin, L1, LPS, ICAM-1-4, iC3b, Fb, Factor X, CD23, NIF, heparin, β-

glucan, VN, vWF or a combination thereof. The bioconjugate's peptide(s) is selected from the group consisting of P-2, P-49, and SEQ ID NOS 1-202 and 205-219.

[0041] In a method of preventing and treating allograft transplant rejection, an anti-rejection amount of a bioconjugate having one or more peptides capable of binding selectively to integrin ligands expressed on T cells implicated in allograft transplant rejection is administered to an individual having transplanted tissue. The integrin ligand may be VCAM-1, FN, MAdCAM-1, TSP, invasin, ICAM-1-4, LPS, iC3b, Fb, Factor X, CD23, NIF, heparin, β-glucan, LN, CN, vWF, OP, BSP, L1 and E-cadherin. The bioconjugate's peptide(s) may be any of P-49 and SEQ ID NOS 9-30, 39-58, 91-200 and 211-218. Transplant rejection also may be concurrently treated with an Immunosuppressant, such as cyclosporine.

[0042] In a method of preventing and treating Crohn's disease, an effective amount of the bioconjugate comprising one or more peptides capable of binding selectively to integrin ligands expressed on inflamed cells in gut tissue is administered. The integrin ligand may be VCAM-1, FN, MAdCAM-1, TSP, invasin, ICAM-1-4, iC3b, Fb, Factor X, CD23, NIF, heparin, β-glucan, CN I, VN, LN, OP, BSP, L1, vWF and/or E-cadherin. The bioconjugate may have one or more peptides selected from the group consisting of P-49 and SEQ ID NOS 9-30, 30-58, 93-200 and 211-218.

[0043] In a method of preventing and treating inflammatory bowel disease, an effective amount of a bioconjugate includes one or more peptides capable of binding selectively to integrin ligands expressed on inflamed cells in gut tissue is administered. The bioconjugate has one or more peptides selected from the group consisting of P-49 and SEQ ID NOS 9-30, 39-58, 91-200 and 21-218.

[0044] In a method of preventing and treating sequelae of a bacterial infection, an effective amount of the bioconjugate comprising one or more peptides capable of binding selectively to integrin ligands expressed on secretory membranes is administered. The bioconjugate has one or more peptides selected from the group consisting of P-49 and SEQ ID NOS 39-58, 107-192 and 211-216.

[0045] In a method of preventing and treating sepsis or septic shock, an effective amount of a bioconjugate comprising one or more peptides capable of binding selectively to integrin ligands such as LFA-1, ICAM-1, VCAM-1 and a combination thereof is administered. The

bioconjugate includes one or more peptides selected from the group consisting of P2, P-49 and SEQ ID NOS 1-30, 39-58, 91-200 and 211-18.

[0046] In a method of preventing and treating ischemia-reperfusion injury, an effective amount of a bioconjugate comprising one or more peptides capable of binding selectively to integrin ligands is administered intravenously. The bioconjugate includes one or more peptides selected from the group consisting of P-49 and SEQ ID NOS 9-30 and 39-218.

[0047] In a method of preventing and treating cancer metastasis, an anti-metastasis effective amount of the bioconjugate comprising one or more peptides capable of binding selectively to integrin ligands is administered systemically to an individual or locally to tissue containing or suspected of containing cancer. The bioconjugate includes one or more peptides selected from the group consisting of P-49 and SEQ ID NOS 91, 92, 203 and 204.

[0048] In a method of treating conditions caused by viper and rattlesnake bites, an anti-venom-effective amount of the bioconjugate having one or more peptides capable of binding selectively to at least one integrin ligand on a bitten tissue site is administered. In some embodiments, the bioconjugate has a peptide of SEQ ID NOS 153 and 154.

[0049] Also embodied herein are therapeutic replacement fluids including a bioconjugate and a pharmaceutically acceptable diluent.

DETAILS OF THE INVENTION

[0050] We have created a family of bioselective bioconjugates that specifically bind to ligands expressed during cell-cell interactions including immune responses that result in pathology. The bioconjugates selectively target and bind to tissue surfaces, forming a protective barrier against pathologically driven cell-cell interactions. The bioconjugates, provided systemically or locally, selectively target tissues to suppress pathologically excessive damage to healthy tissues and thus limit deleterious outcomes. The various bioconjugates may be used in the prevention and therapy of a number of pathological processes involving leukocyte adhesion to tissue surfaces, including but not limited to, inflammation, septic shock, post-trauma multiple organ failure, ischemic reperfusion injury, transplant rejection, infectious inflammatory diseases, and autoimmune diseases. Other pathological responses that are the result of cell-cell interactions that may be therapeutically treated by the present bioconjugates include, but are not

limited to, thrombosis, atherosclerosis, cancer metastasis, autoimmune diseases, hookworm infection, bacterial and viral infection, and the sequelae of viper and rattlesnake bites.

[0051] The term "bioconjugate" as used herein means a compound in which at least two components, a peptide and a cell-adhesion-barrier polymer are chemically attached, i.e., conjugated. Methods of conjugation of the bioselective peptide and the cell adhesion barrier molecules are generally known in the art. The specific conjugation method is determined by the choice of cell adhesion barrier molecule and the accepted linking methods to the selected bioselective molecule, preferably a protein or peptide. Both univalent and multivalent conjugation methods are suitable. The conjugation method is selected to produce a bioconjugate that retains the bioselective and blockade abilities of the bioconjugate. In preferred embodiments of the invention, the molecules are attached *in vitro* prior to application to the living tissue. In certain other embodiments the molecules may be designed with appropriate linking groups that cause them to congregate *in vivo*.

[0052] As used herein "bioselective" means a molecule that (a) is capable of binding specifically to its ligand, preferably an integrin ligand; (b) is physiologically compatible with living tissue; (c) is generally chemically inert; and (d) exhibits little or no binding affinity for cellular components other than the targeted ligand. Peptides having the amino acid sequence based on the ligand binding site of the integrins have a selective affinity for the targeted ligand, e.g., provide the targeting ability of the bioconjugates for tissue such as injured or diseased tissue that express the ligand. Since normal tissue does not generally express these ligands (or expresses ligand in low quantity), the bioselective bioconjugates may be delivered systemically as well as locally as therapeutic agents to suppress inflammation where these ligands are expressed and to prevent the pathological consequences of excessive tissue inflammation.

[0053] As used herein, the term "integrin ligand" means the moiety on a specific cell type that binds to surface-bound integrins during the course of cellular interactions. Integrin ligands are the target binding site for the bioconjugates of the present invention. Each bioconjugate comprises one or more peptides that bind specifically to one or more particular cell-surface expressed ligands and also comprises a low-adhesive polymer. The bound bioconjugates block binding at the ligand to any subsequent cell surface integrin by forming a blockade or an "internal tissue bandage" that prevents specific, unwanted cell-cell interactions.

[0054] The term "peptide" is used herein in its broadest sense to refer to a sequence of subunit amino acids, amino acid analogs, or peptidomimetics. Peptides may be linked, for example, by peptide bonds, to form polypeptides.

[0055] The term "biointerface" as used herein means a collection of bioconjugates of the present invention bound to their ligand on a cell surface. When a bioconjugate binds to its ligand, an essentially inert blockade results, and subsequent interaction between cells is prevented.

[0056] The term "cell adhesion" as used herein means the binding of at least one cell to another cell or to a component of an extracellular matrix.

[0057] The term "cell adhesion barrier" as used herein means the biointerface that forms *in situ* in a tissue as a result of bioconjugate binding. Cell adhesion barrier molecules have properties that intrinsically inhibit cell adhesion by forming a physical barrier to cell-cell/tissue adhesion when applied to cell, tissue, or biomaterial surfaces. The cell adhesion barrier prevents adhesion of circulating cells to a cell surface, a component of an extracellular matrix or another material.

[0058] The term "polyvalent polymer" as used herein means a polymer having more than one reactive group at which a peptide or other moiety may be chemically linked to the polymer. In preferred embodiments of this invention, the reactive groups are hydroxyl groups that react with the sulfydryl groups on a peptide to form the bioconjugate. The polyvalency of the polymer provides the opportunity to make a bioconjugate comprising multiple connections of a peptide to the polymer or multiple peptides, which may be the same or different.

[0059] The therapeutic bioconjugates of the present invention comprise a polymer that forms the cell adhesion barrier. Preferably the polymer is multivalent, i.e., contains multiple reactive groups to allow a high number of peptides to be incorporated into the bioconjugate. In certain preferred embodiments, the polymer component is a hydrophilic polymer that is highly soluble in aqueous solutions.

[0060] The therapeutic bioconjugates of the present invention also comprise one or more peptides that selectively and strongly bind cell ligands and effectively immobilize the polymeric component at a tissue surface. Tissue ligands are typically in high enough concentrations on tissue surfaces to promote high-density surface binding of bioconjugates, creating a polymer

barrier to cell adhesion on ligand-presenting surfaces. The polymeric barrier is a biointerface on a tissue surface that blocks subsequent binding of circulating cells to the tissue surface.

[0061] The therapeutic bioconjugates of the present invention can be prepared from readily available starting materials using the following general methods and procedures. It will be appreciated that where typical or preferred process conditions (i.e., reaction temperatures, times, mole ratios of reactants, solvents, pressures, etc.) are given, other process conditions can also be used unless otherwise stated. Optimum reaction conditions may vary with the particular reactants or solvent used, but such conditions can be determined by one skilled in the art by routine optimization procedures.

[0062] The bioconjugates are preferably prepared by contacting a cell-adhesion-barrier polymer having multiple reactive chemical groups with a peptide having multiple chemical reactive groups under conditions where the polymer and peptide react to form covalent bonds.

[0063] Disclosed herein is a method for synthesis of a preferred embodiment of the present invention, bioconjugates comprising dextran and one or more peptides having the amino acid sequence of a portion of the integrin binding site. In a preferred method, dextran containing multiple hydroxyl groups is reacted directly with peptide functional groups (usually SH or S-S) to form covalently bound peptide in the dextran bioconjugate. Generally, the reaction is conducted at a temperature and a time such that (1) the solvent is in liquid form, (2) the dextran and the peptide do not degrade, and (3) detectable levels of product is obtained. Preferably, this reaction is conducted in the presence of a suitable solvent, e.g., water, under atmospheric conditions and pH optimal for formation. Upon completion of the reaction, the resulting bioconjugate of activated dextran and covalently attached peptide is recovered by conventional methods including, but not limited to, neutralization, extraction, precipitation, chromatography, filtration and the like.

[0064] Another preferred method for preparing the bioconjugates is presented. In this method a polymer having multiple reactive chemical groups is contacted with linker molecules containing two or more chemical reactive groups under conditions whereby the two compounds react to form covalent bonds. The polymer with covalently bound linker molecules is then contacted with a peptide with multiple chemical reactive groups under conditions whereby the two components react to form covalent bonds and the final therapeutic bioconjugate product.

[0065] Also disclosed is a method for synthesis of a preferred embodiment of the present invention, bioconjugates comprising dextran and one or more peptides having the amino acid sequence of the binding site of an integrin. In this method, dextran is first activated by reaction with a linking molecule, preferably dimethylaminopyridinine (DMAP). Generally, this reaction is conducted at a temperature and time range such that (1) the solvent is in liquid form, (2) the cell adhesion barrier polymer, (3) the linking molecule do not degrade, and (4) detectable levels of product are obtained. Preferably, the reaction is conducted in the presence of a suitable solvent, e.g., DMSO, under atmospheric conditions optimal for product formation. Upon completion of the reaction, the resulting conjugate containing the cell adhesion barrier polymer with covalently attached linking molecules, e.g., activated dextran, is recovered by conventional methods such as neutralization, extraction, precipitation, chromatography, filtration and the like. The multiple functional groups of activated dextran react with a sulfhydryl group, preferably on a cysteine residue in the peptide. Upon completion of the reaction, the resulting bioconjugate containing dextran with covalently attached peptide is recovered by conventional methods including, but not limited to, neutralization, extraction, precipitation, chromatography, filtration and the like.

[0066] Peptides are presented that may be used in the synthesis of the present bioconjugates. The peptides preferably comprise the amino acid sequence of the binding site of an integrin specific for a targeted ligand expressed on a cell surface. The peptides also comprise one or more sulfhydryl groups provided, generally, by cysteine residues. Certain of the peptides comprising amino acid sequences of binding sites of the integrins naturally comprise cysteine. Other preferred peptides may be modified for use in the synthetic methods by the addition of N-terminal or C-terminal cysteine residues. Preferred peptides for use in the preparative methods of the present method are members of the group consisting of SEQ ID NOS 1-112, with a cysteine residue added to the N- or C-terminus of peptide sequences which do not naturally have cysteine. The peptides described herein may be isolated from a naturally occurring protein, may be chemically synthesized, or may be recombinantly expressed by methods well known in the art. Nucleic acids for recombinant preparation of the peptides are presented in SEQ ID NOS 113-225.

[0067] Table 1 (at end) presents the amino acid sequence of the peptides, the nucleic acid sequence corresponding to each peptide, the integrin from which the peptide is derived, the target

ligand for each peptide and therapeutic administration of the preferred bioconjugates of the present invention.

[0068] From Table 1 it can be seen that the bioconjugates of the present invention may be used therapeutically in a large number of diseases and disease states caused by pathological consequences of cell-cell interactions through integrin/ligand binding. Many of these diseases involve inflammation at various tissue sites as, for example, Crohn's disease, intestinal bowel disease, multiple organ failure (MOF), systemic inflammatory response, and septic shock. Other diseases that are the pathological consequences of intercellular reactions mediated by integrins and may be therapeutically treated by the bioconjugates of the present invention include, but are not limited to allograft transplant rejection, cancer metastasis, bacterial or viral infection, thrombosis, atherosclerosis, ischemia-reperfusion injury, autoimmune diseases, and hookworm infection.

[0069] The above table is a compendium of known integrin/ligand pairs and illustrates the therapeutic applications of bioconjugates comprising these known integrins. However, it is anticipated that as new integrins are discovered and characterized, they may likewise be used as sources of peptides in the bioconjugates of the present invention and will find therapeutic use in preventing and treating disease states in which integrin/ligand binding is implicated.

[0070] In certain embodiments of the present invention, peptides other than those derived from integrins may be used to form cell adhesion barriers. Thus, for example, bioconjugates synthesized from a barrier polymer and antibodies or antibody fragments capable of binding to selected antigens expressed on a cell surface, an extracellular matrix or tissue surface may likewise be used in the methods of the present invention to prevent or treat diseases triggered by cellular interactions.

[0071] The therapeutic bioconjugates of the present invention bind to a specific target tissue. This specificity is achieved by selecting the peptide component of the bioconjugate that specifically binds to ligands that are expressed on cells in selected tissues, not generally on cells circulating in the bloodstream. A bioconjugate capable of binding to circulating cells might create aggregates in the bloodstream which could compromise blood flow. Examples of ligands expressed on non-circulating-cell surfaces include, but are not limited to, CN I, CN II, CN III, CN IV, LN, Echovirus-1 receptor, VCA, FN, L1, invasin, MAdCAM-1, TSP, ICAM-1, ICAM-2, ICAM-3, ICAM-4, iC3b, Fb, Factor X, CD23, NIF, heparin, β-glucan, LPS, VN, vWF, FN, LN,

CN, VCAM-1 and MAdCAM-1. The definition of these abbreviations are given at the end of Table 1.

[0072] In an important aspect of the present invention, pharmaceutical compositions comprising one or more bioconjugates of the present invention and a pharmaceutically acceptable carrier are presented. The pharmaceutical combinations and methods of this invention are adapted to therapeutic use as agents in the treatment or prevention of pathological excessive leukocyte adhesion/infiltration and subsequent tissue injury according to the methods described herein. The bioconjugates may be suspended in aqueous solution, e.g., saline solution, for intravenous delivery of the therapeutic compounds.

[0073] The compounds of the present invention are generally administered in the form of a pharmaceutical composition comprising at least one of the bioconjugates of this invention together with a pharmaceutically acceptable carrier or diluent. Thus, the compounds of this invention can be administered either individually or together in any conventional oral, or parenteral dosage form.

[0074] For oral administration the pharmaceutical composition can take the form of solutions, suspensions, tablets, pills, capsules, powders, and the like. Tablets containing various excipients such as sodium citrate, calcium carbonate and calcium phosphate are employed along with various disintegrants such as starch and preferably potato or tapioca starch and certain complex silicates, together with binding agents such as polyvinylpyrrolidone, sucrose, gelatin and acacia. Additionally, lubricating agents such as magnesium stearate, sodium lauryl sulfate and talc are often very useful for tabletting purposes. Fillers in soft and hard-filled gelatin capsules have preferred materials, including lactose or milk sugar as well as high molecular weight polyethylene glycols. When aqueous suspensions and/or elixirs are desired for oral administration, the bioconjugates of this invention can be combined with various sweetening agents, flavoring agents, coloring agents, emulsifying agents and/or suspending agents, as well as such diluents as water, ethanol, propylene glycol, glycerin and combinations thereof.

[0075] The bioconjugates of this invention may also be administered in a controlled release formulation such as a slow release or a fast release formulation. Such controlled release dosage formulations of the combination of this invention may be prepared using methods well known to those skilled in the art. The method of preferred administration will be determined by

the attendant physician or other person skilled in the art after an evaluation of the subject's condition and requirements.

[0076] For purposes of parenteral administration, solutions in sesame or peanut oil or in aqueous propylene glycol can be employed, as well as sterile aqueous solutions of the water-soluble salts and sugars. Such aqueous solutions may be suitably buffered, if necessary, and the liquid diluent first rendered isotonic with sufficient saline or dextrose. These aqueous solutions are especially suitable for intravenous, intramuscular, subcutaneous and intraperitoneal injection. In this connection, the sterile aqueous solutions are all readily obtainable by standard techniques well known to those skilled in the art.

[0077] Methods of preparing various pharmaceutical compositions with a certain amount of active ingredient are known, or will be apparent in light of this disclosure, to those skilled in this art.

[0078] The present invention also relates to pharmaceutical compositions in kit form. The kit may include one or more pharmaceutical compositions. The kit includes container means for containing the compositions. Typically the kit includes directions for the administration of the compositions. The kit form is particularly advantageous when the separate components are administered in different dosage forms (e.g., oral and parenteral) or are administered at different dosage concentrations as desired by the prescribing physician.

[0079] In an important aspect of the present invention, improved biomedical devices are presented. The devices are improved by the incorporation of one or more bioconjugates of the present invention disposed on or in the biomedical device.

[0080] As used herein, a "biomedical device" refers to a device to be implanted into or attached to a tissue in a subject, for example, a human being, in order to bring about a desired result. Particularly preferred improved biomedical devices according to this aspect of the invention include, but are not limited to catheters coated with the present bioconjugates to prevent localized inflammation around the biodevice. Similarly, wound dressings are biomedical devices that may be improved by coating with the present bioconjugates and then applied to inflamed surfaces.

[0081] As used herein, "disposed on or in" means that the one or more bioselective bioconjugates can be either directly or indirectly in contact with an outer surface, an inner surface, or embedded within the biomedical device. "Direct" contact refers to disposition of the

bioconjugates directly on or in the device, including, but not limited to, soaking a biomedical device in a solution containing the one or more bioconjugates, spin coating or spraying a solution containing the one or more bioconjugates onto the device, implanting a device that would deliver the bioconjugate, and administering the bioconjugate through a catheter directly on to the surface or into any organ or transplant.

[0082] "Indirect" contact means that the one or more bioconjugates do not directly contact the biomedical device. For example, the one or more bioconjugates may be disposed in a matrix, such as a gel matrix or a viscous fluid, which in turn is disposed on the biomedical device. Such matrices can be prepared to, for example, modify the binding and release properties of the one or more bioconjugates as required.

[0083] Exact dosing of bioconjugate therapy depends on many factors, among them the binding affinity of a particular bioconjugate for the targeted tissue ligands and the rate at which the bioconjugate is cleared from targeted tissue sites. Binding affinity of the bioconjugate for tissue ligands affects the amount of local tissue requirements for maintaining saturated coverage of bioconjugate on ligand-expressing tissue. Two major factors affect binding affinity: 1) the number of ligand-binding peptides per conjugate molecule; and 2) the affinity of the complexed peptide for the targeted ligand. The rate at which the bioconjugate is cleared from targeted tissue sites is dependent in part on the turnover rate of cells presenting tissue ligands. The turnover rate is driven by a constant internalization of surface molecules, and ligand internalization rate determines the duration of the ligand-bound bioconjugates on cell/tissue surfaces. The amount of bioconjugate delivered to a particular tissue in an individual in need of therapy varies by size of person, affinity of the peptide of the bioconjugate for the target ligand, turn-over rate of cells at the specific stage of disease at the time of administration and the mode of administration. It is anticipated that continuous or multiple administrations of bioconjugate will be most effective in treating and controlling the progress of disease.

[0084] In an important aspect of the present invention, methods are given for treating diseases caused by the pathological reactions triggered by interaction between different cell types in a living tissue. The methods comprise the step of administering to a subject in need thereof an amount of a bioselective bioconjugate of the present invention effective to block target ligands and thereby suppress subsequent cell-cell interaction and prevent the diseases.

[0085] In the methods of the present invention, the therapeutic bioselective bioconjugates may be administered by targeted delivery or by localized delivery. As used herein "targeted delivery" means systemic delivery of the present bioconjugates to an internal inflamed tissue surface. The biospecific bioconjugates target tissue surfaces with selected ligands and thus are agents of targeted delivery.

[0086] As used herein "localized delivery" means, for example, the direct application of the present bioconjugates to an exposed tissue surface. Topical application to a wound or inflamed burned tissue, for example, would be most suitable for localized delivery. Delivery systems such as aerosols or swabs may be used in localized delivery to other tissue or mucosal surfaces. Intra-arterial delivery of bioconjugate to a particular organ also is contemplated.

Therapy of inflammation in tissue

[0087] It has been discovered that the normal response to vascular injury may be suppressed by certain therapeutic bioconjugates that selectively target and locally bind to inflamed tissue surfaces that express certain ligands, such as ICAM-1. The bound bioconjugates form a protective barrier against abnormally excessive leukocyte adhesion/infiltration and subsequent tissue injury. The effective blockade suppresses the pathological consequences of excessive leukocyte adhesion/infiltration into vulnerable tissue.

[0088] To exemplify the biospecific activity and adhesion of the bioconjugates of the present invention, the characteristics of a preferred embodiment, the dextran/ICAM-1-binding A domain peptide conjugates, to inflammatory cells were measured as described in Experiments 2 and 3 hereinbelow.

[0089] FIG 1 depicts the reaction of bioselective dextran bioconjugate at inflamed endothelial cells expressing ICAM-1. In FIG 1, the intravascular action of the present bioconjugates is illustrated. In FIG 1, the lumen of the vessel and circulating blood/fluid volume are illustrated above the endothelial layer; the vessel wall is below the endothelium. FIG 1 (A) illustrates a normal blood vessel in uninjured tissues with circulating polymorphic neutrophils (PMNs). FIG 1 (B) illustrates inflamed (ICAM-1-expressing) endothelial cells following tissue injury. PMNs bind to ICAM-1 on inflamed endothelial cells and invade the vessel wall and surrounding tissues. Traumatic shock can induce excessive PMN adhesion and activation resulting in damage to healthy tissues and multiple organ failure (MOF). FIG 1 (C) illustrates

an inflamed blood vessel immediately after infusion of resuscitative fluids containing dextran/ICAM-1-binding peptide bioconjugate of the present invention. FIG 1 (D) illustrates binding of dextran bioconjugate to inflamed endothelial cells forming a non-adhesive barrier to PMNs. Invasion of PMNs into healthy tissues is thus reduced. Other leukocytes that interact with ICAM-1 are also blocked by this therapeutic strategy. Other endothelial cell surface ligands, e.g., VCAM-1, could also be targeted using peptides that selectively bind to other endothelial cell surface ligands.

[0090] Methods are presented for suppressing inflammation in a tissue. In certain instances, an inflamed tissue is contacted locally with one or more bioconjugates in an amount effective to inhibit tissue/leukocyte binding and suppress inflammation. The topical methods may also be used to enhance healing of inflamed flesh wounds caused by trauma or heat. In other instances the bioselective bioconjugates are delivered systemically to target the inflamed tissue sites. These methods are useful for preventing and treating inflammatory diseases including chronic inflammation of gut, cervix, eyes and lung.

[0091] In preferred methods for preventing and treating inflammatory diseases, an anti-inflammation-effective amount of a bioconjugate comprising one or more peptides capable of binding selectively to integrin ligands expressed on tissues containing the inflamed cells is applied to inflamed tissue such as such as gut, cervix, eyes, lung and inflamed flesh wounds. In these methods the bioconjugate comprises peptides capable of binding to the target ligands expressed on inflamed tissue cells. Most preferably the bioconjugate comprises one or more peptides selected from the group consisting of P6-P16, P21-P30, P48-P104, P109-P112 (Table 1).

[0092] In preferred methods for preventing and treating systemic inflammatory response syndrome (SIRS), there is administered an anti-SIRS-effective amount of bioconjugate comprising one or more peptides capable of binding selectively to integrin ligands expressed on cells in inflamed tissue. Preferably, the bioconjugate comprises peptides capable of binding to a target ligand from the group shown in Table 1. Most preferably the bioconjugate comprises one or more peptides selected from the group consisting of P1-99, P104 and P106-112 (Table 1).

[0093] In preferred methods for preventing and treating inflammatory bowel disease (IBD), an anti-IBD-effective amount of bioconjugate comprising one or more peptides capable of binding selectively to target ligands expressed on cells in inflamed bowel tissue is applied to

the tissue. Preferably, the bioconjugate comprises peptides capable of binding to an integrin ligand from the group shown in Table 1. Most preferably the bioconjugate comprises one or more peptides selected from the group consisting of P6-P16, P21-P30, P48-P104 and P109-P112 (Table 1).

[0094] In preferred methods for preventing and treating Crohn's disease (CD), there is administered an anti-CD-effective amount of bioconjugate comprising one or more peptides capable of binding selectively to target ligands expressed on cells in inflamed bowel tissue. Preferably, the bioconjugate comprises peptides capable of binding to the target ligand from the group shown in Table 1. Most preferably the bioconjugate comprises one or more peptides selected from the group consisting of P6-P16, P21-P30, P48-P104 and P109-112 (Table 1). The nucleotide sequences are provided in Table 2.

[0095] The utility of the compounds of the present invention as medical agents in the prevention and suppression of inflammatory cell responses to vulnerable tissue and as a therapeutic agent to prevent the pathological consequences of excessive inflammation in mammals (e.g., humans) is demonstrated by the activity of the compounds of this invention in cell adhesion assays described below in Examples 2 and 3.

Therapy of disorders due to pathogenic immune responses

[0096] In a further aspect, the invention provides methods for treating or inhibiting a disorder due to pathogenic immune responses. Although leukocyte adhesion to tissue surfaces is essential for normal immune system function, leukocyte/tissue adhesion plays a major role in a number of pathological processes including septic shock, post-trauma multiple organ failure, ischemic reperfusion injury, transplant rejection, inflammatory diseases, and autoimmune diseases. Accordingly, these methods provide targeted therapeutics for these diseases.

[0097] Topical and systemic anti-inflammatory/immunosuppressant therapeutic methods are presented for treating and preventing leukocyte adhesion/infiltration, to suppress inflammation and to prevent the pathological processes that result from excess inflammation. Integrin-mediated leukocyte/tissue adhesion plays a major role in a number of these pathological processes.

[0098] Methods for treating and preventing ischemia-reperfusion injury are provided. In the methods an anti-ischemia-reperfusion-injury-effective amount of a bioconjugate comprising

one or more peptides capable of binding selectively to target ligands expressed on endothelium is administered intravenously. In the methods the bioconjugate comprises peptides capable of binding to the target ligand. Most preferably the peptides may be selected from the group consisting of P6-P16, P21-P104 and P106-P112 (Table 1).

Therapy and prevention of infection by pathological agents

[0099] Methods are presented for preventing or treating pathogenic immune responses resulting from infection by bacteria, a biological warfare agent, anthrax or small pox, for example. Sexually transmitted diseases caused by bacterial pathogens or viral pathogens may likewise be prevented and treated. In these methods an effective immunosuppressive amount of a bioselective bioconjugate of the present invention is administered to an individual in need thereof.

[0100] Methods are presented for treatment of septic shock resulting from bacterial infection. Many bacteria (including agents of biological warfare, like anthrax) not only invade and infect host organisms, but also release endotoxins that promote a massive, systemic inflammatory response, resulting in an immune attack on healthy as well as diseased tissue. The present method protects tissues against injurious pathogenic immune responses. In certain instances the therapeutic method is used in adjunct with antibiotics to increase patient/casualty survival.

[0101] Infections of many types can result in hypersensitivity reactions, which are typically treated with steroids such as hydrocortisone and prednisolone, which have the drawback of side effects and interference with clearing the parasite (bacterial, viral or ameboid). Examples include SARS-related pulmonary hypersensitivity and hookworm infestation. In pulmonary infections, inflammatory exudates form in alveoli and bronchi and are organized by extensive matrix deposits and scarring. Ligands for integrins include CN III and CN IV.

[0102] Pancreatic infection results in damage to the ducts (epithelial cells), periductal inflammation, and new extracellular matrix expansion. Collagen also may be present and attract integrin-expressing cells.

[0103] In an important aspect, methods are presented for treatment of septic shock resulting from bacterial infection. Many bacteria (including agents of biological warfare like anthrax) not only invade and infect host organisms but also release endotoxins that promote a

massive and systemic inflammatory response resulting in an immune attack on healthy as well as diseased tissue. Among the abnormalities is deposition of platelets on damaged epithelium. The present method protects tissues against injurious pathogenic immune responses. In certain instances the therapeutic method is used in adjunct with antibiotics to increase patient/casualty survival.

[0104] In methods for preventing and treating septic shock, an anti-septic shock effective amount of a bioconjugate comprising one or more peptides capable of binding selectively to integrin ligands expressed on endothelium. The product must be infused intravenously. Preferably, the bioconjugate comprises one or more peptides selected from the group consisting of P1-P16, P21-P30, P48-P102, P109-P110 (Table 1).

Therapy of post-trauma multiple organ failure

[0105] Methods are presented to prevent and treat post trauma multiple organ failure. A bioselective bioconjugate of the present invention in a resuscitative fluid for preventing post-trauma multiple organ failure is presented.

[0106] Severe trauma can invoke a massive and systemic inflammatory response resulting in an immune attack on healthy as well as diseased tissue. The present methods may be used to protect tissues against injurious pathogenic immune responses that promote multiple organ failure. In this aspect, methods are presented for preventing the pathogenic results of intestinal ischemia and reperfusion that promote leukosequestration and injury in the gut as well as other organs resulting in multiple organ failure (MOF). Polymorphonuclear neutrophils (PMNs) play a key role in MOF since they respond to injury by adhering to tissues in multiple organs and releasing injurious oxidative agents.

[0107] In methods for preventing and treating multiple organ failure (MOF), an anti-MOF-effective amount of a bioconjugate comprising one or more peptides capable of binding selectively to target ligands expressed on endothelial cells. Preferably the bioconjugate comprises one or more peptides selected from the group consisting of P1-16, P21-104 and P106-P112 (Table 1).

Treatment of wound trauma

[0108] Means are presented for preventing and treating individuals suffering from severe trauma and injuries. Although massive blood loss and dehydration are the primary life-threatening factors in trauma patients, a major downstream effect of these severe injuries is a massive arousal of the immune system. Unfortunately this immune response is so aggressive that healthy tissues are destroyed by immune system cells (typically white blood cells) attempting to clean up and eliminate dead, injured tissues. This collateral damage of healthy tissue can promote failure of healthy organs and decrease patient survivability. The present bioconjugates may be used in intravenous replacement fluids, such as Ringer's lactate, where they circulate in the blood and selectively form a barrier on the endothelium to prevent attack by PMNs. Preferably the bioconjugates are incorporated into a formulation that replaces fluid loss to curtail collateral damage to healthy tissues that inevitably occurs following severe injuries. In these embodiments, the bioselective bioconjugates may be incorporated into blood replacements that are shipped in a dry or lyophilized formulation in conventional fluid therapy bags or are otherwise added to the conventional intravenous fluids.

[0109] Targeted and localized protection from pathogenic immune responses triggered by diseases that cause ischemic injury (injury due to lack of oxygen), e.g., heart attack and stroke, are also presented.

Prevention of transplant rejection

[0110] In another aspect of the invention, methods are presented for locally suppressing transplant rejection of allograft organ transplants including heart, lung, liver, kidney, skin, pancreatic islets, and cornea. In these methods biospecific bioconjugates target ICAM-1 on organ transplants, reducing or eliminating inflammation and the need for traditional systemic immunosuppression therapy, which is less specific.

Prevention and treatment of autoimmune disease.

[0111] Also presented are targeted and localized methods for protection from autoimmune diseases, including, but not limited to, diabetes and rheumatoid arthritis. At least ICAM-1 and LFA-1 are implicated in autoimmune diseases. Blocking those receptors is a

strategy for blocking autoimmune reactions and limiting conditions such as diabetes and rheumatoid arthritis. MAdCAM-1 receptors also have been implicated in diabetes.

Prevention of atherosclerosis

[0112] Atherosclerosis is an inflammatory condition. Endothelium is injured by a variety of sources (e.evated cholesterol, hypertension, etc.) and begins to display receptors that are ligands for integrins. The receptors include but are not limited to ICAM-1, VCAM-1 (vascular cell adhesion molecule) and PDGF.

Treatment and Prevention of Cirrhosis

[0113] Cirrhosis is the replacement of hepatocytes with fibrotic cells and is due to an inflammatory processes such as hepatitis and toxic reactions. Ligands for integrins also are present in cirrhosis. These include collagen I and III (CN I and CN III).

Treatment and Preventions of Glomerulosclerosis

[0114] This disorder is characterized by inflammatory destruction of renal glomeruli and replacement by fibrotic scar tissue. Such pathology is associated with the presence of CN I, CN IV and fibrinogen, which serve as ligands for integrins.

Prevention of Cancer Metastasis

[0115] Tumor metastasis is a fine-tuned balance between the formation and loosening of adhesive cell contacts within the tumor, which is regulated by various integrins. For example, human ovarian cancer cells express integrin $\alpha_v\beta_3$, which associates with vitronectin in the extracellular matrix and correlates with cancer progression. Exposure of such cancer cells to vitronectin results in proliferation and motility increase of five fold. Once blood-borne metastatic cancer cells may lodge in the lungs, causing early, intravascular metastatic tumors. Pulmonary vasculature contains integrin ligands known as calcium-activated chloride channels (CLCA) which are specific for the specific-determining loop (SDL) of β_4. Two mechanisms of fighting cancer metastasis are blocking vitronectin with the ligand-binding portion of $\alpha_v\beta_3$ and

blocking the CLCA ligand with a peptide including amino acids (SEQ ID NOS 184-203) of integrin β_4.

Sequelae of Viper and Rattlesnake Bites

[0116] Snake bites may cause excessive capillary permeability, which may be mediated by integrins.

Examples

Example 1

[0117] This experiment presents the synthesis of a preferred embodiment of the present invention, an anti-inflammatory dextran/peptide bioconjugate. This reaction scheme is illustrated in FIG 2.

Synthesis and chemical characterization of methacroylated dextran

[0118] Dextran, molecular weight about 70kD (25 g), and dimethylaminopyridinine (DMAP) (5 g) were dissolved in dimethylsulfoxide (DMSO) (225 ml) under nitrogen atmosphere at room temperature. Glycidyl methacrylate (GMA), a linking molecule, was added to the mixture to produce GMA-derivatized dextran (dex-GMA). The amount of GMA was adjusted to obtain 10 degrees of substitution (DS) (DS: molar ratio of GMA per glucopyranose residue). The reaction was terminated after 48 hours. The product was purified from the reaction mixture by solvent removal and size exclusion chromatography. Aqueous solutions of methacroylated dextran were rapidly frozen in liquid nitrogen, lyophilized, and stored frozen. FIG 2 illustrates the chemical structures of dextran, GMA, and methacroylated dextran and the dextran-peptide bioconjugate. FIG 3 is an NMR of dextran.

Synthesis of the anti-inflammatory dextran/peptide bioconjugate by coupling a synthetic peptide (CNAFKILVVITDGEK) to activated dextran

[0119] The synthetic peptide was based on the portion of integrin $\alpha_m\beta_2$ (CD11b/CD18) that fits in the ICAM-1-binding pocket. Synthesis with this peptide is illustrative and other peptides may likewise be coupled to dextran or other polyvalent polymers. The synthetic peptide (CNAFKILVVITDGEK) was added to phosphate buffered saline (PBS) with 1.5 mM EDTA at a final concentration of 20 mM. The pH was adjusted to 8.0-8.5 with triethanolamine (TEA). Methacroylated dextran (2mM) was then added to the reaction mixture and the pH was adjusted

again to pH 8.0-8.5 with TEA. All solutions were maintained under inert conditions to minimize disulfide bond formation. Crosslinking was allowed to proceed at room temperature for two hours. The reaction mixture was then dialyzed against deionized water in 25,000 MWCO membrane to remove any unreacted or disulfide-bonded peptide. The purified dextran/peptide conjugates were recovered by lyophilization.

[0120] A bioconjugate containing an inactive scrambled sequence of the above A-domain peptide CTVDLKFGIKNIEAV, was similarly synthesized and was conjugated to dextran and used as the sham control in the *in vitro* assays described below. Synthetic peptides were added to phosphate buffered saline (PBS) with 1.5 mM EDTA at a final concentration of 20 mM. The pH was adjusted to 8.0-8.5 with TEA. Methacroylated dextran (2mM) was then added to the reaction mix and the pH was adjusted again to pH 8.0-8.5 with TEA. All solutions were maintained under inert conditions to minimize disulfide bond formation. Crosslinking was allowed to proceed at room temperature for two hours. The reaction mixture was then dialyzed against deionized water in 25,000 MWCO membrane to remove any unreacted or disulfide-bonded peptide. The purified dextran/peptide conjugates were recovered by lyophilization.

Example 2

[0121] This experiment illustrates the activity of the bioconjugate, whose synthesis was described above, in the inflammatory cell adhesion assay. Bovine endothelial cell (BEC) monolayers were established in 24-well culture dishes. At 24h prior to the assay, normal medium (Minimal Eagle's Medium with 10% fetal bovine serum, 1% ABAM and 1% L-glutamine) (Gibco, CA, USA) was replaced with medium containing tumor necrosis factor α (TNF-α, 10 ng/ml). Following the 24h incubation period, each sample well received a medium change.

[0122] Treated sample groups received medium containing 6% dextran bioconjugate or 6% bioconjugate. Negative control samples received medium containing dextran bioconjugate whose peptide had a scrambled A domain sequence. Two other control treatments were given: a medium change with no dextran or peptide was given to a sample group pretreated with TNF-α, and a positive control that was not pretreated with TNF-α. After a 30-minute incubation period, the medium in all wells was replaced with medium containing the human monocyte cell line U937 (1×10^5/ml) (ATCC, Manassas, VA). All samples were incubated for another 30 minutes,

then washed three times with PBS to remove non-adherent cells. The average number of adherent cells per 100x microscopic field was determined for each sample group.

[0123] Referring to FIG 4, the results of this assay illustrate the biospecific binding of the peptide/dextran conjugate to bovine endothelial cells. In this assay all but the positive control were activated with TNF-α to induce ICAM expression. The negative control represents 100%. Treatment with active peptide conjugate resulted in a relative monocyte adherence of 3.34±1.69%. The positive control, where the endothelial cells were not induced, had monocyte adherence of 5.741±4.81%, which is not statistically different from samples where ICAM expression was induced preceding treatment with the active conjugate. The treatment with the inactive peptide conjugate yielded a relative adherence of 55.65±23.42%, while treatment with the active peptide alone led to a monocyte adherence of 56.28±22.67%. The treatment with the inactive peptide alone was comparable to no treatment after the TNF-α activation. Inactive peptide treatment gave a relative monocyte adherence of 95.71±21.03%. The standard deviation for the negative control was 54.5.

[0124] The active dextran bioconjugate effectively bound to TNF-α stimulated, ICAM-expressing BECs and prevented monocyte adhesion to the extent observed in non-stimulated BECS (positive control). Unconjugated peptides, dextran, and the inactive peptide conjugate inhibited cell adhesion poorly, suggesting that only the combined effect of specific binding of active peptide conjugates to ICAM and formation of an ICAM-bound nonadhesive dextran layer promoted reduced monocyte adhesion to TNF-α stimulated, ICAM-expressing BECs. Since leukocyte/tissue adhesion plays a major role in a number of the pathological processes discussed above, these bioconjugates could be utilized as targeted therapeutics for many applications.

Example 3

[0125] This experiment illustrates the inhibition of leukocyte/inflamed cell binding in human umbilical vein endothelial cell (HUVEC) monolayers by the bioselective bioconjugates of the present invention.

[0126] To assess the effect of these peptide-dextran bioconjugates on inflammatory cell adhesion, the following *in vitro* ICAM-1-mediated leukocyte cell adhesion assay was performed. HUVEC monolayers were established in 24-well culture dishes. At 24h prior to the assay,

normal culture media were replaced with medium containing TNF-α (10 ng/ml). Following the 24h incubation period, each sample well received a medium change. Treated sample groups received medium containing 6% dextran bioconjugate (dextran conjugated to the A domain peptide CNAFKILVVITDGEK). Untreated control samples received normal medium. Negative sham control samples received medium containing dextran conjugate with a scrambled A domain sequence (KCENGADFTKIIVLV). All samples were then incubated for 30 min prior to the adhesion assay. Medium was removed from all wells following the 30 min incubation and replaced with medium containing U937 monocytic cells (1 x 10^5/ml). All samples were then incubated for another 30 min. After this incubation period, samples were washed three times with PBS to remove non-adherent monocytes. The samples were then fixed, and an average number of adherent monocytes per 100x microscopic field was determined for each sample group. Statistical comparisons between sample groups (n = 4 replicate wells per group) were performed using a student's t-test.

[0127] U937 cell adhesion to inflammatory HUVECs was reduced by 87.7% in the sample group treated with bioconjugate containing the active A-domain sequence CNAFKILVVITDGEK. No significant reductions in cell adhesion were observed in untreated and sham-treated (scrambled A domain peptide conjugated to dextran) sample groups.

[0128] It should be understood that the invention is not limited to the particular embodiments described herein, but that various changes and modifications may be made without departing from the spirit and scope of this novel concept as defined by the following claims. The following references are incorporated by reference.

REFERENCES

1 DS Tuckwell, L Smith, M Korda, JA Askari, S Santosof, MJ Barnes, RW Farndale, and MJ Humphries, Monoclonal antibodies identify residues 199-216 of the integrin a2 vWFA domain as a functionally important region within α_2/β_1. Biochem J (2000) 350: 485-493.

2 SL King, T Kamata, JA Cunningham, J Emsley, RC Liddington, Y Takada, and JM Bergelson, Echovirus-1 interaction with the human very late antigen-2 (integrin α_2/β_1) I domain. J Biol Chem (1997) 272: 285518-28522.

3 T Kamata, RC Liddington, and Y Takada, Interaction between collagen and α_2 I domain of integrin α_2/β_1. J Biol Chem (1999) 274: 32108-32111.

4 T Kamata, W Puzon, and Y Takada, Identification of putative ligand binding sites within I domain of integrin α_2/β_1(VLA-2, CD49b/CD29). J Biol Chem (1994) 269: 9659-9663.

5 SG Schiffer, ME Hemler, RR Lobb, R Tizard, and L Osborn, Molecular mapping of functional antibody binding sites of α_4 integrin. J Biol Chem (1995) 270: 14270-14273.

6 A Irie, T Kamata, and Y Takada, Multiple loop structures critical for ligand binding of the integrin α_4 subunit in the upper face of the beta-propeller mode 1. Proc Natl Acad Sci USA 1997; 94: 7198-7203.

7 A Irie, T Kamata, W Puzon-McLaughlin, and Y Takada, Critical amino acid residues for ligand-binding are clustered in a predicted beta-turn of the 3rd N-terminal repeat in the integrin α_4 and α_5 subunits. EMBO J (1995) 14: 5550-5556.

8 T Kamata, W Puzon, and Y Takada, Identification of putative ligand-binding sites within of the integrin $\alpha_4\beta_1$ (VLA-2, CD49d/CD29). Biochem J (1995) 305: 945-951.

9 Z Cao, K Huang, and AF Horwitz, Identification of a domain on the integrin α_5 subunit implicated in cell spreading and signaling. J Biol Chem (1998) 273: 31670-31679.

10 JL Baneres, F Roquet, M Green, H LeCalvez, and J Parello, The cation-binding domain from the alpha subunit of integrin $\alpha_5\beta_1$ is a minimal domain for fibronectin recognition. J Biol Chem (1998) 273: 24744-24753.

11 AP Mould, J Askari, Humphries MJ, Molecular basis of ligand recognition by integrin $\alpha_5\beta_1$. J Biol Chem (2000) 275: 20324-20336.

12 U.S. Patent No. 5,843,885, Benedict et al (1998)

13 Yusuf-Makagiansar H, Siahaan TJ. Binding and internalization of an LFA-1-derived cyclic peptide by ICAM receptors on activated lymphocyte: A potential ligand for drug targeting to ICAM-1 expressing cells. Pharm Res 2001:18:329-335.

14 Yusuf-Makagiansar H, Makagiansar IT, Siahaan TJ. Inhibition of the adherence of T-lymphocytes to epithelial cells by a cyclic peptide derived from inserted domain of lymphocyte function-associated antigen-1. Inflammation 2001:25:203-214.

15 Jois SD, Tibbetts SA, Chan MA, Benedict SH, Siahaan TJ. A Ca^{2+} binding cyclic peptide derived from the a-subunit of LFA-1: Inhibitor of ICAM-1/LFA-l-mediated T-cell adhesion. J Pept Res 1999:53:18-29.

16 T Kamata, KK Tieu, T Tarui, W Puzon-McLaughlin, N Hogg, and Y Takada. The role of CPNKEKEC sequence in the beta 2 subunit I domain in regulation of integrin α_L β_2 (LFA-1). (2002) J Immunol 168: 2296-2301.

17 L Zhang and E Plow, Amino acid sequences within the alpha subunit of integrin α_m β_2 (Mac-1) critical for specific recognition of C3bi. Biochem (1999) 38: 8064-8071.

18 VP Yakubenko, DA Solovjov, L Zhang, VC Yee, EF Plow, and TP Ugarova. Identification of the binding site for fibrinogen recognition peptide gamma 383-395 within the alpha m I-domain of integrin α_m β_2 (2001) 276: 13995-14003.

19 J Plescia, MS Conte, G VanMeter, G Ambrosini, and DC Altieri. Molecular identification of the cross-reacting epitope on $\alpha_b\beta_2$ integrin I domain recognized by anti-$\alpha_{IIb}\beta_3$ monoclonal antibody 7E3 and its involvement in leukocyte adherence. J Biol Chem (1998) 273: 20372-20377.

20 JJ Calvete, W Schafer, K Mann, A Henschen, and J Gonzalez-Rodriguez. Localisation of the cross-linking sites of RGD and KQAGDV peptides to the isolated fibrinogen receptor, the human platelet integrin glycoprotein IIb/IIIa- Influence of peptide length. (1992) Eur J Biochem 206: 759-765.

21 JJ Calvete, G Rivas, W Schafer, MA McLane, and S Niewiarowski. Glycoprotein IIb peptide 656-667 mimics the fibrinogen gamma chain 402-411 binding site on platelet integrin GPIIb/IIIa (1993) FEBS Lett 235: 132-135.

22 DB Taylor, JM Derrick, and TK Gartner. Antibodies to GPIIb (alpha)(300-312) inhibit FG binding, clot retraction, and platelet adhesion to multiple ligands (1994) Proc Soc Exp Biol Med 205: 35-43.

23 JM Grunkemeier and TA Horbett. Fibrinogen receptor-like biomaterials made by pre-adsorbing peptides to polystyrene substrates (1996) J Mol Recog 9: 247-257.

24 LJ Yao and KH Mayo. Interactions of integrin GPIIb/IIIa-derived peptides with fibrinogen investigated by NMR spectroscopy (1996) Biochem J 315: 161-170.

25 EM Makogonenko, VP Yakubenko, KC Ingham, and LV Medved. Thermal stability of individual domains in platelet glycoprotein IIbIIIa (1996) Eur J Biochem 237: 205-211.

26 SE D'Souza, MH Ginsberg, TA Burke, and EF Plow. The ligand binding site of the platelet integrin receptor GPIIb-IIIa is proximal to the second calcium binding domain of its alpha subunit (1990) J Biol Chem 265: 3440-3446.

27 D Gulino, C Boudignon, L Zhang, E Concord, MJ Rabiet, and G Maguerie. Calcium-binding properties of the platelet glycoprotein IIb ligand-interacting domain (1992) J Biol Chem 267: 1001-1007.

28 W Puzon-McLaughlin, T Kamata, and Y Takada. Multiple discontinuous ligand-mimetic antibody binding sites define a ligand binding pocket in integrin α_{IIb} β_3. (2000) J Biol Chem 275: 7795-7802.

29 YK Liu, A Nemoto, Y Feng, T Uemura. The binding ability of matrix proteins and the inhibitory effects on cell adhesion of synthetic peptides derived from a conserved sequence of integrins. (1997) J Biochem 121: 961-968.

30 G Bazzoni, DT Shih, CA Buck, and ME Hemler. Monoclonal antibody 9EG7 defines a novel β_1 integrin epitope induced by soluble ligand and manganese, but inhibited by calcium. (1995) J Biol Chem 270: 25570-25577.

31 J Takagi, Kamata T, J Meredith and W Puzon-McLaughim. Changing ligand specificities of $\alpha_v\beta_1$ and $\alpha_v\beta_3$ integrins by swapping a short diverse sequence of the beta subunit. (1997) J Biol Chem 272: 19794-19800.

32 W Puzon-McLaughlin and Y Takada. Critical residues for ligand binding in an I domain-like structure of the integrin β_1 subunit. (1996) J Biol Chem 271: 20438-20443.

33 Y Takada and W Puzon. Identification of regulatory region of integrin β_1 subunit using activating and inhibiting antibodies. (1993) J Biol Chem 268: 17597-17601.

34 HY Ni and JA Wilkins. Localisation of a novel adhesion blocking epitope on the human beta 1 integrin chain. (1998) Cell Adhesion and Comm 5: 257-271.

35 LL Chen, RR Lobb, JH Cuervo, KC Lin, SP Adams, and EB Pepinsky. Identification of ligand binding sites on integrin α_4 β_1 through chemical cross-linking. (1998) 37: 8743-8753.

36 DT Shih, D Boettiger, and CA Buck. Epitopes of adhesion-perturbing antibodies map within a predicted alpha helical domain of the integrin β_1 subunit. (1997) 110: 2619-2628.

37 C Huang, Q Zang, J Takagi, and TA Springer. Structural and functional studies with antibodies to the integrin β_2 subunit. (2000) 275: 21514-21524.

38 YM Xiong and L Zhang. Structure-function of the putative I-domain within the integrin β_2 subunit. (2001) 276: 19340-19349.

39 YM Xiong, TA Haas, and L Zhang. Identification of functional segments within the β_2 I-domain of integrin α_m β_2. (2002) 277: 46639-46644.

40 CF Lu, M Ferzly, J Tagaki, and Springer TA. Epitope mapping of antibodies to the C-terminal region of the integrin β_2 subunit reveals regions that become exposed upon receptor activation. (2001) 166: 5629-5637.

41 P Rieu, T Ueda, I Haruta, CP Sharma, and MA Arnaout, The A domain of β_2 integrin CR3 (CD11b/CD18) is a receptor for the hookworm-derived neutrophils adhesion inhibitor NIF. J Cell Biol 1994; 127: 2081-2091.

42 Tibbetts SA, Chirathawom C, Nakashima M, Jois SDS, Siahaan TJ, Chan MA, Benedict SH. Peptides derived from ICAM-1 and LFA-1 modulate T cell adhesion and immune function in a mixed lymphocyte culture. Transplantation 1999:68:685-692.

43 Jois SDS, Hughes R, Siahaan TJ. Comparison of solution conformations of a cell-adhesive peptide LBE and its reverse sequence EBL. J Biomol Struc Dyn 1999:17:429-444.

44 SE D'Souza, MH Ginsberg, TA Burke, SCT Lam, and EF Plow. Localization of an Arg-Gly-Asp recognition site within and integrin adhesion receptor. Science (1990) 242: 91-93.

45 JJ Cook, M Trybulec, EC Lasz, S Khan, and S Niewiaeowski. Binding of glycoprotein-IIIa-derived peptide 217-231 to fibrinogen and von Willebrand factor and its inhibition by platelet glycoprotein IIb/IIIa complex. (1992) Biochim Biophys Acta 1119: 312-321.

46 JJ Calvete, K Mann, MV Alvarez, MM Lopez, and J Gonzales-Rodriguez. Proteolytic dissection of the isolated platelet fibrinogen receptor, integrin gp IIb/IIIa-localization of gpIIb and gp IIIa putatively involved in the subunit interface and in intrasubunit and intrachain contacts. (1992) Biochem J 282: 523-532.

47 ML Bajt, MH Ginsberg, AL Frelinger, MC Berndt, and JC Loftus. A spontaneous mutation of integrin α_{IIb} β_3 (platelet glycoprotein IIb-IIIa) helps define a binding site. (1992) J Biol Chem 267: 3789-3794.

48 B Steiner, A Trzeciak, G Pfenninger, and WC Kouns. Peptides derived from a sequence within β_3 integrin bind to a platelet α_{IIb} β_3 (gpIIb-IIIa) and inhibit ligand binding. (1993) J Biol Chem 268: 6870-6873.

49 EC Lasz, MA McLane, M Trybulec, MA Kowalska, S Khan, AZ Budzynski, and S Niewiarowski. β_3 integrin derived peptide 217-230 inhibits fibrinogen binding and platelet aggregation: significance of RGD sequences and fibrinogen A alpha chain. (1993) Biochem Biophys Res Comm 190: 118-124.

50 JJ Calvete, MA McLane, GJ Stewart, and S Niewiarowski. Characterization of the cross-linking site of disintegrins albolabrin, bitistatin, echistatin, and eristostatin on isolated human platelet integrin gpIIb/IIIa. (1994) Biochem Biophys Res Comm 202: 135-140.

51 SE D'Souza, TA Haas, RS Piotrowicz, V Byersward, DE McGrath, HR Soule, C Cherniewski, EF Plow, JW Smith. Ligand and Cation-binding are dual functions of a discrete segment of the integrin β_3 subunit – cation displacement is involved in ligand-binding. (1994) Cell 79: 659-667.

52 S Honda, Y Tomiyama, AJ Pelletier, D Annis, Y Honda, R Oechekowski, Z Ruggeri, and TJ Kunicki. Topography of ligand-induced binding sites, including a novel cation-sensitive epitope (AP5) at the amino terminus, of the human integrin β_3 subunit. (1995) J Biol Chem 270: 11947-11954.

53 WC Kouns, PJ Newman, KJ Puckett, AA Miller, CD Wall, CF Fox, JM Seyer, and Lennings LK. Further characterization of the loop structure of platelet glycoprotein IIIa- partial mapping of functionally significant glycoprotein IIIa epitopes. (1991) Blood 78: 3215-3223.

54 X Du, M Gu, JW Weisel, C Nagaswami, JS Bennett, R Bowditch, and MH Ginsberg. Long range propagation of conformational changes in integrin α_{IIb} β_3. J Biol Chem (1993) 268: 23087-23092.

55 R Pasqualini, E Koivunen, and E Ruoslahti. A peptide isolated from phage display libraries is a structural and functional mimic of an RGD-binding site on integrins. (1995) J Cell Biol 130: 1189-1196.

56 M Alemany, E Concord, J Garin, M Vincon, A Giles, G Marguerie, and D Gulino. Sequence 274-368 in the β_3 subunit of the integrin α_{IIb} β_3 provides a ligand recognition and binding domain for the gamma chain of fibrinogen that is independent of platelet activation. Blood 87: 592-601.

57 ECK Lin, BI Ratnikov, PM Tsai, CP Carron, DM Myers, CF Barbas, and JW Smith. Identification of a region in the integrin β_3 subunit that confers ligand binding specificity. (1997) J Biol Chem 272: 23912-23920.

58 I Wierzbicka, MA Kowalska, EC Lasz, DH Farrell, AZ Budzynski, and S Niewiarowski. Interaction of β_3 integrin-derived peptides 214-218 and 217-231 with α_{IIb} β_3 complex and with fibrinogen A alpha chain (1997) Thromb Res 85: 115-126.

59 M Triantafilou, K Triantafilou, KM Wilson, Y Takada, and N Fernandez. High affinity interactions of coxsackievirus A9 with integrin α_v β_3 (CD51/61) require the CYDMKTTC sequence of β_3, but do not require the RGD sequence of the CAV-9 VP-1 protein. (2000) Human Immnol 61: 453-459.

60 G Bitan, L Scheibler, Z Greenberg, M Rosenblatt, and M Chorev. Mapping of the integrin α_v β_3–ligand interface by photoaffinity cross-linking. Biochem (1999) 38: 3414-3420.

61 G Bitan, L Scheibler, DF Mierke, M Rosenblatt, and M Chorev. Ligand-integrin α_v β_3 interaction determined by photoaffinity cross-linking. Biochem (2000) 39: 11014-11023.

62 L Scheibler, DF Mierke, G Bitan, M Rosenblatt, and M Chorev. Identification of a contact domain between echistatin and the integrin α_v β_3 by photoaffinity cross-linking. Biochem (2001) 40: 15117-15126.

63 A Cierniewska-Cieslak, CS Cierniewska, K Blecka, M Paperak, L Michalec, L Zhang, and EF Plow. Identification and characterization of two cation binding sites in the integrin β_3 subunit. J Biol Chem (2002) 277: 11126-11134.

64 M Tidswell, R Pachynski, SW Wu, SQ Qiu, E Dunham, N Cochran, MJ Briskin, PJ Kilshaw, AI Lazarovitis, DP Andrew, Butcher EC, Yednock TA, and Earle DJ. Structure-function analysis of the integrin β_7 subunit: identification of domains involved in adhesion to MAdCAM-1. J Immunol (1997) 159: 1497-1505.

65 TK Gartner and DB Taylor. The peptide Glu-His-Ile-Pro-Ala binds fibrinogen and inhibits platelet aggregation and adhesion to fibrinogen and vitronectin. (1991) Proc Soc Exp Biol Med 198: 649-655.

66 V Castronovo, G Tarboletti, and ME Sobel. Laminin receptor complementary DNA-deduced synthetic peptide inhibits cancer cell attachment to endothelium. (1991) Canc Res 51: 5672-5678.

67 SE D'Souza, VJ Byers-Ward, EE Gardiner, H Wang, and SS Sung. Identification of an active sequence within the first immunoglobulin domain of intercellular molecule-1 (ICAM-1) that interacts with fibrinogen (1996) J Biol Chem 271: 24270-24277.

68 JP Shannon, MV Silva, DC Brown, and RS Larson. Novel cyclic peptide inhibits intercellular adhesion molecule-1 mediated cell aggregation. (2001) J Peptide Res 58: 140-150.

69 Kam JL, Regimbald LH, Hilgers JHM, Hoffman P, Krantz MJ, Longenecker BM, Hugh JC. MUC1 synthetic peptide inhibition of intercellular adhesion molecule-1 and MUC1 binding requires six tandem repeats. (1998) Canc Res 58: 5577-5581.

70 JK Welply, CN Steininger, M Caparon, ML Michener, SC Howard, LE Pegg, DM Meyer, PA De Ciechi, CS Devine, GF Casperson. A peptide isolated by phage display binds to ICAM-1 and inhibits binding to LFA-1. (1996) Proteins Struct Funct Genetics 26: 262-270.

ADDENDUM A

TABLE 1 – NUCLEOTIDE SEQUENCES

TABLE 1 – NUCLEOTIDE SEQUENCES

SEQ ID #	ID #	Nucleotide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
1	D-1	ACT TAC AAA ACA AAG GAG GAA ATG ATA GTA GCA ACG AGT CAG ACC AGT CAA TAT	Integrin α_2 subunit (CD49b, VLA-2, platelet gpIa) I domain	CN I-IV, LN, Echovirus-1 receptor	Thromb, Ather, SIRS, MOF, SS, ID	1
NA	D-2	ACT TAC AAA	Integrin α_2 subunit (CD49b, VLA-2, platelet gpIa) I domain	CN I-IV, LN, Echovirus-1 receptor	Thromb, Ather, SIRS, MOF, SS, ID	2
3	D-3	CAG ACC AGT CAA TAT	Integrin α_2 subunit (CD49b, VLA-2, platelet gpIa) I domain	CN I-IV, LN, Echovirus-1 receptor	Thromb, Ather, SIRS, MOF, SS, ID	2
5	D-4	ATA GCA GTA ATA GGA	Integrin α_2 subunit (CD49b, VLA-2, platelet gpIa) I domain	CN I-IV, LN, Echovirus-1 receptor	Thromb, Ather, SIRS, MOF, SS, ID	3
7	D-5	AAT TTC CTA GAG AAG TTT GTT CAG GGT CTC GAT ATC GGC CCT ACC AAA ACC CAG GTC GGT CTG ATA CAA TAT GCG AAT AAT CCA CGC TGG TTC AAT CTA AAT ACT TAT AAG ACT AAG GAA GAG ATG ATT GTT GCT ACC TCC CAG ACT AGC CAG TAC GGC GGT GAT CTA ACA AAT ACA TTC GGA GCG ATC CAG TAT GCG CGA AAA TAT GCG TAT TCA GCG GCC TCT GGA GGC CGT CGA AGT GCA ACA CTT AAA GTA ATG GTG	Integrin α_2 subunit (CD49b, VLA-2, platelet gpIa) I domain	CN I-IV, LN, Echovirus-1 receptor	Thromb, Ather, SIRS, MOF, SS, ID	4
9	D-6	TAC AAC GTC GAC ACA GAA TCT GCA CTT TTA TAT CAG GGC CCG CAT AAT ACA CTG TTT GGC TAC AGT TGG CTC CAC TCC CAT GGA GCT CAT AGA TGG CTA CTG GTA GGA GCG CCA ACA GCA ATG TGG TTA GCA ATG GCA AGC GTT ATT AAT CCT GGG GCC ATC TAT AGA TGC AGA ATA GGA AAA AAC CCA GGG CAG ACG TGT GAA TTG CAA TTG GGT TCA TTC CAC GGT GAG CCC GGC GGT AAG ACT TGT CTA GAG GAA AGA GAT CAC CAA TGG CTT GGG GTG ACC CTC TCG AGA	Integrin α_4 subunit (CD49b, VLA-4)	VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	5
11	D-7	CAG GAT TAT GTA AAG AAA TTC GGC GAA CAT TTT GCA AGT TGT CAA GCA GGG ATA TCC TCG TTC TAT ACG AAA GAC TTA ATC GTA ATG GGT GCA CCA GGA TCT TCA TAC TGG ACA GGA AGC TTA TTT GTA TAC ATG ATT ACC ACT AAT AAG TAT AAA	Integrin α_4 subunit (CD49d, VLA-4)	VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	5

SEQ ID #	ID #	Nucleotide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
13	D-8	CAG GAT TAT GTA AAG AAA TTC GGC GAA CAT TTT GCA AGT TGT CAA GCA GGG ATA TCC TCG TTC TAT ACG AAA GAC TTA ATC GTA ATG GGT GCA CCA GGA TCT TCA TAC TGG ACA GGA AGC TTA TTT GTA TAC ATG ATT ACC ACT AAT AAG TAT AAA	Integrin α_4 subunit (CD49d, VLA-4)	VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	5
15	D-9	GGA CAT AGA TGG AAA AAC ATA TTT TAT ATA AAG AAT GAA AAT AAA TTA CCA ACA GGA GGA	Integrin α_4 subunit (CD49d, VLA-4)	VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	6
17	D-10	GGA GGA GCA CCA CAG CAT GAA CAA ATA GGA AAA	Integrin α_4 subunit (CD49d, VLA-4)	VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	6
19	D-11	AGT TAT TGG ACA GGA AGT	Integrin α_4 subunit (CD49d, VLA-4)	VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	6
21	D-12	ATG GGA GCA CCA GGA AGT AGT TAT TGG ACA GGA	Integrin α_4 subunit (CD49d, VLA-4)	VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	7
23	D-13	TAC AAT GTA GAT ACA GAA AGT GCA TTA CTC TAT CAA GGT CCA CAC AAC ACA TTG TTT GGG TAT AGT TGG CTT CAT AGT CAT GGA GCA CAC AGA TGG CTG CTA GTA GGC GCA	Integrin α_4 subunit (CD49d, VLA-4)	VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	8
25	D-14	ATA GTA ACG TGT GGC CAT AGA TGG AAA AAT ATT TTT TAT ATC AAA CAC GAA AAC AAA TTA CCA ACA GGA GGG TGT TAT GGC GTG CCC CCG GAT TTA AGA ACC GAA TTA AGT AAG AGA ATA GCC CCT GGT TAT CAG GAC TAC GTT AAA AAG TTC GGA GAG CAT TTT GCT AGT TGC CAA GCA GGT ATC AGT AGT TTC TAC ACT AAG GAT TTA ATT GTC ATG GGG GCG	Integrin α_4 subunit (CD49d, VLA-4)	VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	8
27	D-15	TAC ATG ATT ACC ACT AAC AAG TAT AAA GCG TTT TTA GGG AAG CAA AAT CAG GTG AAG CCA GGA AGT TAT TTA GGG TAT AGT GTA GGT GCC GGC CAT TTC AGA AGT CAA CAC ACG ACA GAA GTT GTC GGC GGT GCA CCA CAA CAT GAG CAG ATA GGA AAA GCT TAC ATC TTT AGT ATA GAT GAA AAA GAA TTA AAT ATA TTA CAC GAG ATG AAG GGA AAA AAA	Integrin α_4 subunit (CD49d, VLA-4)	VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	8

SEQ ID #	ID #	Nucleotide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
29	D-16	TTA GGA TCA TAT TTC GGA GCA TCC GTC GGC GCA GTC GAC TTA CAC GCT GAT GGC TTC TCA GAC CTG CTC GTC GGT GCT CCC ATG CAA TCG ACG ATA AGA GAA GAG GGT AGA GTT TTT GTT TAC ATC AAT TCT GGA AGC GGG GCA GTT ATG AAC GCA ATG GAG ACA AAC TTA GTG GGA AGT GAC AAA TAC GCA GCG CGA TTT GGG GAA TCC ATC GTG AAT TTG GGA GAT ATT GAC AAT GAC GGG TTT GAA GAC GTA GCG ATT GGA GCA CCA CAG GAG GAC GAT CTC CAG GGA GCT ATC TAT ATC TAC AAC GGC AGA GCG GAT GGT ATA TCT TCA ACA TTT TCC CAA AGA ATT GAG GGC CTA CAA ATA TCG AAG TCG CTA TCC ATG TTT GGG CAG AGT ATT TCT GGT CAG ATC GAC GCG GAT AAC AAT GGC TAT GTG GAT GTA GCA GTA GGC GCG TTC AGG AGT GAT CGT AGC GAT TCT GCT GTT TTG TTA AGA ACG CGT CCA GTC GTC ATA GTG GAC GCT TCA CTT AGT CAT CCT GAA TCA GTA AAC CGA ACA AAG TTT GAT TGT GTC GAG AAT GGG TGG CCG AGC GTG TGT ATA GAT CTG ACA TTA TGC TTC TCG TAC AAA GGG AAG GAA GTT CCT GGT TAT ATT GTA TTA TTC TAC AAT ATG AGT CTT GAT GTT AAC CGC AAA GCC GAA TCG CCA CCG CGG TTT TAT TTC AGT AGC AAT GGT ACT AGT GAT GTA ATT ACT GGA AGC ATA CAA GTG TCT TCC AGA GAA GCC AAC TGC CGG ACC CAT CAA GCC TTC ATG CGC AAA GAC GTA AGG GAC ATA TTA ACC CCC ATA CAG ATC GAG GCC GCC TAT	Integrin α_4 subunit (CD49d, VLA-4)	VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	8

SEQ ID #	ID #	Nucleotide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
31	D-17	TCC TCA ATA TAT GAC GAC TCC TAC CTC GGA TAC AGT GTA GCG GTC GGC GAA TTT TCG GGA GAC GAC ACA GAA GAT TTT GTA GCT GGG GTG CCC AAA GGG AAT TTG ACT TAT GGC TAC GTT ACC ATA CTA AAT GGT TCT GAT ATT CGT AGT TTA TAT AAT TTC AGT GGG GAG CAA ATG GCA AGC TAT TTC GGA TAT GCG GTA GCA GCG ACC GAC GTC AAC GGT GAT GGG CTG GAC GAT TTG CTT GTC GGG GCC CCG TTA CTT ATG GAC CGC ACT CCA GAT GGA AGA CCA CAG GAA GTG GGT CGT GTA TAT GTG TAC TTA CAG CAC CCA GCA GGT ATA GAG CCG ACA CCG ACT TTG ACG CTA ACC GGA CAC GAC GAG TTC GGC CGG TTT GGC AGT TCA TTA ACA CCC CTT GGA GAC TTA GAT CAG GAT GGA TAC AAT GAC GTT GCT ATT GGG GCA CCA TTT GGT GGC GAA ACG CAA CAA GGT GTA GTA TTC GTG TTT CCT GGA GGC CCT GGA GGC TTA GGC AGT AAA CCT TCG CAA GTT TTG CAG CCA CTA TGG GCC GCT AGC CAT ACG CCC GAT TTC TTT GGC AGC GCT CTG AGA GGG GGG AGG GAC CTC GAC GGT AAC GGG TAT CCT GAT CTG ATC GTT GGT AGT TTT GGA GTC GAT AAG GCG GTG GTC TAC AGA GGG CGG CCC ATA GTT TCA GCA AGT GCC AGC CTT ACG ATA TTC CCC GCC ATG TTT AAT CCT GAG GAG AGA TCT TGC TCA TTG GAA GGT AAC CCG GTC GCG TGT ATC AAC CTC TCC TTC TGT TTA AAC GCA TCG GGT AAA CAT GTG GCT GAT TCG ATC GGA TTT ACA GTA GAA CTT CAA CTA GAT TGG CAG AAG CAA AAA GGC GGA GTT AGA CGA GCC CTC TTC CTC GCA TCC AGG CAG GCG ACT TTA ACA CAA ACC CTA CTG ATA CAG AAC GGA GCC AGA GAG GAT TGC CGC GAA ATG AAG ATC TAC CTG AGA AAT GAA TCT GAG TTC CGA GAC AAG TTA TCT CCG ATT CAT ATT GCT	Integrin α_5 subunit (CD49e, VLA-5)	FN, L1, invasin	Thromb, Ather, SIRS, ID	9

SEQ ID #	ID #	Nucleotide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
33	D-18	AGC TAC CTA GGA TAT AGT GTT GCT GTA GGC GAG TTC AGC GGA GAT GAT ACA GAA GAC TTT GTT GCA GGG GTG CCT AAG GGG AAT CTA ACA TAT GGG TAC GTA ACA ATC CTC AAC GGA TCG GAT ATT CGT AGT TTA TAC AAT TTC TCC GGT GAG CAA ATG GCC TCA TAT TTT GGA TAC GCC GTT GCG GCT ACG GAC GTT AAC GGT GAC GGA TTA GAC GAT CTT CTT GTG GGA GCT CCC CTG CTG ATG GAC CGA ACC CCT GAT GGT AGA CCC CAG GAA GTC GGA AGA GTC TAC GTC TAC TTG CAA CAT CCC GCC GGC ATA GAA CCA ACG CCA ACT TTA ACT CTC ACT GGG CAT GAC GAA TTT GGT AGA TTC GGT TCC TCT TTA ACC CCT CTT GGC GAC TTG GAC CAG GAT GGA TAT AAT GAT GTG GCA ATA GGC GCG CCG TTT GGG GGC GAG ACC CAG CAA GGC GTG GTG TTC GTC TTT CCA GGT GGA CCG GGT GGG CTA GGG TCT AAA CCA TCA CAA GTT TTA CAG CCA TTA TGG GCA GCG AGT CAC ACG CCA GAT TTT TTC GGC AGT GCA CTC AGG GGT GGA CGG GAC TTG GAC GGC AAC GGC TAT CCG GAT CTG ATA GTA GGG TCG TTC GGT GTA GAT AAA GCA GTA GTC TAT CGC GGG	Integrin α_5 subunit (CD49e, VLA-5)	FN, L1, invasin	Thromb, Ather, SIRS, ID	10
35	D-19	GCA CAT GGT TCG AGC ATC TTA GCA TGC GCT CCT CTC TAC AGC TGG AGA ACG GAA AAA GAA CCC TTA TCT GAT CCG GTC GGG ACG TGT TAT TTA TCG ACC GAC AAC TTT ACA AGA ATC TTA GAG TAC GCG CCA TGT AGA TCT GAT TTC AGT TGG GCA GCG GGT CAA GGG TAT TGC CAA GGC GGC TTC AGT GCC GAA TTT ACT AAG ACC GGA AGA GTA GTG CTT GGA GGT CCA GGA TCA TAC TTT TGG CAG GGG CAA ATT CTA TCC GCT ACA CAA GAG CAG ATA GCA GAG AGT TAT TAT CCA GAA TAC CTG ATA AAT TTA GTT CAG GGC CAG TTG CAG ACT AGA CAA GCC TCA TCC ATT TAT	Integrin α_5 subunit (CD49e, VLA-5)	FN, L1, invasin	Thromb, Ather, SIRS, ID	11
37	D-20	GAT TTT AGT TGG GCA GCA	Integrin α_5 subunit (CD49e, VLA-5)	FN, L1, invasin	Thromb, Ather, SIRS, ID	11

SEQ ID #	ID #	Nucleotide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
39	D-21	GGA GTA GAC GTA GAT CAG GAT GGC GAA ACA GAG TTA ATA GGA GCA CCA TTA TTT TAT GGT GAA CAA AGA GGG	Integrin α_L subunit (CD11a) I domain	ICAM-1, ICAM-2, ICAM-3, LPS,	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	12
41	D-22	ATA ACA GAT GGA GAA GCA ACA GAC AGT GGA CAA ATT GAT GCA GCA AAA GAC ATC ATA TAT ATT ATA GGA ATC	Integrin α_L subunit (CD11a) I domain	ICAM-1, ICAM-2, ICAM-3, LPS,	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	12
43	D-23	ATA ACA GAT GGA GAA GCA ACA AGT GGA TGT	Integrin α_L subunit (CD11a) I domain	ICAM-1, ICAM-2, ICAM-3, LPS,	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	13-14
45	D-24	GGA GTA GAC GTA GAT CAA GAT GGA GAA ACA TGT	Integrin α_L subunit (CD11a) I domain	ICAM-1, ICAM-2, ICAM-3, LPS,	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	15
47	D-25	TGC CCA AAT AAG GAA AAA GAG TGT	Integrin α_L subunit (CD11a) I domain	ICAM-1, ICAM-2, ICAM-3, LPS,	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	16
49	D-26	AAA GAA TTT GTA AGT ACA	Integrin α_m subunit (CD11b) I domain	iC3b, ICAM-1, ICAM-2, ICAM-4, Fb, Factor X, CD23, NIF, heparin, β-glucan, LPS	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	17
51	D-27	CCA ATA ACA CAA TTA TTA GGA AGA ACC CAT ACG GCA ACT GGA ATA AGA AAA	Integrin α_m subunit (CD11b) I domain	iC3b, ICAM-1, ICAM-2, ICAM-4, Fb, Factor X, CD23, NIF, heparin, β-glucan, LPS	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	17
53	D-28	AAA TTT GGA GAC CCA TTA GGA TAT GAA GAT GTA ATA CCA GAG GCA GAT AGA	Integrin α_m subunit (CD11b) I domain	iC3b, ICAM-1, ICAM-2, ICAM-4, Fb, Factor X, CD23, NIF, heparin, β-glucan, LPS	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	17, 18
55	D-29	GGA TGT CCA CAA GAA GAT AGT GAC ATT GCA TTC TTA ATA GAT GGA AGT GGA AGT ATA ATC CCA CAT GAC TTT	Integrin α_m subunit (CD11b) I domain	iC3b, ICAM-1, ICAM-2, ICAM-4, Fb, Factor X, CD23, NIF, heparin, β-glucan, LPS	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	19
57	D-30	TTT AGA AGA ATG AAA GAG TTT GTA AGT ACA GTA ATG GAA CAA TTA AAG AAA AGT AAG ACA TTA TTC AGT	Integrin α_m subunit (CD11b) I domain	iC3b, ICAM-1, ICAM-2, ICAM-4, Fb, Factor X, CD23, NIF, heparin, β-glucan, LPS	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	19

SEQ ID #	ID #	Nucleotide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
59	D-31	GGA AAT AGT TTT CCA GCA AGT TTA GTA GTA GCA GCA GAA GAG GGA GAG AGA GAA	Integrin α_{IIb} subunit (CD41) heavy chain	Fb, FN, VN, TSP, vWF	Thromb, Ather, SIRS, MOF, IR, ID	20
61	D-32	AAC GCA CAA ATC GGA ATT GCA ATG TTA GTA AGT GTA GGA AAT TTA GAG GAA GCA GGA GAA AGT GTA AGT TTT CAA TTA CAG ATA	Integrin α_{IIb} subunit (CD41) heavy chain	Fb, FN, VN, TSP, vWF	Thromb, Ather, SIRS, MOF, IR, ID	20
63	D-33	ACA TTA GGA CCA AGT CAA GAA GAG ACA GGA GGA GTA TTT TTA TGT CCA TGG AGA	Integrin α_{IIb} subunit (CD41) heavy chain	Fb, FN, VN, TSP, vWF	Thromb, Ather, SIRS, MOF, IR, ID	20
65	D-34	GCA GAA GGA GGA CAA TGT CCA AGT TTA TTA TTT GAT TTA	Integrin α_{IIb} subunit (CD41) heavy chain	Fb, FN, VN, TSP, vWF	Thromb, Ather, SIRS, MOF, IR, ID	20
67	D-35	GCC ATG GTC ACA GTA TTG GCA TTT CTT TGG CTC CCA AGT CTA TAT CAG AGA CCA CTG GAT CAA TTT GTG TTA CAA AGT CAT GCT TGG TTC AAT GTT AGT AGT TTA CCA TAC GCG GTA	Integrin α_{IIb} subunit (CD41) light chain	Fb, FN, VN, TSP, vWF	Thromb, Ather, SIRS, MOF, IR, ID	20
69	D-36	GGA GCA CAT TAT ATG AGA GCA TTA AGT AAT GTA GAA	Integrin α_{IIb} subunit (CD41)	Fb, FN, VN, TSP, vWF	Thromb, Ather, SIRS, MOF, IR, ID	21
71	D-37	GGA GCA CCA TTA	Integrin α_{IIb} subunit (CD41)	Fb, FN, VN, TSP, vWF	Thromb, Ather, SIRS, MOF, IR, ID	22
73	D-38	GGA GAT GGA AGA CAT GAC TTA TTA GTA GGA GCA CCA TTA	Integrin α_{IIb} subunit (CD41)	Fb, FN, VN, TSP, vWF	Thromb, Ather, SIRS, MOF, IR, ID	22
75	D-39	ACA GAT GTA AAT GGA GAC GGA AGA CAT GAT TTA	Integrin α_{IIb} subunit (CD41)	Fb, FN, VN, TSP, vWF	Thromb, Ather, SIRS, MOF, IR, ID	23
77	D-40	GGA GAT GGA AGA CAT GAC TTA TTA GTA GGA GCA CCA	Integrin α_{IIb} subunit (CD41)	Fb, FN, VN, TSP, vWF	Thromb, Ather, SIRS, MOF, IR, ID	23
79	D-41	GGA GAC GGA AGA CAT GAT TTA TTA GTA GGA GCA CCA TTA TAT	Integrin α_{IIb} subunit (CD41)	Fb, FN, VN, TSP, vWF	Thromb, Ather, SIRS, MOF, IR, ID	24

SEQ ID #	ID #	Nucleotide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
81	D-42	GAA TTT GAC GGT GAT CTT AAT ACG ACT GAG TAC GTC GTC GGA GCA CCA ACT TGG TCG TGG ACA TTA GGC GCA GTC GAG ATA CTC GAC AGT TAT TAT CAG AGG TTA CAT AGA TTA CGT GCA GAA CAG ATG GCG TCC TAC TTT GGT CAC AGC GTA GCG GTA ACG GAT GTG AAC GGA GAC GGC CGC CAT GAC TTG CTA GTT GGA GCT CCG CTC TAC ATG GAG AGT CGA GCA GAT CGC AAG CTT GCT GAA GTG GGC CGA GTA TAT CTT TTC CTT CAA CCA CGG GGT CCC CAC GCC CTA GGC GCT CCT AGT TTA TTG TTA ACC GGA ACA CAG TTG TAT GGT AGA TTC GGA TCT GCA ATA GCG CCA CTC GGG GAT TTG GAT AGA GAT GGC TAT AAC GAT ATA GCT GTG GCC GCC CCT TAC GGA GGA CCC TCC GGC AGA GGG CAG GTT CTG GTT TTC CTA GGG CAA AGT GAA GGG TTA AGG TCA AGA CCG TCT CAA GTC TTA GAC TCG CCA TTT CCA ACC GGA AGT GCG TTT GGG TTC AGT CTC CGT GGT GCA GTG GAC ATC GAT GAC AAT GGT TAC CCG GAT CTA ATT GTT GGA GCC TAC GGG GCC AAT CAA GTA GCA GTA TAT CGG GCG CAG CCC GTA GTT AAA GCT TCA GTC CAA CTG CTG GTG CAA GAC AGC CTG AAC CCT GCA	Integrin α_{IIb} subunit (CD41)	Fb, FN, VN, TSP, vWF	Thromb, Ather, SIRS, MOF, IR, ID	25
83	D-43	GCA GTA ACA GAT GTA AAT GGA GAC GGA AGA CAT GAT TTA TTA GTA GGA GCA CCA TTA TAT	Integrin α_{IIb} subunit (CD41)	Fb, FN, VN, TSP, vWF	Thromb, Ather, SIRS, MOF, IR, ID	26

SEQ ID #	ID #	Nucleotide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
85	D-44	TTT TCC TCA GTC GTG ACA CAA GCT GGC GAG TTA GTA TTG GGG GCT CCC GGA GGC TAC TAC TTC CTG GGG CTA CTC GCA CAG GCA CCC GTG GCG GAC ATA TTC TCG TCT TAT AGA CCT GGG ATT TTG TTG TGG CAC GTC TCC TCT CAG TCT TTA AGT TTC GAT AGT AGC AAT CCA GAA TAT TTT GAC GGA TAC TGG GGG TAT TCT GTG GCA GTC GGT GAG TTC GAT GGT GAT CTG AAT ACT ACA GAA TAT GTG GTA GGG GCT CCT ACA TGG AGT TGG ACT TTA GGC GCG GTC GAG ATA TTA GAT AGC TAC TAC CAA CGC TTA CAC AGA TTG CGT GCT GAA CAA ATG GCC TCC TAC TTT GGT CAT TCA GTC GCC GTT ACC GAT GTG AAT GGT GAT GGA CGG CAT GAC CTC CTA GTT GGA GCT CCA CTT TAC ATG GAG AGC AGA GCG GAC CGA AAG TTA GCT GAA GTA GGA AGA GTT TAT TTG TTC CTA CAA CCG AGG GGC CCG CAT GCG CTT GGC GCA CCT TCC TTA CTT CTG ACC GGT ACG CAA CTT TAC GGG CGA TTT GGG TCG GCC ATT GCG CCA CTG GGG GAC CTT GAT CGC GAC GGA TAT AAC GAC ATC GCA GTT GCC GCG CCT TAT GGA GGC CCA TCG GGT CGG GGA CAG GTT CTA GTG TTC CTC GGT CAA AGT GAA GGC CTC CGT AGT AGA CCG AGC CAG GTA CTG GAC AGT CCG TTT CCC ACG GGC TCG GCT TTT GGT TTT TCA TTA AGA GGT GCG GTA GAC ATC GAT GAT AAC GGA TAC CCC GAT CTC ATA GTA GGG GCC TAT GGC GCC AAC CAG GTC GCA GTT TAT AGG GCC CAG CCA GTA GTG AAA GCA TCA GTC CAA TTA CTA GTT CAG GAC	Integrin α_{IIb} subunit (CD41)	Fb, FN, VN, TSP, vWF	Thromb, Ather, SIRS, MOF, IR, ID	27
87	D-45	GTA GAA AAT GAT TTT AGT TGG	Integrin α_{IIb} subunit (CD41)	Fb, FN, VN, TSP, vWF	Thromb, Ather, SIRS, MOF, IR, ID	28
NA	D-46	GAA TAT	Integrin α_{IIb} subunit (CD41)	Fb, FN, VN, TSP, vWF	Thromb, Ather, SIRS, MOF, IR, ID	28
89	D-47	GGA GAA TTA GTA TTA	Integrin α_{IIb} subunit (CD41)	Fb, FN, VN, TSP, vWF	Thromb, Ather, SIRS, MOF, IR, ID	28
91	D-48	GAT TTA TAT TAT TTA ATG GAC TTA AGT TAC AGT ATG AAA	All integrin β subunits	FN, Fb, CN I, VN	All named pathologies	29

SEQ ID #	ID #	Nucleotide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
NA	D-49	D$$$$$DXSXS$KDDL; $, any hydrophobic residue; X, any residue	All integrin β subunits	All named ligands	All named pathologies	29
93	D-50	TAC TGC CGA AAA GAA AAC TCA TCG GAA ATA TGT AGT AAC AAT GGG GAG TGC GTC TGC GGC CAA TGT GTA TGC CGG AAA CGT GAC AAC ACA AAC GAA ATC TAT AGT GGA AAG TTT TGT GAG TGT GAT AAT TTC AAC TGT GAT CGC AGC AAT GGC TTA ATA TGC GGT GGC AAT GGA GTT TGC AAG TGT AGG GTG TGT GAA TGC AAT CCA AAT TAT ACA GGG AGT GCA TGC GAT TGC TCT TTA GAC ACT AGT ACG TGC GAG GCA TCC AAC GGG CAG ATA TGT AAT GGA AGA GGT ATT TGT GAG TGT GGT GTA TGC AAA TGT ACC GAC	Integrin β_1 subunit (CD29)	FN, LN, CN, VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	30
95	D-51		Integrin β_1 subunit (CD29)	FN, LN, CN, VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	31

SEQ ID #	ID #	Nucleotide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
97	D-52	TTG CGA TTA CGC TCG GGC GAA CCC CAG ACA TTT ACG CTT AAG TTC AAA CGG GCT GAG GAT TAT CCT ATC GAC CTT TAC TAT CTT ATG GAT CTC TCA TAT AGT ATG AAA GAT GAT CTG GAG AAT GTT AAG TCC TTA GGG ACC GAT TTA ATG AAC GAG ATG AGA AGA ATC ACT TCA GAC TTC AGA ATT GGA TTT GGC TCT TTT GTC GAA AAA ACC GTA ATG CCA TAC ATA AGC ACA ACC CCA GCA AAG CTG AGG AAT CCG TGT ACA TCG GAG CAA AAC TGC ACT ACT CCC TTC AGT TAT AAG AAT GTT CTC AGT CTG ACG AAC AAA GGG GAA GTA TTT AAC GAG CTA GTG GGA AAA CAG AGA ATT AGC GGT AAC CTC GAC TCT CCA GAA GGT GGT TTT GAT GCA ATT ATG CAA GTT GCA GTG TGT GGA TCT CTA ATA GGG TGG CGT AAT GTA ACT AGA CTA TTG GTG TTT TCC ACC GAC GCC GGC TTC CAC TTC GCT GGA GAC GGC AAG CTA GGG GGA ATC GTA TTG CCT AAC GAT GGT CAG TGC CAT TTG GAA AAT AAT ATG TAT ACG ATG TCG CAC TAC TAC GAC TAC CCA TCC ATA GCC CAT TTA GTC CAA AAG CTG AGC GAA AAC AAT ATT CAA ACA ATA TTT GCG GTA ACG GAA GAG TTC CAG CCA GTC TAT AAG GAG CTT AAA AAT CTC ATC CCG AAA TCA GCG	Integrin β_1 subunit (CD29)	FN, LN, CN, VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	32
99	D-53	AAC AAG GGA GAA GTA TTT AAT GAG TTA GTA GGA AAA	Integrin β_1 subunit (CD29)	FN, LN, CN, VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	33
101	D-54	ACA GCA GAA AAA TTA	Integrin β_1 subunit (CD29)	FN, LN, CN, VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	34
103	D-55	GAT TAC CCA ATA GAC TTA TAC TAT TTA ATG GAC TTA AGT TAT AGT ATG AAG GAT GAT TTA GAA GTA AAA AGT TTA GGA	Integrin β_1 subunit (CD29)	FN, LN, CN, VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	35
105	D-56	AAT GTA AAG AGT TTA GGA ACA GCA TTA ATG AGA GAG ATG GAA AAA ATA ACA AGT GAT TTT	Integrin β_1 subunit (CD29)	FN, LN, CN, VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	36

SEQ ID #	ID #	Nucleotide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
107	D-57	GGA CAA AAA CAG TTA AGT CCG CAG AAG GTC ACT CTA TAC TTG CGT CCC GGG CAA GCA GCC GCG TTC AAC GTA ACG TTT CGT CGC GCA AAA GGA TAC CCA ATA GAC CTT TAT TAT TTA ATG GAT TTA TCC TAC TCA ATG CTC GAT GAT TTA AGA AAC GTT AAG AAG TTA GGC GGG GAT CTG CTC AGA GCT CTC AAT GAG ATA ACT GAA AGT GGT CGG ATA GGT TTC GGT TCG TTC GTT GAT AAG ACG GTG CTG CCC TTT GTA AAT ACA CAC CCA GAC AAA CTG AGG AAC CCC TGC CCA AAT AAG GAG AAA GAA TGC CAG CCG CCT TTC GCT TTT CGC CAT GTC CTA AAA TTA ACA AAT AAT AGC AAT CAA TTT CAG ACC GAG GTA GGA AAA CAA CTT ATT AGT GGA AAC TTA GAC GCC CCA GAG GGC GGC TTA GAC GCA ATG ATG CAA GTA GCA GCC TGT CCG GAG GAA ATT GGT TGG CGG AAT GTC ACC AGG TTG TTG GTA TTT GCC ACT GAC GAT GGA TTC CAT TTT GCT GGA GAT GGC AAG CTA GGG GCG ATT CTT ACC CCT AAC GAC GGG CGA TGT CAC CTC GAA GAC AAC CTA TAT AAG AGA AGT AAT GAA TTC GAT TAT CCA TCT GTG GGA CAA CTG GCG CAT AAG TTG GCT GAG AAC AAC ATA CAG CCA ATC TTT GCA GTT ACA AGT CGA ATG GTG AAA ACA TAC GAA AAA CTT ACG GAA ATC ATC CCT AAA AGT GCG	Integrin β_2 subunit (CD18)	ICAM-1, ICAM-2, ICAM-3, ICAM-4, LPS, iC3b, Fb, Factor X, CD23, NIF, heparin, β-glucan,	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	37

SEQ ID #	ID #	Nucleotide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
109	D-58	TAC CCA ATA GAT CTC TAC TAC CTG ATG GAT CTA TCC TAT TCA ATG CTG GAC GAT CTA CGT AAC GTT AAG AAA CTT GGA GGT GAT TTA CTA AGA GCT CTT AAC GAA ATC ACG GAG AGT GGG CGA ATC GGC TTC GGC TCA TTC GTC GAC AAG ACA GTA TTG CCC TTC GTA AAC ACG CAC CCA GAC AAG CTT AGA AAC CCC TGC CCA AAT AAA GAG AAA GAG TGT CAA CCC CCG TTT GCC TTT AGA CAT GTC TTA AAG CTC ACG AAT AAC AGC AAT CAG TTT CAG ACA GAA GTT GGA AAA CAA CTG ATA TCG GGT AAT CTA GAC GCA CCA GAG GGG GGA CTT GAT GCC ATG ATG CAG GTG GCA GCC TGC CCG GAG GAA ATT GGG TGG AGG AAT GTC ACA AGA CTG CTA GTT TTC GCA ACT GAT GAC GGG TTT CAT TTT GCT GGA GAT GGT AAA CTG GGC GCA ATT TTG ACT CCT AAC GAT GGA CGG TGT CAT TTG GAA GAC AAC CTC TAT AAA AGA AGC AAT GAA TTC GAC TAT CCT AGT GTA GGT CAA TTA GCG CAC AAG TTA GCA GAA AAC AAT ATA CAA CCG ATA TTT GCG GTT ACC AGT CGC ATG GTG AAA ACA TAC GAA AAG TTA ACC GAG ATA ATT CCA AAA TCT GCT GTG GGC GAG CTC TCC GAA GAT AGT AGT AAT GTC GTA CAC TTG ATC AAG AAT GCA TAT AAC AAA TTA TCT AGT AGA GTA TTT TTG GAC CAT AAT GCG CTT CCT GAT ACT CTC AAG GTG ACC TAT GAC TCG TTC	Integrin β_2 subunit (CD18)	ICAM-1, ICAM-2, ICAM-3, ICAM-4, LPS, iC3b, Fb, Factor X, CD23, NIF, heparin, β-glucan,	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	38
111	D-59	AGA AAT GTA AAA AAG	Integrin β_2 subunit (CD18)	ICAM-1, ICAM-2, ICAM-3, ICAM-4, LPS, iC3b, Fb, Factor X, CD23, NIF, heparin, β-glucan,	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	39

SEQ ID #	ID #	Nucleotide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
113	D-60	CAA CCA CCA TTT GCA	Integrin β_2 subunit (CD18)	ICAM-1, ICAM-2, ICAM-3, ICAM-4, LPS, iC3b, Fb, Factor X, CD23, NIF, heparin, β-glucan,	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	39
115	D-61	TTA ATA AGT GGA AAT TTA	Integrin β_2 subunit (CD18)	ICAM-1, ICAM-2, ICAM-3, ICAM-4, LPS, iC3b, Fb, Factor X, CD23, NIF, heparin, β-glucan,	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	39
117	D-62	GGA CAA TTA GCA CAT	Integrin β_2 subunit (CD18)	ICAM-1, ICAM-2, ICAM-3, ICAM-4, LPS, iC3b, Fb, Factor X, CD23, NIF, heparin, β-glucan,	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	39
119	D-63	GAG CTC TCA GAA GAT TCT AGT AAT GTC GTC CAT TTA ATC AAA AAC GCC TAT AAC AAA CTA AGT TCG AGA GTT TTC TTA GAC CAC AAT GCA CTG CCA GAT ACG TTG AAG GTA ACA TAC GAC AGC TTT TGC TCC AAT GGG GTG ACC CAT AGA AAC CAG CCA AGA GGC GAT TGT GAC GGA GTA CAA ATA AAT GTA CCA ATA ACA TTC CAG GTT AAG GTG ACA GCT ACT GAG TGT ATA CAA GAA CAA AGT TTT GTA ATT AGA GCG CTT GGT	Integrin β_2 subunit (CD18)	ICAM-1, ICAM-2, ICAM-3, ICAM-4, LPS, iC3b, Fb, Factor X, CD23, NIF, heparin, β-glucan,	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	40
121	D-64	GGT TTC ACC GAC ATT GTA ACA GTA CAG GTA TTA CCA CAA TGC GAA TGC AGA TGT AGA GAT CAA AGT AGA GAC AGA AGT TTA TGC CAT GGA AAG GGC TTT TTA GAA TGT GGA ATC TGT AGA TGC GAT ACG GGA TAT ATA GGA AAA AAT TGT GAG TGT CAG ACT CAA GGG	Integrin β_2 subunit (CD18)	ICAM-1, ICAM-2, ICAM-3, ICAM-4, LPS, iC3b, Fb, Factor X, CD23, NIF, heparin, β-glucan,	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	40

SEQ ID #	ID #	Nucleotide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
123	D-65	TGT AAT GCA TTT AAG ATA TTA GTA GTA ATA ACA GAT GGA GAA AAA	Integrin β_2 subunit (CD18) A domain	ICAM-1, ICAM-2, ICAM-3, ICAM-4, LPS, iC3b, Fb, Factor X, CD23, NIF, heparin, β-glucan,	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	41
125	D-66	ACA GGA ATA AGA AAG GTA GTA AGA GAA TTA TTT AAT ATA ACA AAC GGA GCA AGA AAA AAT	Integrin β_2 subunit (CD18) A domain	ICAM-1, ICAM-2, ICAM-3, ICAM-4, LPS, iC3b, Fb, Factor X, CD23, NIF, heparin, β-glucan,	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	41
127	D-67	GAT TTA AGT TAT AGT CTC GAC GAT CTG AGA AAT GTA AAG AAA CTT GGA GGA GAC CTA TTA AGA GCA TTG AAC GAA	Integrin β_2 subunit (CD18)	ICAM-1, ICAM-2, ICAM-3, ICAM-4, LPS, iC3b, Fb, Factor X, CD23, NIF, heparin, β-glucan,	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	42, 43
129	D-68	GAC TAT CCC GTA GAC ATA TAC TAC CTT ATG GAT TTA AGT TAC TCC ATG AAG GAC GAT CTC TGG TCA ATT CAG AAC TTG GGA ACA AAA CTA GCA ACA CAA ATG AGA AAG CTG ACA TCG AAT TTA AGA ATA GGA TTT GGA GCA TTC GTA GAT AAA CCA GTA AGC CCT TAT ATG TAT ATC TCT CCA CCG GAA	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	44
131	D-69	GAC GCA CCA GAA GGA GGA TTT GAT GCA ATA ATG CAA GCA ACA GTA	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	45

SEQ ID #	ID #	Nucleotide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
133	D-70	TTT TCC ATA CAG GTT CGA CAG GTA GAG GAT TAT CCA GTA GAC ATC TAT TAC TTA ATG GAC TTA AGC TAT AGT ATG AAG GAC GAT CTC TGG AGT ATA CAA AAT TTA GGT ACC AAG TTG GCC ACC CAA ATG CGT AAA TTA ACT TCA AAT TTA CGG ATA GGA TTC GGG GCA TTT GTG GAT AAA CCC GTA TCG CCG TAC ATG TAT ATT AGT CCA CCT GAG GCG CTT GAA AAC CCC TGC TAC GAC ATG AAA ACA ACG TGT CTG CCT ATG TTT GGC TAC AAG CAT GTC CTA ACA TTA ACG GAT CAA GTC ACT AGG TTC AAC GAG GAA GTT AAA AAG CAG AGT GTG TCT CGC AAT AGA GAT GCT CCG GAA	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	46
135	D-71	GGA GTA AGT AGT TGC CAG CAA TGT TTA GCA GTA AGT CCA ATG TGT GCA TGG TGC AGT GAT GAA GCA TTA CCA TTA GGA AGT CCA AGA	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	20
137	D-72	GTA TTA GAA GAC AGA CCA TTA AGT GAT AAA GGA AGT GGA GAT AGT AGT CAA GTA ACA CAG GTA	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	20
139	D-73	AAC ATC AAT TTA ATA TTT GCA GTC ACA GAA AAC GTA GTG AAT CTT TAC CAG AAC TAT AGT GAG CTA ATA CCA GGA ACA ACA GTA GGA GTT CTC AGT ATG GAT AGT AGT AAT GTA CTG CAA TTG ATT GTA GAC GCA TAT GGA AAA ATA AGA AGT	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	20
141	D-74	ATA GGA TTT GGA GCA TTC GTA GAC AAA CCA GTA AGT CCT TAC ATG TAT ATA AGT CCA CCC GAA GCA TTA GAG AAT CCA TGC TAC GAT ATG AAG ACA ACA TGT TTA CCG ATG TTT GGA TAT AAA	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	20
143	D-75	AGT GTA AGT AGA AAT AGA GAT GCA CCA GAA GGA GGA	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	47
145	D-76	AGT GTA AGT AGA AAT AGA GAT GCA CCA GAA GGA	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	48

SEQ ID #	ID #	Nucleotide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
147	D-77	AGA AAT AGA GAT GCA	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	48
149	D-78	GAT GCA CCA GAA GGA GGA TTT GAC GCA ATA ATG CAA GCA ACA	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	49
151	D-79	GAT GCA CCA GAA GGA GGA TTT GAC GCA ATA ATG CAA GCA ACA GTA	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	49
153	D-80	GAT GCG CCA GAA GGT GGG TTT GAC GCG ATC ATG CAA GCT ACA GTG TGC GAC GAA AAA ATA GGC TGG AGA AAC GAT GCA AGT CAC CTC CTT GTC TTC ACA ACC GAT GCA AAA ACA CAT ATT GCC CTG GAC GGG AGA TTG GCC GGC ATA GTT CAA CCA AAT GAT GGT CAG TGT CAT GTA GGA TCA GAC AAT CAC TAT TCT GCT AGC ACT ACG ATG GAT TAC CCA TCC TTA GGA TTA ATG ACA GAG AAG CTA TCG CAG AAG	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1, viper and rattlesnake venom components: albolabrin, bitistatin, echistatin, eristostatin	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID, viper and rattlesnake bites	50
155	D-81	ATG GAC TTA AGT TAT AGT ATG AAA GAT GAT TTA TGG AGT ATA	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	51
157	D-82	GGA CCA AAT ATA TGT ACA	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	52
159	D-83	GGA CCA AAT ATA TGT ACA ACA AGA GGA GTAAGT AGT TGC	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	52
161	D-84	AAA GAT TCT TTA ATA GTA CAG GTA ACA TTT GAC TGT GAC TGT GCA TGT CAG GCA CAA GCA GAA CCC AAC TCG CAT AGA TGC AAC AAT GGA AAT GGC ACA TTC GAA TGC GGA GTA TGC AGA TGC GGA CCG GGT TGG TTA GGG AGT CAG TGT GAA TGC TCA GAG GAA GAT TAT AGA CCT TCC CAA CAA GAT GAG TGT AGC CCA AGA GAG	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	53

SEQ ID #	ID #	Nucleotide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
163	D-85	CCT ACT TGC CCG GAT GCT TGC ACT TTT AAA AAA GAA TGT GTA GAA TGC AAA AAA TTT GAC CGT GAG CCC TAT ATG ACA GAA AAT ACT TGC AAC AGG TAT TGT AGA GAT GAA ATA GAG AGC GTT AAA GAG TTA AAA GAT ACA GGT AAA GAT GCA GTT AAC TGT ACA TAT AAA AAT GAG GAC GAT TGT GTG GTA CGA TTC CAA TAT TAT GAA GAC AGT TCA GGA AAA TCT ATA TTG TAT GTA GTG GAA GAG CCA GAA TGT CCA AAA GGG	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	54
165	D-86	AAA GAT GAC TTA TGG	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	55
167	D-87	AGT GTA AGT AGA AAT AGA GAT GCA CCA GAA GGA GGA TTT	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	24
169	D-88	CAC GTG GGG AGT GAC AAC CAT TAT TCC GCA TCT ACA ACT ATG GAC TAT CCA AGT CTG GGC TTA ATG ACA GAG AAG TTA AGC CAA AAG AAT TTA AAC TTG ATC TTT GCA GTT ACA GAG AAC GTA GTC AAT CTT TAC CAG AAT TAC AGT GAG CTA ATT CCA GGA ACG ACC GTA GGA GTA TTG TCG ATG GAT AGT TCA AAT GTC CTC CAA CTA ATA GTG GAT GCA TAT GGT AAA ATA AGA AGT AAA GTT GAA TTA GAA GTA AGA GAT CTC CCA GAA GAA CTT AGT CTG	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	56

SEQ ID #	ID #	Nucleotide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
171	D-89	GAC GAT AGT AAA AAT TTC AGT ATT CAA GTA CGA CAA GTA GAA GAC TAT CCC GTT GAC ATC TAC TAT CTA ATG GAT TTA AGT TAC AGT ATG AAA GAT GAT TTA TGG AGT ATA CAG AAT TTG GGG ACC AAG CTT GCA ACC CAA ATG AGA AAG CTG ACA TCG AAC TTA AGG ATT GGA TTT GGA GCA TTC GTT GAT AAG CCT GTG TCA CCG TAT ATG TAC ATC TCT CCC CCA GAG GCT TTA GAA AAT CCG TGT TAC GAC ATG AAA ACG ACA TGT TTA CCT ATG TTT GGT TAT AAA CAT GTA TTA ACG CTC ACT GAC CAG GTA ACA CGT TTT AAC GAA GAG GTC AAG AAA CAG AGC GTG TCC CGG AAC CGC GAT GCG CCA GAG GGC GGA TTC GAC GCC ATA ATG CAA GCA ACT GTC TGC GAT	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	57
173	D-90	TAT ATG TAC ATA AGT CCC CCG GAA GCA TTA GAG AAT CCT TGT TAC GAT ATG AAA ACT ACC TGC TTA CCA ATG TTT GGA TAT AAG CAT GTA TTA ACA TTA ACG GAC CAA GTA ACA AGA	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	57
175	D-91	AGA AAT AGA GAT GCA TAT	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	58
177	D-92	GAC GCA CCA GAA GGA GGA TTT GAT GCA ATA ATG CAA GCA ACA GTA TAT	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	58
179	D-93	TGC TAT GAT ATG AAA ACA ACA TGT	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1, Coxsackievirus A9	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	31, 59
181	D-94	AAT TTT AGT ATA CAG GTA AGA CAA GTA GAA GAC TAT CCA GTA GAT ATA TAT TAC TTA ATG	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	60
183	D-95	GAT ATG AAA ACA ACA	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	28

SEQ ID #	ID #	Nucleotide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
185	D-96	ATA AGT CCA CCA GCA	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	61
187	D-97	AAA CAA AGT GTA AGT AGA AAT AGA GAT GCA CCA GAA	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	62
189	D-98	GAT GAC AGT AAA AAT TTT AGT ATC CAG GTA AGA CAG GTA GAA GAT TAT CCA GTC GAC ATA TAT TAC CTC ATG GAC CTG AGT TAC AGT ATG AAG GAT GAT CTC TGG TCA ATT CAA AAT CTA GGG ACT AAG CTT GCG ACG CAA ATG AGA AAA TTG ACA AGC AAT TTA CGA ATT GGA TTT GGA GCA TTC GTC GAT AAG CCT GTT AGT CCT TAC ATG TAC ATC TCA CCC CCT GAA GCC TTA GAG AAC CCC TGC TAT GAC ATG AAA ACC ACA TGT TTA CCG ATG TTT GGT TAT AAA CAT GTG CTC ACG CTT ACG GAC CAA GTG ACT CGG TTC AAT GAG GAA GTA AAA AAG CAG TCT GTC AGT AGG AAC CGT GAT GCA CCG GAA GGA GGA TTT GAC GCG ATA ATG CAA GCC ACA GTA TGT GAC GAG AAA ATA GGC TGG CGC AAC GAT GCA TCC CAT TTA CTG GTG TTC ACC ACT GAT GCG AAA ACA CAC ATC GCA TTG GAT GGT AGA TTG GCT GGA ATA GTA CAG CCA AAT GAT GGC CAA TGC CAT GTC GGG AGC GAC AAC CAC TAT TCG GCA AGT ACC ACG ATG GAC TAC CCC AGC TTA GGT CTA ATG ACT GAG AAG TTA TCG CAG AAG AAC CTT AAC CTA ATC TTC GCT GTA ACA GAA AAT GTA GTT AAT TTA TAT CAA AAC TAC TCG GAA CTG ATA CCG GGA ACA ACA GTT GGG GTC TTG TCC ATG GAC TCA AGT AAT GTT TTA CAG CTA ATT GTG GAC GCT TAT GGC AAG ATT AGA TCC AAA GTG GAG TTA GAA GTT AGA GAT CTT CCA GAG GAG CTC TCT CTG TCT TTT AAC GCC ACC	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	63

SEQ ID #	ID #	Nucleotide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
191	D-99	GAT GAT TCT AAG AAT TTT TCC ATC CAG GTT CGA CAG GTC GAA GAT TAC CCA GTA GAC ATA TAT TAC CTA ATG GAT CTC AGT TAT AGT ATG AAG GAC GAT CTA TGG AGT ATC CAA AAC CTG GGC ACG AAA CTT GCC ACT CAA ATG CGG AAA TTA ACA TCA AAC TTG AGG ATT GGC TTT GGG GCA TTC GTG GAT AAA CCC GTA TCC CCA TAT ATG TAC ATC TCT CCA CCG GAG GCA CTC GAA AAC CCT TGC TAC GAC ATG AAG ACC ACA TGC CTT CCT ATG TTT GGG TAT AAA CAC GTG CTT ACT TTA ACC GAC CAG GTT ACG AGA TTC AAT GAA GAG GTA AAA AAG CAA AGT GTA AGC CGT AAC AGA GAC GCA CCG GAG GGA GGG TTC GAC GCA ATA ATG CAA GCT ACT GTC TGT GAC GAG AAG ATT GGA TGG AGA AAT GAT GCG TCG CAT TTG TTA GTC TTT ACA ACA GAT GCC AAA ACA CAC ATT GCG CTG GAC GGT CGC CTC GCA GGC ATA GTT CAG CCA AAT GAT GGT CAG TGT CAT GTG GGT AGT GAT AAT CAT TAT AGC GCT TCA ACA ACC ATG GAC TAC CCC AGT CTA GGA CTG ATG ACG GAA AAG TTG TCG CAA	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	63

SEQ ID #	ID #	Nucleotide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
193	D-100	AAG CAA CTG AAT TTC ACG GCC TCT GGA GAG GCA GAG GCC CGC AGA TGC GCA CGG AGG GAA GAG CTC CTA GCT AGG GGA TGC CCC CTG GAG GAG CTA GAA GAG CCA CGT GGA CAG CAA GAG GTA CTA CAG GAT CAG CCG CTG TCG CAA GGA GCC CGA GGT GAG GGT GCG ACC CAG CTA GCA CCA CAA CGC GTA CGC GTT ACA TTA CGG CCA GGC GAA CCA CAA CAA TTA CAG GTA AGA TTT TTG CGT GCT GAA GGG TAT CCG GTG GAT TTA TAC TAT CTC ATG GAT CTT AGT TAC TCC ATG AAG GAT GAT CTA GAA AGG GTA CGC CAA CTG GGT CAT GCC TTA TTG GTA AGA TTA CAA GAA GTA ACA CAT AGC GTA CGT ATC GGG TTT GGA TCT TTC GTA GAC AAA ACC GTT TTA CCT TTC GTG AGT ACC GTG CCT AGC AAA TTG CGT CAC CCT TGT CCA ACT AGG CTT GAG CGA TGC CAG AGT CCG TTC TCA TTC CAC CAT GTT TTG AGT TTA ACT GGA GAT GCC CAG GCC TTC GAG CGA GAA GTC GGC CGG CAA TCC GTT TCT GGG AAT TTA GAC AGT CCC GAG GGA GGG TTT GAC GCG ATA CTT CAA GCA GCG CTC TGT CAG GAA CAG ATT GGC TGG CGA AAC GTC AGC AGA CTA TTA GTC TTT ACG AGT GAC GAT ACT TTT CAC ACA GCA GGG GAC GGA AAG CTT GGC GGT ATT TTT ATG CCC AGC GAC GGT CAT TGT CAC CTC GAT TCA AAT GGA TTG TAC AGT CGG TCC ACA GAA TTC GAT TAT CCT TCG GTG GGC CAG GTG GCG CAG GCA CTG AGT GCT GCA AAC ATC CAG CCA ATA TTT GCT GTT ACA TCG GCG GCG TTG CCG GTT TAC CAA GAA CTC TCA AAA TTA ATA CCC AAA TCC GCT GTC GGC GAA TTA TCT GAG GAC TCC TCA AAC GTG GTC CAA CTC ATC ATG GAC GCT TAT AAT TCG CTT AGT AGC ACG GTA ACA CTG GAA CAC TCA TCG CTT CCG CCC GGT GTC CAT ATT TCT TAT GAG AGT CAA TGT GAA GGG CCT	Integrin β_7 subunit (LPAM-1)	VCAM-1 FN, MAdCAM-1, E-cadherin (cadherin-1)	Auto, SS, MOF, Trans, Crohn's, IBD, IR, ID	64

SEQ ID #	ID #	Nucleotide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
195	D-101	AGT TTT GTT GAT AAA ACA GTC CTG CCG TTC GTA AGT ACC GTA CCA AGT AAG TTA CGC CAT CCA TGT CCA ACG AGG TTG GAG AGA TGC CAG TCT CCT TTT TCC TTC CAC CAT GTC TTA AGC CTA ACT GGT GAC GCT CAA GCC TTT GAA CGG GAA GTA GGA AGA CAA TCG GTG AGT GGG AAC CTT GAT TCA CCC GAA GGA GGC TTC GAC GCA ATA TTA CAG GCG GCA CTC TGT CAG GAG CAA ATA GGA TGG CGA AAT GTT AGT CGT TTA TTA GTG	Integrin β_7 subunit (LPAM-1)	VCAM-1 FN, MAdCAM-1, E-cadherin (cadherin-1)	Auto, SS, MOF, Trans, Crohn's, IBD, IR, ID	64
197	D-102	AAA CAA CTC AAT TTC ACA GCT AGT GGC GAA GCA GAG GCT AGG AGA TGC GCC AGG CGA GAA GAA TTA TTG GCA CGC GGG TGT CCC CTG GAG GAG CTT GAA GAG CCA CGG GGT CAG CAG GAA GTT TTA CAA GAT CAA CCA TTA AGT CAG GGA GCA CGC GGC GAA GGG GCG ACA CAA TTA GCG CCA CAG CGT GTC AGA GTG ACA TTG CGA CCA GGA GAG CCT CAA CAG TTA CAA GTA CGT TTT CTT CGG GCC GAG GGT TAC CCG GTA GAT CTG TAT TAC CTA ATG GAC CTC AGT TAT AGT ATG AAG GAC GAT CTA	Integrin β_7 subunit (LPAM-1)	VCAM-1 FN, MAdCAM-1, E-cadherin (cadherin-1)	Auto, SS, MOF, Trans, Crohn's, IBD, IR, ID	64

SEQ ID #	ID #	Nucleotide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
199	D-103	GAA AAA CGT GAG GGA AAA GCC GAA GAC AGA GGC CAG TGT AAC CAC GTG AGG ATA AAC CAA ACC GTA ACC TTC TGG GTC TCG CTT CAG GCA ACT CAT TGT TTA CCC GAA CCA CAT TTG CTA CGC CTC CGG GCT TTA GGG TTT TCT GAG GAG CTC ATA GTT GAG CTA CAC ACG TTA TGT GAC TGC AAT TGC TCA GAC ACG CAA CCA CAA GCG CCA CAC TGT TCC GAT GGG CAG GGC CAC CTT CAA TGT GGA GTC TGT AGT TGC GCT CCT GGT AGA TTG GGT AGG CTG TGC GAG TGC AGT GTA GCT GAG TTA TCG AGT CCT GAT CTC GAA AGC GGA TGT CGC GCG CCG AAT GGG ACT GGA CCT CTG TGT TCC GGA AAA GGG CAT TGC CAG TGT GGT CGG TGC TCT TGC TCG GGT CAG TCA AGT GGC CAT TTG TGC GAA TGT GAC GAC GCC AGC TGT GAA CGG CAT GAG GGC ATT TTG TGC GGG GGT TTC GGC AGG TGC CAG TGT GGG GTG TGT CAC TGT CAT GCA AAC CGA ACA GGT CGA GCA TGC GAG TGT TCC GGC GAC ATG GAT TCT TGT ATA AGT CCG GAG GGA GGT TTA TGC AGT GGT CAT GGA AGA TGC AAG TGC AAT CGC TGC CAA TGC TTA GAT GGT TAC TAC GGA GCC CTA TGT GAT CAG TGC CCA GGC TGT AAG ACT CCA TGT GAA AGA CAC CGA GAC TGC GCA GAG TGC GGT GCG TTT AGA ACA GGC CCC CTG GCC ACC AAT TGC AGC ACA GCT TGT GCT CAC ACT AAT GTG ACG CTT GCA CTT GCG CCC ATA TTA GAT GAC GGC TGG TGT AAA GAA AGA ACA TTG GAT AAC CAA CTG TTT TTT TTC CTA GTA GAA GAC GAT GCC AGA GGC ACG GTA GTT CTC CGT GTT AGA CCG CAA GAA AAG GGA GCA GAT CAT ACC CAA GCA ATT GTA CTG GGG TGT GTT GGG GGA ATC GTC GCA GTG GGG CTA GGG CTC GTA CTT GCG TAT CGT TTA TCA GTC GAA ATC TAT GAT	Integrin β_7 subunit (LPAM-1)	VCAM-1 FN, MAdCAM-1, E-cadherin (cadherin-1)	Auto, SS, MOF, Trans, Crohn's, IBD, IR, ID	64

SEQ ID #	ID #	Nucleotide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
201	D-104	GAA CAT ATA CCA GCA	Mimics Integrin $\alpha_{IIb}\beta_3$ subunit	Fb, FN, VN, TSP, vWF	Thromb, Ather, SIRS, MOF, IR, ID	65
203	D-105	ATA CCA TGT AAT AAC AAA GGA GCA CAT AGT GTA GGA TTA ATG TGG TGG ATG TTA GCA AGA	67 kD LN receptor	LN	Meta	66
205	D-106	AAA GTA ATA TTA GAT AGA GGA GGA AGT GTA TTA GTA ACA TGT	ICAM-1	Fb	Thromb, Ather, SIRS, MOF, IR, ID	67
207	D-107	TGC TGG GAC GAT GGA TGG TTA TGT	Phage display library-mimics RGD binding site in integrins	FN, VN	Thromb, Ather, SIRS, MOF, IR, ID	55
209	D-108	TGC TGG GAT GAC TTA TGG TTA TGT	Phage display library-mimics RGD binding site in integrins	FN, VN	Thromb, Ather, SIRS, MOF, IR, ID	55
211	D-109	TGC TTA TTA AGA ATG AGA AGT ATA TGT	Phage display library	ICAM-1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	68
213	D-110	CCA GAT ACA AGA CCC GCC CCT GGA AGT ACA GCA CCG CCA GCG CAT GGA GTA ACA AGT GCT	MUC-1 protein	ICAM-1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	69
215	D-111	GAG TGG TGT GAA TAT TTA GGA GGA TAT TTA AGA TGC TAC GCA	Phage display library	ICAM-1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	70
217	D-112	GAA TGG CCA GAG TAT TTA	Rhinovirus coat protein 14	ICAM-1	Thromb, Auto, IBD, Ather, SIRS, MOF, Trans, Crohn's, SS, IR, ID	70

Ligand Abbreviations
CN I- Type I collagen
CN II- Type II collagen
CN III- Type III collagen
Up to 19 different collagen types
LN- Laminin
VCAM-1- Vascular cell adhesion molecule-1
FN- Fibronectin
MadCAM-1- Mucosal addressin cell adhesion molecule-1
TSD- Thrombospondin
ICAM-1- Intercellular adhesion molecule-1
ICAM-2- Intercellular adhesion molecule-2
ICAM-3- Intercellular adhesion molecule-3
ICAM-4- Intercellular adhesion molecule-4
LPS- bacterial lipopolysaccharide
iC3b- Complement fragment iC3b
Fb- Fibrinogen
VN- Vitronectin
vWF- von Willebrand factor

Pathology Abbreviations
Thromb- Thrombosis
Ather- Atherosclerosis
SIRS- Systemic inflammatory response syndrome
MOF- Multiple organ failure
Auto- Autoimmune diseases
ID- Inflammatory diseases
Trans- Allograft transplant rejection
Crohn's- Crohn's disease (one type of inflammatory disease)
IBD- Inflammatory bowel disease
NIF- hookworm neutrophils inhibitory factor
Bact- Bacterial infection
SS- Septic shock
IR- Ischemia-reperfusion injury
Meta- Metastasis, cancer

ADDENDUM B

TABLE 2 – PEPTIDE SEQUENCES

TABLE 2 – PEPTIDE SEQUENCES

SEQ ID #	ID #	Peptide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
2	P-1	TYKTKEEMIVATSQTSQY	Integrin α_2 subunit (CD49b, VLA-2, platelet gpIa) I domain	CN I-IV, LN, Echovirus-1 receptor	Thromb, Ather, SIRS, MOF, SS, ID	1
NA	P-2	TYK	Integrin α_2 subunit (CD49b, VLA-2, platelet gpIa) I domain	CN I-IV, LN, Echovirus-1 receptor	Thromb, Ather, SIRS, MOF, SS, ID	2
4	P-3	QTSQY	Integrin α_2 subunit (CD49b, VLA-2, platelet gpIa) I domain	CN I-IV, LN, Echovirus-1 receptor	Thromb, Ather, SIRS, MOF, SS, ID	2
6	P-4	IAVIG	Integrin α_2 subunit (CD49b, VLA-2, platelet gpIa) I domain	CN I-IV, LN, Echovirus-1 receptor	Thromb, Ather, SIRS, MOF, SS, ID	3
8	P-5	TKEEMIVATSQTSQYGGDL TNTFGAIQYARKYAYSAAS GGRRSATIKVMVVVTDGES HDGSMLKAVIDQCNHDNIL RFGIAVLGYLNRN	Integrin α_2 subunit (CD49b, VLA-2, platelet gpIa) I domain	CN I-IV, LN, Echovirus-1 receptor	Thromb, Ather, SIRS, MOF, SS, ID	4
10	P-6	YNVDTESALLYQGPHNTLF GYSWLHSHGAHRWLLVG APTAMWLAMASVINPGAI YRCRIGKNPGQTCEOLQLG SFHGEPGGKTCLEERDHQ WLGVTLSR	Integrin α_4 subunit (CD49b, VLA-4)	VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	5
12	P-7	QDYVKKFGEHFASCQAGIS SFYTKDLIVMGAPGSSYWT GSLFVYMITTNKYK	Integrin α_4 subunit (CD49d, VLA-4)	VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	5
14	P-8	QDYVKKFGEHFASCQAGIS SFYTKDLIVMGAPGSSYWT GSLFVYMITTNKYK	Integrin α_4 subunit (CD49d, VLA-4)	VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	5
16	P-9	GHRWKNIFYIKNENKLPTG G	Integrin α_4 subunit (CD49d, VLA-4)	VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	6
18	P-10	GGAPQHEQIGK	Integrin α_4 subunit (CD49d, VLA-4)	VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	6
20	P-11	SYWTGS	Integrin α_4 subunit (CD49d, VLA-4)	VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	6
22	P-12	MGAPGSSYWTG	Integrin α_4 subunit (CD49d, VLA-4)	VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	7
24	P-13	YNVDTESALLYQGPHNTLF GYSWLHSHGAHRWLLVG A	Integrin α_4 subunit (CD49d, VLA-4)	VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	8
26	P-14	IVTCGHRWKNIFYIKHENK LPTGGCYGVPPDLRTELSK RIAPGYQDYVKKFGEHFAS CQAGISSFYTKDLIVMGA	Integrin α_4 subunit (CD49d, VLA-4)	VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	8

SEQ ID #	ID #	Peptide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
28	P-15	YMITTNKYKAFLGKQNQV KPGSYLGYSVGAGHFRSQ HTTEVVGGAPQHEQIGKA YIFSIDEKELNILHEMKGKK	Integrin α_4 subunit (CD49d, VLA-4)	VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	8
30	P-16	LGSYFGASVGAVDLHADG FSDLLVGAPMQSTIREEGR VFVYINSGSGAVMNAMET NLVGSDKYAARFGESIVNL GDIDNDGFEDVAIGAPQED DLQGAIYIYNGRADGISSTF SQRIEGLQISKSLSMFGQSIS GQIDADNNGYVDVAVGAF RSDRSDSAVLLRTRPVVIV DASLSHPESVNRTKFDCVE NGWPSVCIDLTLCFSYKGK EVPGYIVLFYNMSLDVNRK AESPPRFYFSSNGTSDVITG SIQVSSREANCRTHQAFMR KDVRDILTPIQIEAAY	Integrin α_4 subunit (CD49d, VLA-4)	VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	8
32	P-17	SSIYDDSYLGYSVAVGEFS GDDTEDFVAGVPKGNLTY GYVTILNGSDIRSLYNFSGE QMASYFGYAVAATDVNG DGLDDLLVGAPLLMDRTP DGRPQEVGRVYVYLQHPA GIEPTPTLTLTGHDEFGRFG SSLTPLGDLDQDGYNDVAI GAPFGGETQQGVVFVFPGG PGGLGSKPSQVLQPLWAAS HTPDFFGSALRGGRDLDGN GYPDLIVGSFGVDKAVVYR GRPIVSASASLTIFPAMFNP EERSCSLEGNPVACINLSFC LNASGKHVADSIGFTVELQ LDWQKQKGGVRRALFLAS RQATLTQTLLIQNGAREDC REMKIYLRNESEFRDKLSPI HIA	Integrin α_5 subunit (CD49e, VLA-5)	FN, L1, invasin	Thromb, Ather, SIRS, ID	9
34	P-18	SYLGYSVAVGEFSGDDTED FVAGVPKGNLTYGYVTILN GSDIRSLYNFSGEQMASYF GYAVAATDVNGDGLDDLL VGAPLLMDRTPDGRPQEV GRVYVYLQHPAGIEPTPTL TLTGHDEFGRFGSSLTPLG DLDQDGYNDVAIGAPFGG ETQQGVVFVFPGGPGGLGS KPSQVLQPLWAASHTPDFF GSALRGGRDLDGNGYPDLI VGSFGVDKAVVYRG	Integrin α_5 subunit (CD49e, VLA-5)	FN, L1, invasin	Thromb, Ather, SIRS, ID	10
36	P-19	AHGSSILACAPLYSWRTEK EPLSDPVGTCYLSTDNFTRI LEYAPCRSDFSWAAGQGY CQGGFSAEFTKTGRVVLGG PGSYFWQGQILSATQEQIA ESYYPEYLINLVQGQLQTR QASSIY	Integrin α_5 subunit (CD49e, VLA-5)	FN, L1, invasin	Thromb, Ather, SIRS, ID	11
38	P-20	LACAPL	Integrin α_5 subunit (CD49e, VLA-5)	FN, L1, invasin	Thromb, Ather, SIRS, ID	11
40	P-21	GVDVDQDGETELIGAPLFY GEQRG	Integrin α_L subunit (CD11a) I domain	ICAM-1, ICAM-2, ICAM-3, LPS,	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	12

SEQ ID #	ID #	Peptide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
42	P-22	ITDGEATDSGQIDAAKDIIY IIGI	Integrin α_L subunit (CD11a) I domain	ICAM-1, ICAM-2, ICAM-3, LPS,	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	12
44	P-23	PENITDGEATSGC	Integrin α_L subunit (CD11a) I domain	ICAM-1, ICAM-2, ICAM-3, LPS,	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	13-14
46	P-24	PENGVDVDQDGETC	Integrin α_L subunit (CD11a) I domain	ICAM-1, ICAM-2, ICAM-3, LPS,	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	15
48	P-25	CPNKEKEC	Integrin α_L subunit (CD11a) I domain	ICAM-1, ICAM-2, ICAM-3, LPS,	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	16
50	P-26	LIDGSG	Integrin α_m subunit (CD11b) I domain	iC3b, ICAM-1, ICAM-2, ICAM-4, Fb, Factor X, CD23, NIF, heparin, β-glucan, LPS	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	17
52	P-27	FKEFQNNPNPRSLVKP	Integrin α_m subunit (CD11b) I domain	iC3b, ICAM-1, ICAM-2, ICAM-4, Fb, Factor X, CD23, NIF, heparin, β-glucan, LPS	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	17
54	P-28	ARKNAFKILVVITDGEK	Integrin α_m subunit (CD11b) I domain	iC3b, ICAM-1, ICAM-2, ICAM-4, Fb, Factor X, CD23, NIF, heparin, β-glucan, LPS	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	17, 18
56	P-29	GCPQEDSDIAFLIDGSGSIIP HDF	Integrin α_m subunit (CD11b) I domain	iC3b, ICAM-1, ICAM-2, ICAM-4, Fb, Factor X, CD23, NIF, heparin, β-glucan, LPS	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	19
58	P-30	FRRMKEFVSTVMEQLKKS KTLFS	Integrin α_m subunit (CD11b) I domain	iC3b, ICAM-1, ICAM-2, ICAM-4, Fb, Factor X, CD23, NIF, heparin, β-glucan, LPS	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	19
60	P-31	GNSFPASLVVAAEEGERE	Integrin α_{IIb} subunit (CD41) heavy chain	Fb, FN, VN, TSP, Vwf	Thromb, Ather, SIRS, MOF, IR, ID	20

SEQ ID #	ID #	Peptide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
62	P-32	NAQIGIAMLVSVGNLEEAG ESVSFQLQI	Integrin α_{IIb} subunit (CD41) heavy chain	Fb, FN, VN, TSP, vWF	Thromb, Ather, SIRS, MOF, IR, ID	20
64	P-33	TLGPSQEETGGVFLCPWR	Integrin α_{IIb} subunit (CD41) heavy chain	Fb, FN, VN, TSP, vWF	Thromb, Ather, SIRS, MOF, IR, ID.	20
66	P-34	AEGGQCPSLLFDL	Integrin α_{IIb} subunit (CD41) heavy chain	Fb, FN, VN, TSP, vWF	Thromb, Ather, SIRS, MOF, IR, ID	20
68	P-35	AMVTVLAFLWLPSLYQRP LDQFVLQSHAWFNVSSLPY AV	Integrin α_{IIb} subunit (CD41) light chain	Fb, FN, VN, TSP, vWF	Thromb, Ather, SIRS, MOF, IR, ID	20
70	P-36	GAHYMRALSNVE	Integrin α_{IIb} subunit (CD41)	Fb, FN, VN, TSP, vWF	Thromb, Ather, SIRS, MOF, IR, ID	21
72	P-37	GAPL	Integrin α_{IIb} subunit (CD41)	Fb, FN, VN, TSP, vWF	Thromb, Ather, SIRS, MOF, IR, ID	22
74	P-38	GDGRHDLLVGAPL	Integrin α_{IIb} subunit (CD41)	Fb, FN, VN, TSP, vWF	Thromb, Ather, SIRS, MOF, IR, ID	22
76	P-39	TDVNGDGRHDL	Integrin α_{IIb} subunit (CD41)	Fb, FN, VN, TSP, vWF	Thromb, Ather, SIRS, MOF, IR, ID	23
78	P-40	GDGRHDLLVGAP	Integrin α_{IIb} subunit (CD41)	Fb, FN, VN, TSP, vWF	Thromb, Ather, SIRS, MOF, IR, ID	23
80	P-41	GDGRHDLLVGAPLY	Integrin α_{IIb} subunit (CD41)	Fb, FN, VN, TSP, vWF	Thromb, Ather, SIRS, MOF, IR, ID	24
82	P-42	EFDGDLNTTEYVVGAPTW SWTLGAVEILDSYYQRLHR LRAEQMASYFGHSVAVTD VNGDGRHDLLVGAPLYME SRADRKLAEVGRVYLFLQP RGPHALGAPSLLLTGTQLY GRFGSAIAPLGDLDRDGYN DIAVAAPYGGPSGRGQVLV FLGQSEGLRSRPSQVLDSPF PTGSAFGFSLRGAVDIDDN GYPDLIVGAYGANQVAVY RAQPVVKASVQLLVQDSL NPA	Integrin α_{IIb} subunit (CD41)	Fb, FN, VN, TSP, vWF	Thromb, Ather, SIRS, MOF, IR, ID	25
84	P-43	AVTDVNGDGRHDLLVGAP LY	Integrin α_{IIb} subunit (CD41)	Fb, FN, VN, TSP, vWF	Thromb, Ather, SIRS, MOF, IR, ID	26
86	P-44	FSSVVTQAGELVLGAPGGY YFLGLLAQAPVADIFSSYRP GILLWHVSSQSLSFDSSNPE YFDGYWGYSVAVGEFDGD LNTTEYVVGAPTWSWTLG AVEILDSYYQRLHRLRAEQ MASYFGHSVAVTDVNGDG RHDLLVGAPLYMESRADR KLAEVGRVYLFLQPRGPHA LGAPSLLLTGTQLYGRFGS AIAPLGDLDRDGYNDIAVA APYGGPSGRGQVLVFLGQS EGLRSRPSQVLDSPFPTGSA FGFSLRGAVDIDDNGYPDL IVGAYGANQVAVYRAQPV VKASVQLLVQD	Integrin α_{IIb} subunit (CD41)	Fb, FN, VN, TSP, vWF	Thromb, Ather, SIRS, MOF, IR, ID	27

SEQ ID #	ID #	Peptide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
88	P-45	DKLSPIV	Integrin α_{IIb} subunit (CD41)	Fb, FN, VN, TSP, vWF	Thromb, Ather, SIRS, MOF, IR, ID	28
NA	P-46	QM	Integrin α_{IIb} subunit (CD41)	Fb, FN, VN, TSP, vWF	Thromb, Ather, SIRS, MOF, IR, ID	28
90	P-47	VVLH	Integrin α_{IIb} subunit (CD41)	Fb, FN, VN, TSP, vWF	Thromb, Ather, SIRS, MOF, IR, ID	28
92	P-48	DLYYLMDLSYSMK	All integrin β subunits	FN, Fb, CN I, VN	All named pathologies	29
NA	P-49	D$$$$$DXSXS$KDDL; $ = any hydrophobic residue; X = any residue	All integrin β subunits	All named ligands	All named pathologies	29
94	P-50	YCRKENSSEICSNNGECVC GQCVCRKRDNTNEIYSGKF CECDNFNCDRSNGLICGGN GVCKCRVCECNPNYTGSA CDCSLDTSTCEASNGQICN GRGICECGVCKCTD	Integrin β_1 subunit (CD29)	FN, LN, CN, VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	30
96	P-51	See sequence listing	Integrin β_1 subunit (CD29)	FN, LN, CN, VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	31
98	P-52	LRLRSGEPQTFTLKFKRAE DYPIDLYYLMDLSYSMKD DLENVKSLGTDLMNEMRR ITSDFRIGFGSFVEKTVMPY ISTTPAKLRNPCTSEQNCTT PFSYKNVLSLTNKGEVFNE LVGKQRISGNLDSPEGGFD AIMQVAVCGSLIGWRNVT RLLVFSTDAGFHFAGDGKL GGIVLPNDGQCHLENNMY TMSHYYDYPSIAHLVQKLS ENNIQTIFAVTEEFQPVYKE LKNLIPKSA	Integrin β_1 subunit (CD29)	FN, LN, CN, VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	32
100	P-53	NKGEVFNELVGK	Integrin β_1 subunit (CD29)	FN, LN, CN, VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	33
102	P-54	TAEKL	Integrin β_1 subunit (CD29)	FN, LN, CN, VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	34
104	P-55	DYPIDLYYLMDLSYSMKD DLENVKSLG	Integrin β_1 subunit (CD29)	FN, LN, CN, VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	35
106	P-56	NVKSLGTALMREMEKITSD F	Integrin β_1 subunit (CD29)	FN, LN, CN, VCAM-1, FN, MAdCAM-1, TSP, invasin	Auto, Ather, SIRS, MOF, Trans, SS, ID Crohn's, IBD, IR	36

SEQ ID #	ID #	Peptide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
108	P-57	GQKQLSPQKVTLYLRPGQ AAAFNVTFRRAKGYPIDLY YLMDLSYSMLDDLRNVKK LGGDLLRALNEITESGRIGF GSFVDKTVLPFVNTHPDKL RNPCPNKEKECQPPFAFRH VLKLTNNSNQFQTEVGKQ LISGNLDAPEGGLDAMMQ VAACPEEIGWRNVTRLLVF ATDDGFHFAGDGKLGAILT PNDGRCHLEDNLYKRSNEF DYPSVGQLAHKLAENNIQP IFAVTSRMVKTYEKLTEIIP KSA	Integrin β_2 subunit (CD18)	ICAM-1, ICAM-2, ICAM-3, ICAM-4, LPS, iC3b, Fb, Factor X, CD23, NIF, heparin, β-glucan,	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	37
110	P-58	YPIDLYYLMDLSYSMLDDL RNVKKLGGDLLRALNEITE SGRIGFGSFVDKTVLPFVNT HPDKLRNPCPNKEKECQPP FAFRHVLKLTNNSNQFQTE VGKQLISGNLDAPEGGLDA MMQVAACPEEIGWRNVTR LLVFATDDGFHFAGDGKL GAILTPNDGRCHLEDNLYK RSNEFDYPSVGQLAHKLAE NNIQPIFAVTSRMVKTYEK LTEIIPKSAVGELSEDSSNV VHLIKNAYNKLSSRVFLDH NALPDTLKVTYDSF	Integrin β_2 subunit (CD18)	ICAM-1, ICAM-2, ICAM-3, ICAM-4, LPS, iC3b, Fb, Factor X, CD23, NIF, heparin, β-glucan,	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	38
112	P-59	RNVKK	Integrin β_2 subunit (CD18)	ICAM-1, ICAM-2, ICAM-3, ICAM-4, LPS, iC3b, Fb, Factor X, CD23, NIF, heparin, β-glucan,	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	39
114	P-60	QPPFA	Integrin β_2 subunit (CD18)	ICAM-1, ICAM-2, ICAM-3, ICAM-4, LPS, iC3b, Fb, Factor X, CD23, NIF, heparin, β-glucan,	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	39
116	P-61	LISGNL	Integrin β_2 subunit (CD18)	ICAM-1, ICAM-2, ICAM-3, ICAM-4, LPS, iC3b, Fb, Factor X, CD23, NIF, heparin, β-glucan,	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	39
118	P-62	GQLAH	Integrin β_2 subunit (CD18)	ICAM-1, ICAM-2, ICAM-3, ICAM-4, LPS, iC3b, Fb, Factor X, CD23, NIF, heparin, β-glucan,	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	39
120	P-63	ELSEDSSNVVHLIKNAYNK LSSRVFLDHNALPDTLKVT YDSFCSNGVTHRNQPRGD CDGVQINVPITFQVKVTAT ECIQEQSFVIRALG	Integrin β_2 subunit (CD18)	ICAM-1, ICAM-2, ICAM-3, ICAM-4, LPS, iC3b, Fb, Factor X, CD23, NIF, heparin, β-glucan,	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	40

SEQ ID #	ID #	Peptide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
122	P-64	GFTDIVTVQVLPQCECRCR DQSRDRSLCHGKGFLECGI CRCDTGYIGKNCECQTQG	Integrin β_2 subunit (CD18)	ICAM-1, ICAM-2, ICAM-3, ICAM-4, LPS, iC3b, Fb, Factor X, CD23, NIF, heparin, β-glucan,	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	40
124	P-65	CNAFKILVVITDGEK	Integrin β_2 subunit (CD18) A domain	ICAM-1, ICAM-2, ICAM-3, ICAM-4, LPS, iC3b, Fb, Factor X, CD23, NIF, heparin, β-glucan,	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	41
126	P-66	TGIRKVVRELFNITNGARK N	Integrin β_2 subunit (CD18) A domain	ICAM-1, ICAM-2, ICAM-3, ICAM-4, LPS, iC3b, Fb, Factor X, CD23, NIF, heparin, β-glucan,	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	41
128	P-67	DLSYSLDDLRNVKKLGGD LLRALNE	Integrin β_2 subunit (CD18)	ICAM-1, ICAM-2, ICAM-3, ICAM-4, LPS, iC3b, Fb, Factor X, CD23, NIF, heparin, β-glucan,	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, hookworm, IR, ID	42, 43
130	P-68	DYPVDIYYLMDLSYSMKD DLWSIQNLGTKLATQMRK LTSNLRIGFGAFVDKPVSPY MYISPPE	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	44
132	P-69	DAPEGGFDAIMQATV	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	45
134	P-70	FSIQVRQVEDYPVDIYYLM DLSYSMKDDLWSIQNLGT KLATQMRKLTSNLRIGFGA FVDKPVSPYMYISPPEALE NPCYDMKTTCLPMFGYKH VLTLTDQVTRFNEEVKKQS VSRNRDAPE	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	46
136	P-71	GVSSCQQCLAVSPMCAWC SDEALPLGSPR	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	20
138	P-72	VLEDRPLSDKGSGDSSQVT QV	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	20
140	P-73	NINLIFAVTENVVNLYQNY SELIPGTTVGVLSMDSSNV LQLIVDAYGKIRS	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	20

SEQ ID #	ID #	Peptide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
142	P-74	IGFGAFVDKPVSPYMYISPP EALENPCYDMKTTCLPMF GYK	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	20
144	P-75	SVSRNRDAPEGG	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	47
146	P-76	SVSRNRDAPEG	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	48
148	P-77	RNRDA	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	48
150	P-78	DAPEGGFDAIMQAT	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	49
152	P-79	DAPEGGFDAIMQATV	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	49
154	P-80	DAPEGGFDAIMQATVCDE KIGWRNDASHLLVFTTDA KTHIALDGRLAGIVQPNDG QCHVGSDNHYSASTTMDY PSLGLMTEKLSQK	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1, viper and rattlesnake venom components: albolabrin, bitistatin, echistatin, eristostatin	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID, viper and rattlesnake bites	50
156	P-81	MDLSYSMKDDLWSI	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	51
158	P-82	GPNICT	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	52
160	P-83	GPNICTTRGVSSC	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	52
162	P-84	KDSLIVQVTFDCDCACQAQ AEPNSHRCNNGNGTFECG VCRCGPGWLGSQCECSEE DYRPSQQDECSPRE	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	53

SEQ ID #	ID #	Peptide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
164	P-85	PTCPDACTFKKECVECKKF DREPYMTENTCNRYCRDEI ESVKELKDTGKDAVNCTY KNEDDCVVRFQYYEDSSG KSILYVVEEPECPKG	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	54
166	P-86	KDDLW	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	55
168	P-87	SVSRNRDAPEGGF	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	24
170	P-88	HVGSDNHYSASTTMDYPS LGLMTEKLSQKNINLIFAVT ENVVNLYQNYSELIPGTTV GVLSMDSSNVLQLIVDAYG KIRSKVELEVRDLPEELSL	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	56
172	P-89	DDSKNFSIQVRQVEDYPVD IYYLMDLSYSMKDDLWSIQ NLGTKLATQMRKLTSNLRI GFGAFVDKPVSPYMYISPP EALENPCYDMKTTCLPMF GYKHVLTLTDQVTRFNEE VKKQSVSRNRDAPEGGFD AIMQATVCD	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	57
174	P-90	YMYISPPEALENPCYDMKT TCLPMFGYKHVLTLTDQV TR	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	57
176	P-91	RNRDAY	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	58
178	P-92	DAPEGGFDAIMQATVY	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	58
180	P-93	CYDMKTTC	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1, Coxsackievirus A9	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	31, 59
182	P-94	NFSIQVRQVEDYPVDIYYL M	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	60
184	P-95	DMKTT	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	28

SEQ ID #	ID #	Peptide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
186	P-96	ISPPA	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	61
188	P-97	KQSVSRNRDAPE	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	62
190	P-98	DDSKNFSIQVRQVEDYPVD IYYLMDLSYSMKDDLWSIQ NLGTKLATQMRKLTSNLRI GFGAFVDKPVSPYMYISPP EALENPCYDMKTTCLPMF GYKHVLTLTDQVTRFNEE VKKQSVSRNRDAPEGGFD AIMQATVCDEKIGWRNDA SHLLVFTTDAKTHIALDGR LAGIVQPNDGQCHVGSDN HYSASTTMDYPSLGLMTE KLSQKNINLIFAVTENVVN LYQNYSELIPGTTVGVLSM DSSNVLQLIVDAYGKIRSK VELEVRDLPEELSLSFNAT	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	63
192	P-99	DDSKNFSIQVRQVEDYPVD IYYLMDLSYSMKDDLWSIQ NLGTKLATQMRKLTSNLRI GFGAFVDKPVSPYMYISPP EALENPCYDMKTTCLPMF GYKHVLTLTDQVTRFNEE VKKQSVSRNRDAPEGGFD AIMQATVCDEKIGWRNDA SHLLVFTTDAKTHIALDGR LAGIVQPNDGQCHVGSDN HYSASTTMDYPSLGLMTE KLSQ	Integrin β_3 subunit (CD 61; platelet glycoprotein gpIIIa)	Fb, FN, VN, TSP, vWF, OP,BSP, LN, CN, L1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	63
194	P-100	KQLNFTASGEAEARRCARR EELLARGCPLEELEEPRGQ QEVLQDQPLSQGARGEGA TQLAPQRVRVTLRPGEPQQ LQVRFLRAEGYPVDLYYL MDLSYSMKDDLERVRQLG HALLVRLQEVTHSVRIGFG SFVDKTVLPFVSTVPSKLR HPCPTRLERCQSPFSFHHVL SLTGDAQAFEREVGRQSVS GNLDSPEGGFDAILQAALC QEQIGWRNVSRLLVFTSDD TFHTAGDGKLGGIFMPSDG HCHLDSNGLYSRSTEFDYP SVGQVAQALSAANIQPIFA VTSAALPVYQELSKLIPKSA VGELSEDSSNVVQLIMDAY NSLSSTVTLEHSSLPPGVHI SYESQCEGP	Integrin β_7 subunit (LPAM-1)	VCAM-1 FN, MAdCAM-1, E-cadherin (cadherin-1)	Auto, SS, MOF, Trans, Crohn's, IBD, IR, ID	64
196	P-101	SFVDKTVLPFVSTVPSKLR HPCPTRLERCQSPFSFHHVL SLTGDAQAFEREVGRQSVS GNLDSPEGGFDAILQAALC QEQIGWRNVSRLLV	Integrin β_7 subunit (LPAM-1)	VCAM-1 FN, MAdCAM-1, E-cadherin (cadherin-1)	Auto, SS, MOF, Trans, Crohn's, IBD, IR, ID	64

SEQ ID #	ID #	Peptide Sequence	Derived from	Targeted Ligand	Targeted Pathology	Cite #
198	P-102	KQLNFTASGEAEARRCARR EELLARGCPLEELEEPRGQ QEVLQDQPLSQGARGEGA TQLAPQRVRVTLRPGEPQQ LQVRFLRAEGYPVDLYYL MDLSYSMKDDL	Integrin β_7 subunit (LPAM-1)	VCAM-1 FN, MAdCAM-1, E-cadherin (cadherin-1)	Auto, SS, MOF, Trans, Crohn's, IBD, IR, ID	64
200	P-103	EKREGKAEDRGQCNHVRI NQTVTFWVSLQATHCLPEP HLLRLRALGFSEELIVELHT LCDCNCSDTQPQAPHCSDG QGHLQCGVCSCAPGRLGR LCECSVAELSSPDLESGCR APNGTGPLCSGKGHCQCG RCSCSGQSSGHLCECDDAS CERHEGILCGGFGRCQCGV CHCHANRTGRACECSGDM DSCISPEGGLCSGHGRCKC NRCQCLDGYYGALCDQCP GCKTPCERHRDCAECGAFR TGPLATNCSTACAHTNVTL ALAPILDDGWCKERTLDN QLFFFLVEDDARGTVVLRV RPQEKGADHTQAIVLGCV GGIVAVGLGLVLAYRLSVE IYD	Integrin β_7 subunit (LPAM-1)	VCAM-1 FN, MAdCAM-1, E-cadherin (cadherin-1)	Auto, SS, MOF, Trans, Crohn's, IBD, IR, ID	64
202	P-104	EHIPA	Mimics Integrin $\alpha_{IIb}\beta_3$ subunit	Fb, FN, VN, TSP, vWF	Thromb, Ather, SIRS, MOF, IR, ID	65
204	P-105	IPCNNKGAHSVGLMWWM LAR	67 kD LN receptor	LN	Meta	66
206	P-106	KVILDRGGSVLVTC	ICAM-1	Fb	Thromb, Ather, SIRS, MOF, IR, ID	67
208	P-107	CWDDGWLC	Phage display library-mimics RGD binding site in integrins	FN, VN	Thromb, Ather, SIRS, MOF, IR, ID	55
210	P-108	CWDDLWLC	Phage display library-mimics RGD binding site in integrins	FN, VN	Thromb, Ather, SIRS, MOF, IR, ID	55
212	P-109	CLLRMRSIC	Phage display library	ICAM-1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	68
214	P-110	PDTRPAPGSTAPPAHGVTS A	MUC-1 protein	ICAM-1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	69
216	P-111	EWCEYLGGYLRCYA	Phage display library	ICAM-1	Thromb, Auto, SS, Ather, SIRS, MOF, Trans, Crohn's, IBD, bact, SS, IR, ID	70
218	P-112	EWPEYL	Rhinovirus coat protein 14	ICAM-1	Thromb, Auto, IBD, Ather, SIRS, MOF, Trans, Crohn's, SS, IR, ID	70

Ligand Abbreviations
CN I- Type I collagen

Pathology Abbreviations
Thromb- Thrombosis

CN II- Type II collagen
CN III- Type III collagen
Up to 19 different collagen types
LN- Laminin
VCAM-1- Vascular cell adhesion molecule-1
FN- Fibronectin
MadCAM-1- Mucosal addressin cell adhesion molecule-1
TSP- Thrombospondin
ICAM-1- Intercellular adhesion molecule-1
ICAM-2- Intercellular adhesion molecule-2
ICAM-3- Intercellular adhesion molecule-3
ICAM-4- Intercellular adhesion molecule-4
LPS- bacterial lipopolysaccharide
iC3b- Complement fragment iC3b
Fb- Fibrinogen
VN- Vitronectin
vWF- von Willebrand factor
Ather- Atherosclerosis
SIRS- Systemic inflammatory response syndrome
MOF- Multiple organ failure
Auto- Autoimmune diseases
ID- Inflammatory diseases
Trans- Allograft transplant rejection
Crohn's- Crohn's disease (one type of inflammatory disease)
IBD- Inflammatory bowel disease
NIF- hookworm neutrophils inhibitory factor
Bact- Bacterial infection
SS- Septic shock
IR- Ischemia-reperfusion injury
Meta- Metastasis, cancer

We claim:

1. A therapeutic bioconjugate comprising:
   a. a hydrophilic polymer; and
   b. one or more peptides capable of binding specifically to a ligand expressed on a cell surface.

2. The bioconjugate of Claim 1 for blocking interactions between cells in a living tissue wherein said ligand is expressed on the surface of at least one of said cells.

3. The bioconjugate of Claim 1 for blocking interaction between a cell and an extracellular matrix wherein said ligand is capable of binding to a component of said matrix.

4. The bioconjugate of Claim 1 for blocking pathological reactions triggered by cellular interactions in a living tissue.

5. The bioconjugate of Claim 1 wherein said peptide comprises the amino acid sequence of the binding portion of an integrin for said ligand.

6. The bioconjugate of Claim 5 for blocking cell signaling receptors implicated in the regulation of cellular adhesion, migration, tumor metastasis, proliferation, angiogenesis, bone resorption, apoptosis, or gene expression.

7. The bioconjugate of Claim 5 wherein said binding portion is from an integrin α subunit or an integrin β subunit.

8. The bioconjugate of Claim 7 comprising one or more peptides selected from the group consisting of SEQ ID NOS 1-202.

9. The bioconjugate of Claim 7 wherein said binding portion is a portion of the integrin α_2 subunit (CD49b, VLA-2, platelet gpla) I domain, integrin α_4 (CD49b, VLA-4), integrin α_5 (CD49e, VLA-5) , integrin α_L (CD11a) I domain, integrin α_M subunit (CD11b) I domain, integrin α_{IIb} I domain, integrin α_{IIb} (CD41) heavy chain, integrin α_{IIb} (CD41) light chain, integrin β_1 (CD29) subunit, the integrin β_2 (CD18) subunit, integrin β_3 (CD61) subunit, or integrin β_7 (LPAM-1) subunit.

10. The bioconjugate of Claim 9 wherein said peptide comprises the binding portion of the integrin α_2 subunit (CD49b, VLA-2, platelet gpla) I domain and binds specifically to ligands CN I, CN II, CN III, CN IV, LN or the echovirus-1 receptor.

11. The bioconjugate of Claim 9 wherein said peptide comprises a portion of the integrin α_4 (CD49b, VLA-4) subunit that binds specifically to the ligands VCAM-1, FN, MAdCAM-1, TSP or invasin.

12. The bioconjugate of Claim 9 wherein said peptide comprises a portion of the integrin α_5 (CD49e, VLA-5) that binds specifically to ligands FN, L1 or invasin.

13. The bioconjugate of Claim 9 wherein said peptide comprises a portion of the integrin α_1 (CD11a) I domain that binds specifically to the ligands ICAM-1, ICAM-2, ICAM-3 or LPS.

14. The bioconjugate of Claim 9 wherein said peptide comprises a portion of the integrin α_M subunit (CD11b) I domain that binds specifically to the ligands iC3b, ICAM-1, ICAM-2, ICAM-4, Fb, Factor X, CD23, NIF, heparin, beta glucan, or LPS.

15. The bioconjugate of Claim 9 wherein said peptide comprises a portion of the integrin α_{IIb} (CD41) heavy chain that binds specifically to the ligands Fb, FN, VN, TSP or vWF.

16. The bioconjugate of Claim 9 wherein said peptide comprises a portion of the integrin α_{IIb} (CD41) light chain that binds specifically to the ligands Fb, FN, VN, TSP and vWF.

17. The bioconjugate of Claim 9 wherein said peptide comprises a portion of the integrin β_1 (CD29) subunit,, and binds specifically to the ligands FN,LN,CN,VCAM-1, FN, MAdCAM-1, TSP or invasin.

18. The bioconjugate of Claim 9 wherein said peptide comprises a portion of the integrin β_2 (CD18) subunit that binds specifically to the ligands ICAM-1, ICAM-2, ICAM-3, ICAM-4, LPS, iC3b, Fb, Factor X, CD23, NIF, heparin, or betaglucan.

19. The bioconjugate of Claim 9 wherein said peptide comprises a portion of the integrin β_3 (CD61) subunit that binds specifically to ligands fibrinogen, fibronectin, vitronectin, thrombospondin, von Willebrand factor, osteopontin, bone sialoprotein, laminins, collagens, or neural cell adhesion molecule L1.

20. The bioconjugate of Claim 9 wherein said peptide comprises a portion of the integrin β_7 (LPAM-1) subunit that binds specifically to the ligands VCAM-1, fibronectin, MAdCAM-1, or E-cadherin (cadherin-1).

21. The nucleic acids having the sequence coding for peptides of the bioconjugate of Claim 8.

22. The nucleic acids of Claim 21 selected from the group consisting of SEQ ID NOS 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 86, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 186, 185, 187, 189, 191, 193, 195, 1197, 199 and 201.

23. The peptide for preparation of the bioconjugate of Claim 1, said peptide having a sequence selected from the group consisting of SEQ ID NOS 1-112, wherein each sequence comprises additionally an N-terminal and/or a C-terminal cysteine residue.

24. The nucleic acids having the sequence coding for a peptide of Claim 23.

25. The bioconjugate of Claim 1 wherein said polymer is a polysaccharide or an oligosaccharide.

26. The bioconjugate of Claim 1 wherein said polymer is a derivative of a polysaccharide or an oligosaccharide wherein said derivative polymer additionally comprises additional groups capable of reacting chemically with a peptide to form said bioconjugate.

27. The bioconjugate of Claim 1 having the formula XY_b wherein X is a low cell-adhesive, hydrophilic polymer, Y is a peptide comprising a portion of the binding site of an integrin for a ligand expressed on a cell surface, and b is greater than 0.

28. The bioconjugate of Claim 27 wherein X comprises a polysaccharide or an oligosaccharide.

29. The bioconjugate of Claim 27 wherein X comprises a derivative of a polysaccharide or of an oligosaccharide wherein said derivative saccharide comprises reactive groups whereby said derivative saccharide reacts with said peptide to form said bioconjugate.

30. The bioconjugate of Claim 29 wherein said reactive group comprises a hydroxyl group.

31. The bioconjugate of Claim 25 wherein said polysaccharide or oligosaccharide is selected from the group consisting of agarose, dextran, heparin, chondroitin sulfate, hydroxyethyl starch, and hyaluronic acid.

32. The bioconjugate of Claim 1 wherein said polymer comprises a dextran and said peptide comprises the binding portion of an integrin for its ligand.

33. The bioconjugate of Claim 1 wherein said polymer is polyvalent and is selected from the group consisting of poly(ethylene glycol), poly(ethylene oxide), poly(vinyl alcohol), poly(acrylic acid), poly(ethylene-co-vinyl alcohol), poly(vinyl pyrrolidone), poly(ethyloxazoline), and poly(ethylene oxide)-co-poly(propylene oxide) block copolymers.

34. The bioconjugate of Claim 1 wherein said polymer comprises copolymers, block copolymers, graft copolymers, alternating copolymers, or random copolymers.

35. The bioconjugate of Claim 1 wherein said polymer is essentially inert.

36. The bioconjugate of Claim 1 wherein said polymer is degradable by hydrolytic or enzymatic means.

37. The bioconjugate of Claim 36 wherein said degradable polymer comprises one or more blocks selected from the group consisting of lactic acid, glycolic acid, ε-caprolactone, lactic-co-glycolic acid oligomers, trimethylene carbonate, anhydrides, and amino acids.

38. The bioconjugate of Claim 1 wherein said polymer is a serum protein.

39. The bioconjugate of Claim 38 wherein said serum protein is an albumin.

40. The bioconjugate of Claim 1 in a pharmaceutically acceptable carrier.

41. The bioconjugate of Claim 1 immobilized on a solid substrate.

42. The bioconjugate of Claim 41 wherein said substrate is an implantable medical device.

43. The bioconjugate of Claim 42 wherein said medical device is a drug delivery device.

44. The bioconjugate of Claim 41 wherein said substrate is a component of an *in vitro* diagnostic device.

45. The kit comprising one or more bioconjugates of Claim 1 and reagents and apparatus suitable for administering said bioconjugate to an individual.

46. The kit of Claim 45 wherein said bioconjugate is in a pharmaceutically acceptable carrier.

47. The biointerface formed on a mammalian tissue, wherein said biointerface comprises a plurality of bioconjugates of Claim 1 bound to a plurality of ligands on said tissue.

48. A method of preparing a bioconjugate comprising the steps of:

a. providing a hydrophilic polymer having one or more reactive groups;

b. providing a bioselective peptide comprising a chemical group capable of reacting with said reactive groups; and

c. contacting said polymer and said peptide under conditions whereby said reactive and chemical groups react to form said bioconjugate.

49. The method of Claim 48 wherein the reactive groups of said polymer are hydroxyl groups and the chemical group of said peptide is a sulfhydryl group.

50. The method of Claim 48 wherein said polymer is a polysaccharide.

51. The method of Claim 50 wherein said polysaccharide is activated dextran.

52. The method of Claim 50 wherein said polysaccharide is hydroxyl starch.

53. The method of Claim 50 wherein said peptide is selected from the group consisting of SEQ ID NOS 7-14, 25-32, 35-38, 43-48, 55-56, 65, 66, 93, 94, 97, 98, 107-110, 119-124, 133-136, 141, 142, 153, 154, 157-164, 171-174, 179-200, 203-212, 215 and 216, said peptide comprising a cysteine residue.

54. The method of Claim 50 wherein said peptide is selected from the group consisting of SEQ ID NOS 1-218, said peptide comprising in addition an N-terminal or a C-terminal cysteine residue.

55. A method of preparing a bioconjugate comprising the steps of:

a. providing a peptide selected from the group consisting of SEQ ID NOS 1-218;

b. modifying said peptide by addition of an N-terminal or C-terminal cysteine residue;

c. providing an amount of activated dextran; and

d. contacting said activated dextran and said modified peptide under conditions, whereby said dextran and said modified peptide react to form said bioconjugate.

56. A method for preventing adhesion of a mobile cell to a cell immobilized on a substrate comprising the step of applying a bioconjugate specific for said immobilized cell under such conditions that said bioconjugate forms a cell adhesion barrier on said immobilized cell.

57. A method of blocking pathological reactions triggered by cellular interactions in a living tissue, said method comprising the step of administering to the living tissue a bioconjugate selective for a target tissue whereby the bioconjugate forms a cell adhesion barrier at a targeted tissue site.

58. The method of Claim 57, wherein said bioconjugate comprises the binding portion of an integrin for a ligand expressed in said target tissue.

59. The method of Claim 58 wherein said bioconjugate is administered intravascularly, orally, intramuscularly, intraperitoneally, subcutaneously, cerebrospinally, endovascularly, rectally or topically.

60. The method of Claim 59 wherein said bioconjugate is administered intravascularly in a biologically compatible solution at a concentration of between about 1 μg/L and 100 g/L.

61. The method of Claim 58 wherein said bioconjugate is administered to an individual in a pharmaceutically acceptable composition.

62. The method of Claim 58 wherein the amount of administered bioconjugate is between about 1-1000 mg/kg body weight.

63. The method of Claim 57 for preventing and treating thrombosis, wherein an anti-coagulating amount of a bioconjugate comprising one or more peptides capable of binding selectively to integrin ligands expressed on inflamed endovascular cells is administered to tissue containing said inflamed endovascular cells.

64. The method of Claim 63 wherein said integrin ligands are CN I-IV, LN, or the Echovirus-1 receptor.

65. The method of Claim 63 wherein said peptide is selected from the group consisting of P-2, P-49, and SEQ ID NOS 1, 2, 3-8, 91-106, 129-192, 203 and 204.

66. The method of Claim 57 for preventing and treating atherosclerosis, wherein an anti-atherosclerotic effective amount of said bioconjugate comprising one or more peptides capable of binding selectively to integrin ligands expressed on or around atherosclerotic cells is administered to tissue containing said atherosclerotic cells.

67. The method of Claim 66 wherein said integrin ligands are VCAM-1, FN, MAdCAM-1, TSP, invasin or a combination thereof.

68. The method of Claim 66 wherein said peptide is selected from the group consisting of P-49 and SEQ ID NOS 9-38, 59-106, 129-202 and 207-210.

69. The method of Claim 57 for preventing and treating systemic inflammatory response syndrome wherein an effective amount of said bioconjugate comprising one or more peptides

capable of binding selectively to integrin ligands expressed on cells in inflamed tissue is administered to said tissue.

70. The method of Claim 69 wherein said integrin ligands are FN, L1 or invasin.

71. The method of Claim 69 wherein said bioconjugate comprises one or more peptides selected from the group consisting of P-49 and SEQ ID NOS 9-38, 59-106, 129-202 and 207-210.

72. The method of Claim 58 for preventing and treating multiple organ failure wherein an failure effective amount of said bioconjugate comprising one or more peptides capable of binding selectively to integrin ligands expressed on cells in affected tissue is administered to said tissue.

73. The method of Claim 72 wherein said integrin ligands are ICAM-1, ICAM-2, ICAM-3, LPS or a combination thereof.

74. The method of Claim 72 wherein said bioconjugate comprises one or more peptides selected from the group consisting of P-49 and SEQ ID NOS 39-58, 107-128 and 211-218.

75. The method of Claim 57 for preventing and treating autoimmune disease wherein an effective amount of a bioconjugate comprising one or more peptides capable of binding selectively to integrin ligands expressed on cells implicated in the autoimmune disease is administered to tissue containing said cells.

76. The method of Claim 75 wherein said integrin ligand is VCAM-1, FN, MAdCAM-1, TSP, invasin, ICAM-1, ICAM-2, ICAM-3, LPS, iC3b, ICAM-1, ICAM-2, ICAM-4, Fb, Factor X, CD23, NIF, heparin, β-glucan, LPS, FN, Fb, CN I, VN, FN, LN, CN, Fb, Factor X, CD23, NIF, heparin, β-glucan or a combination thereof.

77. The method of Claim 75 wherein said bioconjugate comprises one or more peptides selected from the group consisting of P-2, P-49 and SEQ ID NOS 1-218.

78. The method of Claim 57 for preventing and treating inflammatory diseases wherein an effective amount of a bioconjugate comprising one or more peptides capable of binding selectively to integrin ligands expressed on cells of inflamed tissue is administered to a tissue containing said inflamed cells.

79. The method of Claim 78 wherein said integrin ligand is CN I-IV, LN, Echovirus-1 receptor, VCAM-1, FN, MAdCAM-1, TSP, Invasin, L1, LPS, ICAM-1-4, iC3b, Fb, Factor X, CD23, NIF, heparin, β-glucan, VN, vWF or a combination thereof.

80. The method of Claim 78 wherein said bioconjugate comprises one or more peptides selected from the group consisting of P-2, P-49, and SEQ ID NOS 1-202 and 205-219.

81. The method of Claim 58 for preventing and treating allograft transplant rejection wherein an anti-rejection amount of a bioconjugate comprising one or more peptides capable of binding selectively to integrin ligands expressed on T cells implicated in allograft transplant rejection is administered to an individual having transplanted tissue.

82. The method of Claim 81 wherein said integrin ligand is VCAM-1, FN, MAdCAM-1, TSP, invasin, ICAM-1-4, LPS, iC3b, Fb, Factor X, CD23, NIF, heparin, β-glucan, LN, CN, vWF, OP, BSP, L1 and E-cadherin.

83. The method of Claim 81 wherein said bioconjugate comprises one or more peptides selected from the group consisting of P-49 and SEQ ID NOS 9-30, 39-58, 91-200 and 211-218.

84. The method of Claim 81 further comprising concurrent administration of an immunosuppressant.

85. The method of Claim 84 wherein said immunosuppressant is cyclosporine.

86. The method of Claim 58 for preventing and treating Crohn's disease wherein an effective amount of said bioconjugate comprising one or more peptides capable of binding selectively to integrin ligands expressed on inflamed cells in gut tissue is administered to said gut tissue.

87. The method of Claim 86 wherein said integrin ligand is VCAM-1, FN, MAdCAM-1, TSP, invasin, ICAM-1-4, iC3b, Fb, Factor X, CD23, NIF, heparin, β-glucan, CN I, VN, LN, OP, BSP, L1, vWF and E-cadherin.

88. The method of Claim 86 wherein said bioconjugate comprises one or more peptides selected from the group consisting of P-49 and SEQ ID NOS 9-30, 30-58, 93-200 and 211-218.

89. The method of Claim 58 for preventing and treating inflammatory bowel disease wherein an effective amount of a bioconjugate comprising one or more peptides capable of binding selectively to integrin ligands expressed on inflamed cells in gut tissue is administered to said gut tissue.

90. The method of Claim 89 wherein said bioconjugate comprises one or more peptides selected from the group consisting of P-49 and SEQ ID NOS 9-30, 39-58, 91-200 and 21-218.

91. The method of Claim 58 for preventing and treating sequelae of a bacterial infection wherein an effective amount of said bioconjugate comprising one or more peptides capable of binding selectively to integrin ligands expressed on secretory membranes is administered to said secretory membranes.

92. The method of Claim 91 wherein said bioconjugate comprises one or more peptides selected from the group consisting of P-49 and SEQ ID NOS 39-58, 107-192 and 211-216.

93. The method of Claim 58 for preventing and treating sepsis or septic shock, comprising administering an effective amount of a bioconjugate comprising one or more peptides capable of

binding selectively to integrin ligands such as LFA-1, ICAM-1, VCAM-1 and a combination thereof.

94. The method of Claim 93 wherein said bioconjugate comprises one or more peptides selected from the group consisting of P2, P-49 and SEQ ID NOS 1-30, 39-58, 91-200 and 211-18.

95. The method of Claim 57 for preventing and treating ischemia-reperfusion injury, comprising administering an effective amount of a bioconjugate comprising one or more peptides capable of binding selectively to integrin ligands intravenously.

96. The method of Claim 95 wherein said bioconjugate comprises one or more peptides selected from the group consisting of P-49 and SEQ ID NOS 9-30 and 39-218.

97. The method of Claim 57 for preventing and treating cancer metastasis, comprising administering wherein an anti-metastasis effective amount of said bioconjugate comprising one or more peptides capable of binding selectively to integrin ligands systemically to an individual or locally to tissue containing or suspected of containing said cancer.

98. The method of Claim 97, wherein said bioconjugate comprises one or more peptides selected from the group consisting of P-49 and SEQ ID NOS 91, 92, 203 and 204.

99. The method of Claim 57 for treating conditions caused by viper and rattlesnake bites wherein an anti-venom effective amount of said bioconjugate comprising one or more peptides capable of binding selectively to at least one integrin ligand on a bitten tissue site is administered.

100. The method of Claim 110 wherein said bioconjugate comprises a peptide having SEQ ID NOS 153 and 154.

101. Therapeutic replacement fluids comprising a bioconjugate of Claim 1 and a pharmaceutically acceptable diluent.

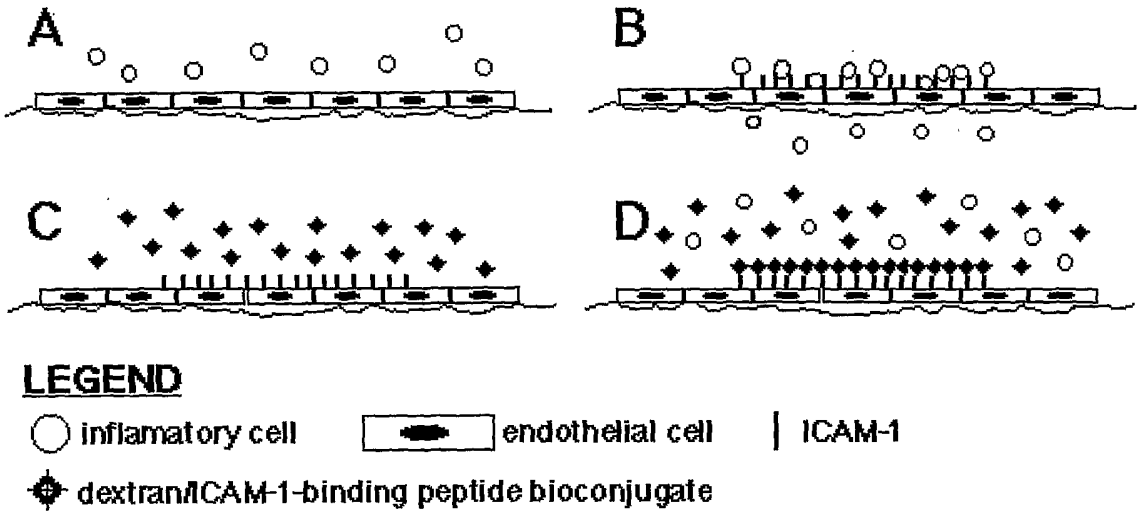

A
B
C
D
LEGEND
inflamatory cell
endothelial cell
ICAM-1
dextran/ICAM-1-binding peptide bioconjugate

FIGURE 1

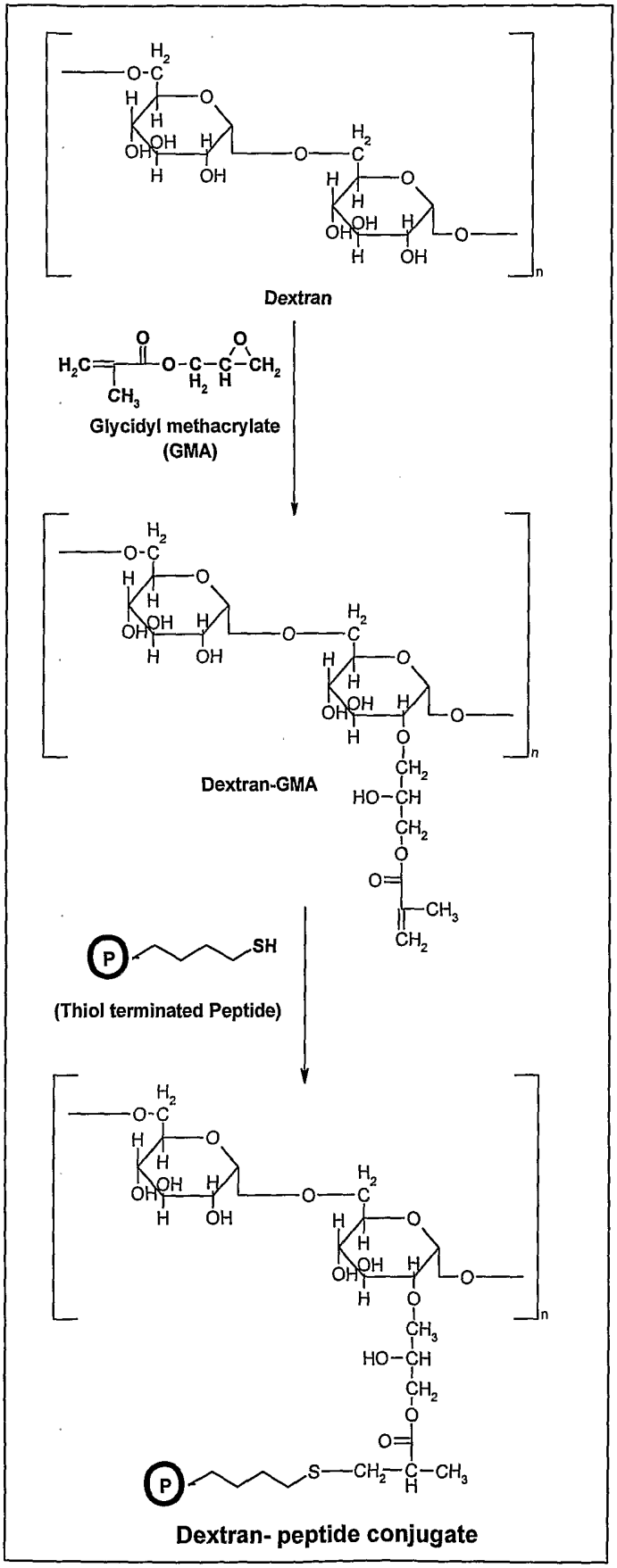

Dextran
Glycidyl methacrylate
(GMA)
Dextran-GMA
(Thiol terminated Peptide)
Dextran- peptide conjugate

FIGURE 2

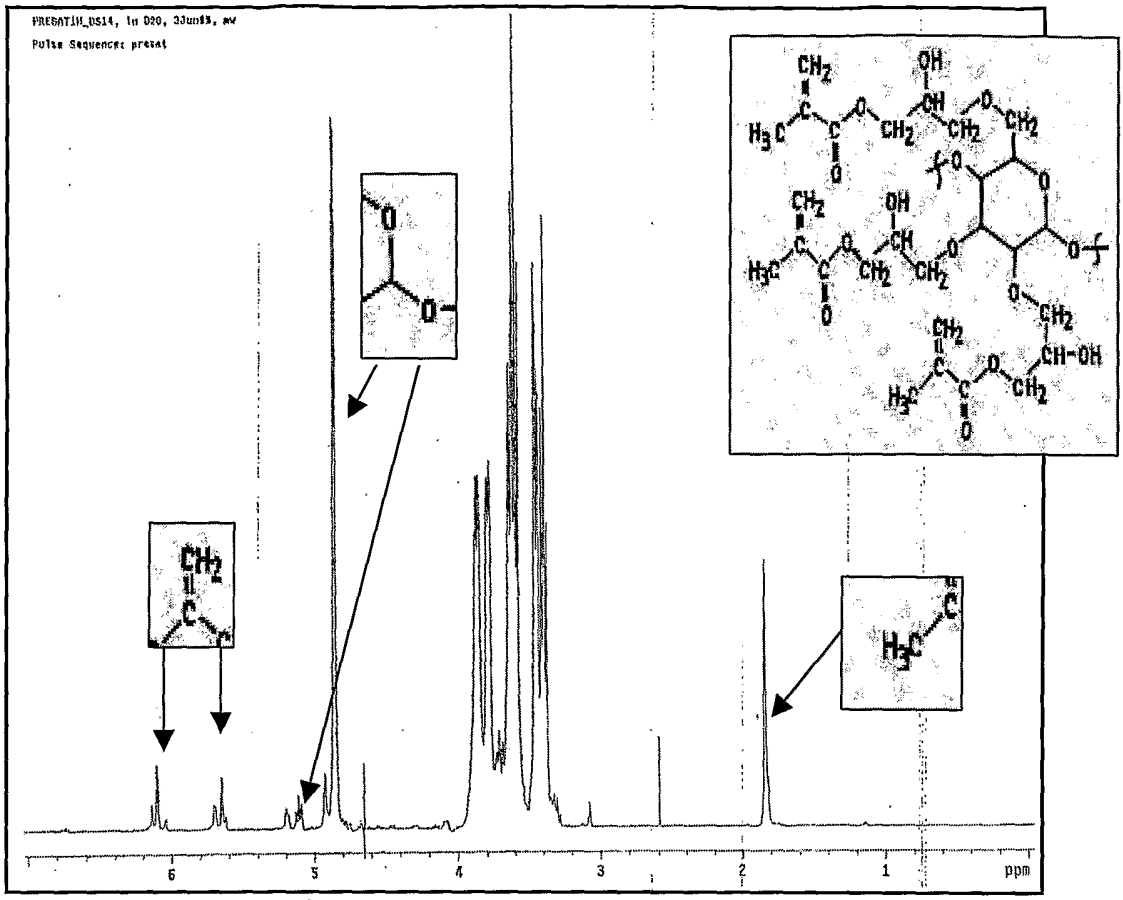

PRESATIH_0514, in D20, 30un03, mv
Pulse Sequence: presat
6
5
4
3
2
1
ppm

FIGURE 3

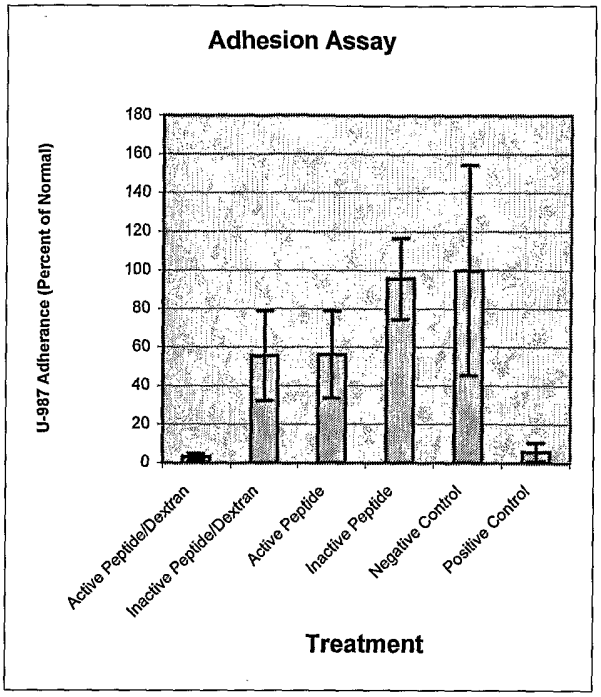


Fig. 2. Monocyte adhesion to bovine endothelial cells. All but the positive control were activated with TNF-α to induce ICAM expression. SM1 is the CD11b/CD18 agonist and SM2 is the scrambled, inactive peptide.

FIGURE 4

130588.00025.ST25.txt
SEQUENCE LISTING

<110> Arizona Board of Regents, acting for and on behalf of,
Arizona State University (ABR/ASU)
Massia, Stephen P.
Ehteshami, Gholam R.

<120> Bioselective bioconjugates for
anti-inflammatory/immunosuppressant therapies

<130> 130588.00025

<150> 10/295,734
<151> 2002-11-15

<160> 219

<170> PatentIn version 3.2

<210> 1
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(54)

<400> 1
act tac aaa aca aag gag gaa atg ata gta gca acg agt cag acc agt
48
Thr Tyr Lys Thr Lys Glu Glu Met Ile Val Ala Thr Ser Gln Thr Ser
1 5 10 15

caa tat
54
Gln Tyr

<210> 2
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 2

Thr Tyr Lys Thr Lys Glu Glu Met Ile Val Ala Thr Ser Gln Thr Ser
1 5 10 15

Gln Tyr

<210> 3
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(15)

<400> 3
cag acc agt caa tat
15
Gln Thr Ser Gln Tyr

1 5

<210> 4
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 4

Gln Thr Ser Gln Tyr
1 5

<210> 5
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(15)

<400> 5
ata gca gta ata gga
15
Ile Ala Val Ile Gly

1 5

<210> 6
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 6

Ile Ala Val Ile Gly
1 5

<210> 7
<211> 261
<212> DNA
<213> Artificial Sequence

<220>

130588.00025.ST25.txt

<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(261)

<400> 7

aat ttc cta gag aag ttt gtt cag ggt ctc gat atc ggc cct acc aaa
48
Asn Phe Leu Glu Lys Phe Val Gln Gly Leu Asp Ile Gly Pro Thr Lys
1 5 10 15

acc cag gtc ggt ctg ata caa tat gcg aat aat cca cgc tgg ttc aat
96
Thr Gln Val Gly Leu Ile Gln Tyr Ala Asn Asn Pro Arg Trp Phe Asn
20 25 30

cta aat act tat aag act aag gaa gag atg att gtt gct acc tcc cag 1
44
Leu Asn Thr Tyr Lys Thr Lys Glu Glu Met Ile Val Ala Thr Ser Gln
35 40 45

act agc cag tac ggc ggt gat cta aca aat aca ttc gga gcg atc cag 1
92
Thr Ser Gln Tyr Gly Gly Asp Leu Thr Asn Thr Phe Gly Ala Ile Gln
50 55 60

tat gcg cga aaa tat gcg tat tca gcg gcc tct gga ggc cgt cga agt 2
40
Tyr Ala Arg Lys Tyr Ala Tyr Ser Ala Ala Ser Gly Gly Arg Arg Ser
65 70 75 80

gca aca ctt aaa gta atg gtg 2
61
Ala Thr Leu Lys Val Met Val
85

<210> 8
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 8

Asn Phe Leu Glu Lys Phe Val Gln Gly Leu Asp Ile Gly Pro Thr Lys
1 5 10 15

Thr Gln Val Gly Leu Ile Gln Tyr Ala Asn Asn Pro Arg Trp Phe Asn
20 25 30

Leu Asn Thr Tyr Lys Thr Lys Glu Glu Met Ile Val Ala Thr Ser Gln
35 40 45

Thr Ser Gln Tyr Gly Gly Asp Leu Thr Asn Thr Phe Gly Ala Ile Gln
50 55 60

Tyr Ala Arg Lys Tyr Ala Tyr Ser Ala Ala Ser Gly Gly Arg Arg Ser
65 70 75 80

Ala Thr Leu Lys Val Met Val
85

<210> 9
<211> 294
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS

<222> (1)..(294)

<400> 9

```
tac aac gtc gac aca gaa tct gca ctt tta tat cag ggc ccg cat aat
48
Tyr Asn Val Asp Thr Glu Ser Ala Leu Leu Tyr Gln Gly Pro His Asn

1               5                  10                  15


aca ctg ttt ggc tac agt tgg ctc cac tcc cat gga gct cat aga tgg
96
Thr Leu Phe Gly Tyr Ser Trp Leu His Ser His Gly Ala His Arg Trp

            20                  25                  30


cta ctg gta gga gcg cca aca gca atg tgg tta gca atg gca agc gtt      1
44
Leu Leu Val Gly Ala Pro Thr Ala Met Trp Leu Ala Met Ala Ser Val

        35                  40                  45


att aat cct ggg gcc atc tat aga tgc aga ata gga aaa aac cca ggg      1
92
Ile Asn Pro Gly Ala Ile Tyr Arg Cys Arg Ile Gly Lys Asn Pro Gly

    50                  55                  60


cag acg tgt gaa ttg caa ttg ggt tca ttc cac ggt gag ccc ggc ggt      2
40
Gln Thr Cys Glu Leu Gln Leu Gly Ser Phe His Gly Glu Pro Gly Gly

65                  70                  75                  80


aag act tgt cta gag gaa aga gat cac caa tgg ctt ggg gtg acc ctc      2
88
Lys Thr Cys Leu Glu Glu Arg Asp His Gln Trp Leu Gly Val Thr Leu

                85                  90                  95


tcg aga                                                             2
94
Ser Arg
```

<210> 10
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 10

Tyr Asn Val Asp Thr Glu Ser Ala Leu Leu Tyr Gln Gly Pro His Asn
1 5 10 15

Thr Leu Phe Gly Tyr Ser Trp Leu His Ser His Gly Ala His Arg Trp
20 25 30

Leu Leu Val Gly Ala Pro Thr Ala Met Trp Leu Ala Met Ala Ser Val
35 40 45

Ile Asn Pro Gly Ala Ile Tyr Arg Cys Arg Ile Gly Lys Asn Pro Gly
50 55 60

Gln Thr Cys Glu Leu Gln Leu Gly Ser Phe His Gly Glu Pro Gly Gly
65 70 75 80

Lys Thr Cys Leu Glu Glu Arg Asp His Gln Trp Leu Gly Val Thr Leu
85 90 95

Ser Arg

<210> 11
<211> 156
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(156)

<400> 11
cag gat tat gta aag aaa ttc ggc gaa cat ttt gca agt tgt caa gca
48
Gln Asp Tyr Val Lys Lys Phe Gly Glu His Phe Ala Ser Cys Gln Ala

1 5 10 15

ggg ata tcc tcg ttc tat acg aaa gac tta atc gta atg ggt gca cca
96
Gly Ile Ser Ser Phe Tyr Thr Lys Asp Leu Ile Val Met Gly Ala Pro

20 25 30

gga tct tca tac tgg aca gga agc tta ttt gta tac atg att acc act 1
44
Gly Ser Ser Tyr Trp Thr Gly Ser Leu Phe Val Tyr Met Ile Thr Thr

35 40 45

aat aag tat aaa 1
56
Asn Lys Tyr Lys

50

<210> 12
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 12

Gln Asp Tyr Val Lys Lys Phe Gly Glu His Phe Ala Ser Cys Gln Ala
1 5 10 15

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

Gly Ser Ser Tyr Trp Thr Gly Ser Leu Phe Val Tyr Met Ile Thr Thr
35 40 45

Asn Lys Tyr Lys
50

<210> 13
<211> 156
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(156)

<400> 13
cag gat tat gta aag aaa ttc ggc gaa cat ttt gca agt tgt caa gca
48
Gln Asp Tyr Val Lys Lys Phe Gly Glu His Phe Ala Ser Cys Gln Ala
1 5 10 15

ggg ata tcc tcg ttc tat acg aaa gac tta atc gta atg ggt gca cca
96
Gly Ile Ser Ser Phe Tyr Thr Lys Asp Leu Ile Val Met Gly Ala Pro
20 25 30

gga tct tca tac tgg aca gga agc tta ttt gta tac atg att acc act 1
44
Gly Ser Ser Tyr Trp Thr Gly Ser Leu Phe Val Tyr Met Ile Thr Thr

35 40 45

aat aag tat aaa 1
56
Asn Lys Tyr Lys

50

<210> 14
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 14

Gln Asp Tyr Val Lys Lys Phe Gly Glu His Phe Ala Ser Cys Gln Ala
1 5 10 15

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

Gly Ser Ser Tyr Trp Thr Gly Ser Leu Phe Val Tyr Met Ile Thr Thr
35 40 45

Asn Lys Tyr Lys
50

<210> 15
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS

<222> (1)..(60)

<400> 15
gga cat aga tgg aaa aac ata ttt tat ata aag aat gaa aat aaa tta
48
Gly His Arg Trp Lys Asn Ile Phe Tyr Ile Lys Asn Glu Asn Lys Leu
1 5 10 15

cca aca gga gga
60
Pro Thr Gly Gly
20

<210> 16
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 16

Gly His Arg Trp Lys Asn Ile Phe Tyr Ile Lys Asn Glu Asn Lys Leu
1 5 10 15

Pro Thr Gly Gly
20

<210> 17
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(33)

<400> 17
gga gga gca cca cag cat gaa caa ata gga aaa
33
Gly Gly Ala Pro Gln His Glu Gln Ile Gly Lys

1 5 10

<210> 18
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 18

Gly Gly Ala Pro Gln His Glu Gln Ile Gly Lys
1 5 10

<210> 19
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(18)

<400> 19
agt tat tgg aca gga agt
18
Ser Tyr Trp Thr Gly Ser

1 5

<210> 20
<211> 6

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 20

Ser Tyr Trp Thr Gly Ser
1 5

<210> 21
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(33)

<400> 21
atg gga gca cca gga agt agt tat tgg aca gga
33
Met Gly Ala Pro Gly Ser Ser Tyr Trp Thr Gly

1 5 10

<210> 22
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 22

Met Gly Ala Pro Gly Ser Ser Tyr Trp Thr Gly
1 5 10

<210> 23
<211> 111
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(111)

<400> 23
tac aat gta gat aca gaa agt gca tta ctc tat caa ggt cca cac aac
48
Tyr Asn Val Asp Thr Glu Ser Ala Leu Leu Tyr Gln Gly Pro His Asn
1 5 10 15

aca ttg ttt ggg tat agt tgg ctt cat agt cat gga gca cac aga tgg
96
Thr Leu Phe Gly Tyr Ser Trp Leu His Ser His Gly Ala His Arg Trp
20 25 30

ctg cta gta ggc gca
11
Leu Leu Val Gly Ala
35

<210> 24
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 24

Tyr Asn Val Asp Thr Glu Ser Ala Leu Leu Tyr Gln Gly Pro His Asn
1 5 10 15

Thr Leu Phe Gly Tyr Ser Trp Leu His Ser His Gly Ala His Arg Trp
20 25 30

Leu Leu Val Gly Ala
35

<210> 25
<211> 225
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(225)

<400> 25
ata gta acg tgt ggc cat aga tgg aaa aat att ttt tat atc aaa cac
48
Ile Val Thr Cys Gly His Arg Trp Lys Asn Ile Phe Tyr Ile Lys His
1 5 10 15

gaa aac aaa tta cca aca gga ggg tgt tat ggc gtg ccc ccg gat tta
96
Glu Asn Lys Leu Pro Thr Gly Gly Cys Tyr Gly Val Pro Pro Asp Leu
20 25 30

aga acc gaa tta agt aag aga ata gcc cct ggt tat cag gac tac gtt 1
44
Arg Thr Glu Leu Ser Lys Arg Ile Ala Pro Gly Tyr Gln Asp Tyr Val
35 40 45

aaa aag ttc gga gag cat ttt gct agt tgc caa gca ggt atc agt agt 1
92
Lys Lys Phe Gly Glu His Phe Ala Ser Cys Gln Ala Gly Ile Ser Ser

50 55 60

ttc tac act aag gat tta att gtc atg ggg gcg 2
25
Phe Tyr Thr Lys Asp Leu Ile Val Met Gly Ala

65 70 75

<210> 26
<211> 75
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 26

Ile Val Thr Cys Gly His Arg Trp Lys Asn Ile Phe Tyr Ile Lys His
1 5 10 15

Glu Asn Lys Leu Pro Thr Gly Gly Cys Tyr Gly Val Pro Pro Asp Leu
20 25 30

Arg Thr Glu Leu Ser Lys Arg Ile Ala Pro Gly Tyr Gln Asp Tyr Val
35 40 45

Lys Lys Phe Gly Glu His Phe Ala Ser Cys Gln Ala Gly Ile Ser Ser
50 55 60

Phe Tyr Thr Lys Asp Leu Ile Val Met Gly Ala
65 70 75

<210> 27
<211> 222
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(222)

<400> 27
tac atg att acc act aac aag tat aaa gcg ttt tta ggg aag caa aat
48
Tyr Met Ile Thr Thr Asn Lys Tyr Lys Ala Phe Leu Gly Lys Gln Asn

1 5 10 15

cag gtg aag cca gga agt tat tta ggg tat agt gta ggt gcc ggc cat
96
Gln Val Lys Pro Gly Ser Tyr Leu Gly Tyr Ser Val Gly Ala Gly His

20 25 30

ttc aga agt caa cac acg aca gaa gtt gtc ggc ggt gca cca caa cat 1
44
Phe Arg Ser Gln His Thr Thr Glu Val Val Gly Gly Ala Pro Gln His

35 40 45

gag cag ata gga aaa gct tac atc ttt agt ata gat gaa aaa gaa tta 1
92
Glu Gln Ile Gly Lys Ala Tyr Ile Phe Ser Ile Asp Glu Lys Glu Leu

50 55 60

aat ata tta cac gag atg aag gga aaa aaa 2
22
Asn Ile Leu His Glu Met Lys Gly Lys Lys

65 70

<210> 28
<211> 74
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 28

Tyr Met Ile Thr Thr Asn Lys Tyr Lys Ala Phe Leu Gly Lys Gln Asn
1 5 10 15

Gln Val Lys Pro Gly Ser Tyr Leu Gly Tyr Ser Val Gly Ala Gly His
20 25 30

Phe Arg Ser Gln His Thr Thr Glu Val Val Gly Gly Ala Pro Gln His
35 40 45

Glu Gln Ile Gly Lys Ala Tyr Ile Phe Ser Ile Asp Glu Lys Glu Leu
50 55 60

Asn Ile Leu His Glu Met Lys Gly Lys Lys
65 70

<210> 29
<211> 849
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(849)

<400> 29
tta gga tca tat ttc gga gca tcc gtc ggc gca gtc gac tta cac gct
48
Leu Gly Ser Tyr Phe Gly Ala Ser Val Gly Ala Val Asp Leu His Ala

1 5 10 15

gat ggc ttc tca gac ctg ctc gtc ggt gct ccc atg caa tcg acg ata

96
Asp Gly Phe Ser Asp Leu Leu Val Gly Ala Pro Met Gln Ser Thr Ile
20 25 30

aga gaa gag ggt aga gtt ttt gtt tac atc aat tct gga agc ggg gca 1
44
Arg Glu Glu Gly Arg Val Phe Val Tyr Ile Asn Ser Gly Ser Gly Ala
35 40 45

gtt atg aac gca atg gag aca aac tta gtg gga agt gac aaa tac gca 1
92
Val Met Asn Ala Met Glu Thr Asn Leu Val Gly Ser Asp Lys Tyr Ala
50 55 60

gcg cga ttt ggg gaa tcc atc gtg aat ttg gga gat att gac aat gac 2
40
Ala Arg Phe Gly Glu Ser Ile Val Asn Leu Gly Asp Ile Asp Asn Asp
65 70 75 80

ggg ttt gaa gac gta gcg att gga gca cca cag gag gac gat ctc cag 2
88
Gly Phe Glu Asp Val Ala Ile Gly Ala Pro Gln Glu Asp Asp Leu Gln
85 90 95

gga gct atc tat atc tac aac ggc aga gcg gat ggt ata tct tca aca 3
36
Gly Ala Ile Tyr Ile Tyr Asn Gly Arg Ala Asp Gly Ile Ser Ser Thr
100 105 110

ttt tcc caa aga att gag ggc cta caa ata tcg aag tcg cta tcc atg 3
84
Phe Ser Gln Arg Ile Glu Gly Leu Gln Ile Ser Lys Ser Leu Ser Met
115 120 125

ttt ggg cag agt att tct ggt cag atc gac gcg gat aac aat ggc tat 4
32
Phe Gly Gln Ser Ile Ser Gly Gln Ile Asp Ala Asp Asn Asn Gly Tyr

130 135 140

gtg gat gta gca gta ggc gcg ttc agg agt gat cgt agc gat tct gct 4
80
Val Asp Val Ala Val Gly Ala Phe Arg Ser Asp Arg Ser Asp Ser Ala

145 150 155 160

gtt ttg tta aga acg cgt cca gtc gtc ata gtg gac gct tca ctt agt 5
28
Val Leu Leu Arg Thr Arg Pro Val Val Ile Val Asp Ala Ser Leu Ser

165 170 175

cat cct gaa tca gta aac cga aca aag ttt gat tgt gtc gag aat ggg 5
76
His Pro Glu Ser Val Asn Arg Thr Lys Phe Asp Cys Val Glu Asn Gly

180 185 190

tgg ccg agc gtg tgt ata gat ctg aca tta tgc ttc tcg tac aaa ggg 6
24
Trp Pro Ser Val Cys Ile Asp Leu Thr Leu Cys Phe Ser Tyr Lys Gly

195 200 205

aag gaa gtt cct ggt tat att gta tta ttc tac aat atg agt ctt gat 6
72
Lys Glu Val Pro Gly Tyr Ile Val Leu Phe Tyr Asn Met Ser Leu Asp

210 215 220

gtt aac cgc aaa gcc gaa tcg cca ccg cgg ttt tat ttc agt agc aat 7
20
Val Asn Arg Lys Ala Glu Ser Pro Pro Arg Phe Tyr Phe Ser Ser Asn

225 230 235 240

ggt act agt gat gta att act gga agc ata caa gtg tct tcc aga gaa 7
68
Gly Thr Ser Asp Val Ile Thr Gly Ser Ile Gln Val Ser Ser Arg Glu
245 250 255

gcc aac tgc cgg acc cat caa gcc ttc atg cgc aaa gac gta agg gac 8
16
Ala Asn Cys Arg Thr His Gln Ala Phe Met Arg Lys Asp Val Arg Asp
260 265 270

ata tta acc ccc ata cag atc gag gcc gcc tat 8
49
Ile Leu Thr Pro Ile Gln Ile Glu Ala Ala Tyr
275 280

<210> 30
<211> 283
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 30

Leu Gly Ser Tyr Phe Gly Ala Ser Val Gly Ala Val Asp Leu His Ala
1 5 10 15

Asp Gly Phe Ser Asp Leu Leu Val Gly Ala Pro Met Gln Ser Thr Ile
20 25 30

Arg Glu Glu Gly Arg Val Phe Val Tyr Ile Asn Ser Gly Ser Gly Ala
35 40 45

Val Met Asn Ala Met Glu Thr Asn Leu Val Gly Ser Asp Lys Tyr Ala
50 55 60

Ala Arg Phe Gly Glu Ser Ile Val Asn Leu Gly Asp Ile Asp Asn Asp
65 70 75 80

Gly Phe Glu Asp Val Ala Ile Gly Ala Pro Gln Glu Asp Asp Leu Gln
85 90 95

Gly Ala Ile Tyr Ile Tyr Asn Gly Arg Ala Asp Gly Ile Ser Ser Thr
100 105 110

Phe Ser Gln Arg Ile Glu Gly Leu Gln Ile Ser Lys Ser Leu Ser Met
115 120 125

Phe Gly Gln Ser Ile Ser Gly Gln Ile Asp Ala Asp Asn Asn Gly Tyr
130 135 140

Val Asp Val Ala Val Gly Ala Phe Arg Ser Asp Arg Ser Asp Ser Ala
145 150 155 160

Val Leu Leu Arg Thr Arg Pro Val Val Ile Val Asp Ala Ser Leu Ser
165 170 175

His Pro Glu Ser Val Asn Arg Thr Lys Phe Asp Cys Val Glu Asn Gly
180 185 190

Trp Pro Ser Val Cys Ile Asp Leu Thr Leu Cys Phe Ser Tyr Lys Gly
195 200 205

Lys Glu Val Pro Gly Tyr Ile Val Leu Phe Tyr Asn Met Ser Leu Asp
210 215 220

Val Asn Arg Lys Ala Glu Ser Pro Pro Arg Phe Tyr Phe Ser Ser Asn
225 230 235 240

Gly Thr Ser Asp Val Ile Thr Gly Ser Ile Gln Val Ser Ser Arg Glu
245 250 255

Ala Asn Cys Arg Thr His Gln Ala Phe Met Arg Lys Asp Val Arg Asp
260 265 270

Ile Leu Thr Pro Ile Gln Ile Glu Ala Ala Tyr
275 280

<210> 31
<211> 1032
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(1032)

<400> 31
tcc tca ata tat gac gac tcc tac ctc gga tac agt gta gcg gtc ggc
48
Ser Ser Ile Tyr Asp Asp Ser Tyr Leu Gly Tyr Ser Val Ala Val Gly

1 5 10 15

gaa ttt tcg gga gac gac aca gaa gat ttt gta gct ggg gtg ccc aaa
96
Glu Phe Ser Gly Asp Asp Thr Glu Asp Phe Val Ala Gly Val Pro Lys

20 25 30

ggg aat ttg act tat ggc tac gtt acc ata cta aat ggt tct gat att 1
44
Gly Asn Leu Thr Tyr Gly Tyr Val Thr Ile Leu Asn Gly Ser Asp Ile

35 40 45

cgt agt tta tat aat ttc agt ggg gag caa atg gca agc tat ttc gga 1
92
Arg Ser Leu Tyr Asn Phe Ser Gly Glu Gln Met Ala Ser Tyr Phe Gly

50 55 60

tat gcg gta gca gcg acc gac gtc aac ggt gat ggg ctg gac gat ttg 2
40
Tyr Ala Val Ala Ala Thr Asp Val Asn Gly Asp Gly Leu Asp Asp Leu

65 70 75 80

ctt gtc ggg gcc ccg tta ctt atg gac cgc act cca gat gga aga cca 2
88
Leu Val Gly Ala Pro Leu Leu Met Asp Arg Thr Pro Asp Gly Arg Pro

85 90 95

cag gaa gtg ggt cgt gta tat gtg tac tta cag cac cca gca ggt ata 3
36
Gln Glu Val Gly Arg Val Tyr Val Tyr Leu Gln His Pro Ala Gly Ile

100 105 110

gag ccg aca ccg act ttg acg cta acc gga cac gac gag ttc ggc cgg 3
84
Glu Pro Thr Pro Thr Leu Thr Leu Thr Gly His Asp Glu Phe Gly Arg

115 120 125

ttt ggc agt tca tta aca ccc ctt gga gac tta gat cag gat gga tac 4
32
Phe Gly Ser Ser Leu Thr Pro Leu Gly Asp Leu Asp Gln Asp Gly Tyr

130 135 140

aat gac gtt gct att ggg gca cca ttt ggt ggc gaa acg caa caa ggt 4
80
Asn Asp Val Ala Ile Gly Ala Pro Phe Gly Gly Glu Thr Gln Gln Gly

145 150 155 160

gta gta ttc gtg ttt cct gga ggc cct gga ggc tta ggc agt aaa cct 5
28
Val Val Phe Val Phe Pro Gly Gly Pro Gly Gly Leu Gly Ser Lys Pro

165 170 175

tcg caa gtt ttg cag cca cta tgg gcc gct agc cat acg ccc gat ttc 5
76
Ser Gln Val Leu Gln Pro Leu Trp Ala Ala Ser His Thr Pro Asp Phe

180 185 190

ttt ggc agc gct ctg aga ggg ggg agg gac ctc gac ggt aac ggg tat 6
24
Phe Gly Ser Ala Leu Arg Gly Gly Arg Asp Leu Asp Gly Asn Gly Tyr

195 200 205

cct gat ctg atc gtt ggt agt ttt gga gtc gat aag gcg gtg gtc tac 6
72
Pro Asp Leu Ile Val Gly Ser Phe Gly Val Asp Lys Ala Val Val Tyr

210 215 220

aga ggg ggg ccc ata gtt tca gca agt gcc agc ctt acg ata ttc ccc 7
20
Arg Gly Gly Pro Ile Val Ser Ala Ser Ala Ser Leu Thr Ile Phe Pro

225 230 235 240

gcc atg ttt aat cct gag gag aga tct tgc tca ttg gaa ggt aac ccg 7
68
Ala Met Phe Asn Pro Glu Glu Arg Ser Cys Ser Leu Glu Gly Asn Pro

245 250 255

gtc gcg tgt atc aac ctc tcc ttc tgt tta aac gca tcg ggt aaa cat 8
16
Val Ala Cys Ile Asn Leu Ser Phe Cys Leu Asn Ala Ser Gly Lys His

260 265 270

gtg gct gat tcg atc gga ttt aca gta gaa ctt caa cta gat tgg cag 8
64

Val Ala Asp Ser Ile Gly Phe Thr Val Glu Leu Gln Leu Asp Trp Gln
275 280 285

aag caa aaa ggc gga gtt aga cga gcc ctc ttc ctc gca tcc agg cag 9
12
Lys Gln Lys Gly Gly Val Arg Arg Ala Leu Phe Leu Ala Ser Arg Gln
290 295 300

gcg act tta aca caa acc cta ctg ata cag aac gga gcc aga gag gat 9
60
Ala Thr Leu Thr Gln Thr Leu Leu Ile Gln Asn Gly Ala Arg Glu Asp
305 310 315 320

tgc cgc gaa atg aag atc tac ctg aga aat gaa tct gag ttc cga gac 10
08
Cys Arg Glu Met Lys Ile Tyr Leu Arg Asn Glu Ser Glu Phe Arg Asp
325 330 335

aag tta tct ccg att cat att gct 10
32
Lys Leu Ser Pro Ile His Ile Ala
340

<210> 32
<211> 344
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 32

Ser Ser Ile Tyr Asp Asp Ser Tyr Leu Gly Tyr Ser Val Ala Val Gly
1 5 10 15

Glu Phe Ser Gly Asp Asp Thr Glu Asp Phe Val Ala Gly Val Pro Lys
20 25 30

Gly Asn Leu Thr Tyr Gly Tyr Val Thr Ile Leu Asn Gly Ser Asp Ile
35 40 45

Arg Ser Leu Tyr Asn Phe Ser Gly Glu Gln Met Ala Ser Tyr Phe Gly
50 55 60

Tyr Ala Val Ala Ala Thr Asp Val Asn Gly Asp Gly Leu Asp Asp Leu
65 70 75 80

Leu Val Gly Ala Pro Leu Leu Met Asp Arg Thr Pro Asp Gly Arg Pro
85 90 95

Gln Glu Val Gly Arg Val Tyr Val Tyr Leu Gln His Pro Ala Gly Ile
100 105 110

Glu Pro Thr Pro Thr Leu Thr Leu Thr Gly His Asp Glu Phe Gly Arg
115 120 125

Phe Gly Ser Ser Leu Thr Pro Leu Gly Asp Leu Asp Gln Asp Gly Tyr
130 135 140

Asn Asp Val Ala Ile Gly Ala Pro Phe Gly Gly Glu Thr Gln Gln Gly
145 150 155 160

Val Val Phe Val Phe Pro Gly Gly Pro Gly Gly Leu Gly Ser Lys Pro
165 170 175

Ser Gln Val Leu Gln Pro Leu Trp Ala Ala Ser His Thr Pro Asp Phe
180 185 190

Phe Gly Ser Ala Leu Arg Gly Gly Arg Asp Leu Asp Gly Asn Gly Tyr
195 200 205

Pro Asp Leu Ile Val Gly Ser Phe Gly Val Asp Lys Ala Val Val Tyr
210 215 220

Arg Gly Gly Pro Ile Val Ser Ala Ser Ala Ser Leu Thr Ile Phe Pro
225 230 235 240

Ala Met Phe Asn Pro Glu Glu Arg Ser Cys Ser Leu Glu Gly Asn Pro
245 250 255

Val Ala Cys Ile Asn Leu Ser Phe Cys Leu Asn Ala Ser Gly Lys His
260 265 270

Val Ala Asp Ser Ile Gly Phe Thr Val Glu Leu Gln Leu Asp Trp Gln
275 280 285

Lys Gln Lys Gly Gly Val Arg Arg Ala Leu Phe Leu Ala Ser Arg Gln
290 295 300

Ala Thr Leu Thr Gln Thr Leu Leu Ile Gln Asn Gly Ala Arg Glu Asp
305 310 315 320

Cys Arg Glu Met Lys Ile Tyr Leu Arg Asn Glu Ser Glu Phe Arg Asp
325 330 335

Lys Leu Ser Pro Ile His Ile Ala
340

<210> 33
<211> 660
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(660)

<400> 33
agc tac cta gga tat agt gtt gct gta ggc gag ttc agc gga gat gat
48
Ser Tyr Leu Gly Tyr Ser Val Ala Val Gly Glu Phe Ser Gly Asp Asp
1 5 10 15

aca gaa gac ttt gtt gca ggg gtg cct aag ggg aat cta aca tat ggg
96
Thr Glu Asp Phe Val Ala Gly Val Pro Lys Gly Asn Leu Thr Tyr Gly
20 25 30

tac gta aca atc ctc aac gga tcg gat att cgt agt tta tac aat ttc 1
44
Tyr Val Thr Ile Leu Asn Gly Ser Asp Ile Arg Ser Leu Tyr Asn Phe
35 40 45

tcc ggt gag caa atg gcc tca tat ttt gga tac gcc gtt gcg gct acg 1
92
Ser Gly Glu Gln Met Ala Ser Tyr Phe Gly Tyr Ala Val Ala Ala Thr
50 55 60

gac gtt aac ggt gac gga tta gac gat ctt ctt gtg gga gct ccc ctg 2
40
Asp Val Asn Gly Asp Gly Leu Asp Asp Leu Leu Val Gly Ala Pro Leu
65 70 75 80

ctg atg gac cga acc cct gat ggt aga ccc cag gaa gtc gga aga gtc 2
88
Leu Met Asp Arg Thr Pro Asp Gly Arg Pro Gln Glu Val Gly Arg Val
85 90 95

tac gtc tac ttg caa cat ccc gcc ggc ata gaa cca acg cca act tta 3
36
Tyr Val Tyr Leu Gln His Pro Ala Gly Ile Glu Pro Thr Pro Thr Leu

100 105 110

act ctc act ggg cat gac gaa ttt ggt aga ttc ggt tcc tct tta acc 3
84
Thr Leu Thr Gly His Asp Glu Phe Gly Arg Phe Gly Ser Ser Leu Thr

115 120 125

cct ctt ggc gac ttg gac cag gat gga tat aat gat gtg gca ata ggc 4
32
Pro Leu Gly Asp Leu Asp Gln Asp Gly Tyr Asn Asp Val Ala Ile Gly

130 135 140

gcg ccg ttt ggg ggg gag acc cag caa ggc gtg gtg ttc gtc ttt cca 4
80
Ala Pro Phe Gly Gly Glu Thr Gln Gln Gly Val Val Phe Val Phe Pro

145 150 155 160

ggt gga ccg ggt ggg cta ggg tct aaa cca tca caa gtt tta cag cca 5
28
Gly Gly Pro Gly Gly Leu Gly Ser Lys Pro Ser Gln Val Leu Gln Pro

165 170 175

tta tgg gca gcg agt cac acg cca gat ttt ttc ggc agt gca ctc agg 5
76
Leu Trp Ala Ala Ser His Thr Pro Asp Phe Phe Gly Ser Ala Leu Arg

180 185 190

ggt gga cgg gac ttg gac ggc aac ggc tat ccg gat ctg ata gta ggg 6
24
Gly Gly Arg Asp Leu Asp Gly Asn Gly Tyr Pro Asp Leu Ile Val Gly

195 200 205

tcg ttc ggt gta gat aaa gca gta gtc tat cgc ggg 6
60
Ser Phe Gly Val Asp Lys Ala Val Val Tyr Arg Gly

210 215 220

<210> 34
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 34

Ser Tyr Leu Gly Tyr Ser Val Ala Val Gly Glu Phe Ser Gly Asp Asp
1 5 10 15

Thr Glu Asp Phe Val Ala Gly Val Pro Lys Gly Asn Leu Thr Tyr Gly
20 25 30

Tyr Val Thr Ile Leu Asn Gly Ser Asp Ile Arg Ser Leu Tyr Asn Phe
35 40 45

Ser Gly Glu Gln Met Ala Ser Tyr Phe Gly Tyr Ala Val Ala Ala Thr
50 55 60

Asp Val Asn Gly Asp Gly Leu Asp Asp Leu Leu Val Gly Ala Pro Leu
65 70 75 80

Leu Met Asp Arg Thr Pro Asp Gly Arg Pro Gln Glu Val Gly Arg Val
85 90 95

Tyr Val Tyr Leu Gln His Pro Ala Gly Ile Glu Pro Thr Pro Thr Leu
100 105 110

Thr Leu Thr Gly His Asp Glu Phe Gly Arg Phe Gly Ser Ser Leu Thr
115 120 125

Pro Leu Gly Asp Leu Asp Gln Asp Gly Tyr Asn Asp Val Ala Ile Gly

130 135 140

Ala Pro Phe Gly Gly Glu Thr Gln Gln Gly Val Val Phe Val Phe Pro
145 150 155 160

Gly Gly Pro Gly Gly Leu Gly Ser Lys Pro Ser Gln Val Leu Gln Pro
165 170 175

Leu Trp Ala Ala Ser His Thr Pro Asp Phe Phe Gly Ser Ala Leu Arg
180 185 190

Gly Gly Arg Asp Leu Asp Gly Asn Gly Tyr Pro Asp Leu Ile Val Gly
195 200 205

Ser Phe Gly Val Asp Lys Ala Val Val Tyr Arg Gly
210 215 220

<210> 35
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(360)

<400> 35
gca cat ggt tcg agc atc tta gca tgc gct cct ctc tac agc tgg aga
48
Ala His Gly Ser Ser Ile Leu Ala Cys Ala Pro Leu Tyr Ser Trp Arg

1 5 10 15

acg gaa aaa gaa ccc tta tct gat ccg gtc ggg acg tgt tat tta tcg
96
Thr Glu Lys Glu Pro Leu Ser Asp Pro Val Gly Thr Cys Tyr Leu Ser

20 25 30

acc gac aac ttt aca aga atc tta gag tac gcg cca tgt aga tct gat 1
44
Thr Asp Asn Phe Thr Arg Ile Leu Glu Tyr Ala Pro Cys Arg Ser Asp

35 40 45

ttc agt tgg gca gcg ggt caa ggg tat tgc caa ggc ggc ttc agt gcc 1
92
Phe Ser Trp Ala Ala Gly Gln Gly Tyr Cys Gln Gly Gly Phe Ser Ala

50 55 60

gaa ttt act aag acc gga aga gta gtg ctt gga ggt cca gga tca tac 2
40
Glu Phe Thr Lys Thr Gly Arg Val Val Leu Gly Gly Pro Gly Ser Tyr

65 70 75 80

ttt tgg cag ggg caa att cta tcc gct aca caa gag cag ata gca gag 2
88
Phe Trp Gln Gly Gln Ile Leu Ser Ala Thr Gln Glu Gln Ile Ala Glu

85 90 95

agt tat tat cca gaa tac ctg ata aat tta gtt cag ggc cag ttg cag 3
36
Ser Tyr Tyr Pro Glu Tyr Leu Ile Asn Leu Val Gln Gly Gln Leu Gln

100 105 110

act aga caa gcc tca tcc att tat 3
60
Thr Arg Gln Ala Ser Ser Ile Tyr

115 120

<210> 36
<211> 120

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 36

Ala His Gly Ser Ser Ile Leu Ala Cys Ala Pro Leu Tyr Ser Trp Arg
1 5 10 15

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

Thr Asp Asn Phe Thr Arg Ile Leu Glu Tyr Ala Pro Cys Arg Ser Asp
35 40 45

Phe Ser Trp Ala Ala Gly Gln Gly Tyr Cys Gln Gly Gly Phe Ser Ala
50 55 60

Glu Phe Thr Lys Thr Gly Arg Val Val Leu Gly Gly Pro Gly Ser Tyr
65 70 75 80

Phe Trp Gln Gly Gln Ile Leu Ser Ala Thr Gln Glu Gln Ile Ala Glu
85 90 95

Ser Tyr Tyr Pro Glu Tyr Leu Ile Asn Leu Val Gln Gly Gln Leu Gln
100 105 110

Thr Arg Gln Ala Ser Ser Ile Tyr
115 120

<210> 37
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(18)

<400> 37
gat ttt agt tgg gca gca
18
Asp Phe Ser Trp Ala Ala

1 5

<210> 38
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 38

Asp Phe Ser Trp Ala Ala
1 5

<210> 39
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(72)

<400> 39
gga gta gac gta gat cag gat ggc gaa aca gag tta ata gga gca cca
48
Gly Val Asp Val Asp Gln Asp Gly Glu Thr Glu Leu Ile Gly Ala Pro

1 5 10 15

tta ttt tat ggt gaa caa aga ggg
72
Leu Phe Tyr Gly Glu Gln Arg Gly

20

<210> 40
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 40

Gly Val Asp Val Asp Gln Asp Gly Glu Thr Glu Leu Ile Gly Ala Pro
1 5 10 15

Leu Phe Tyr Gly Glu Gln Arg Gly
20

<210> 41
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(72)

<400> 41
ata aca gat gga gaa gca aca gac agt gga caa att gat gca gca aaa
48
Ile Thr Asp Gly Glu Ala Thr Asp Ser Gly Gln Ile Asp Ala Ala Lys

1 5 10 15

gac atc ata tat att ata gga atc
72
Asp Ile Ile Tyr Ile Ile Gly Ile

20

<210> 42
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 42

Ile Thr Asp Gly Glu Ala Thr Asp Ser Gly Gln Ile Asp Ala Ala Lys
1 5 10 15

Asp Ile Ile Tyr Ile Ile Gly Ile
20

<210> 43
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(30)

<400> 43
ata aca gat gga gaa gca aca agt gga tgt
30
Ile Thr Asp Gly Glu Ala Thr Ser Gly Cys

1 5 10

<210> 44
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 44

Ile Thr Asp Gly Glu Ala Thr Ser Gly Cys
1 5 10

<210> 45
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(33)

<400> 45
gga gta gac gta gat caa gat gga gaa aca tgt
33
Gly Val Asp Val Asp Gln Asp Gly Glu Thr Cys

1 5 10

<210> 46
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 46

Gly Val Asp Val Asp Gln Asp Gly Glu Thr Cys
1 5 10

<210> 47
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(24)

<400> 47
tgc cca aat aag gaa aaa gag tgt
24
Cys Pro Asn Lys Glu Lys Glu Cys

1 5

<210> 48
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 48

Cys Pro Asn Lys Glu Lys Glu Cys
1 5

<210> 49
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>

<221> CDS
<222> (1)..(18)

<400> 49
aaa gaa ttt gta agt aca
18
Lys Glu Phe Val Ser Thr

1 5

<210> 50
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 50

Lys Glu Phe Val Ser Thr
1 5

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

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(51)

<400> 51
cca ata aca caa tta tta gga aga acc cat acg gca act gga ata aga
48
Pro Ile Thr Gln Leu Leu Gly Arg Thr His Thr Ala Thr Gly Ile Arg

1 5 10 15

aaa

51
Lys

<210> 52
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 52

Pro Ile Thr Gln Leu Leu Gly Arg Thr His Thr Ala Thr Gly Ile Arg
1 5 10 15

Lys

<210> 53
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(51)

<400> 53
aaa ttt gga gac cca tta gga tat gaa gat gta ata cca gag gca gat
48
Lys Phe Gly Asp Pro Leu Gly Tyr Glu Asp Val Ile Pro Glu Ala Asp

1 5 10 15

aga
51

Arg

<210> 54
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 54

Lys Phe Gly Asp Pro Leu Gly Tyr Glu Asp Val Ile Pro Glu Ala Asp
1 5 10 15

Arg

<210> 55
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(72)

<400> 55
gga tgt cca caa gaa gat agt gac att gca ttc tta ata gat gga agt
48
Gly Cys Pro Gln Glu Asp Ser Asp Ile Ala Phe Leu Ile Asp Gly Ser

1 5 10 15

gga agt ata atc cca cat gac ttt
72
Gly Ser Ile Ile Pro His Asp Phe

20

<210> 56
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 56

Gly Cys Pro Gln Glu Asp Ser Asp Ile Ala Phe Leu Ile Asp Gly Ser
1 5 10 15

Gly Ser Ile Ile Pro His Asp Phe
20

<210> 57
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(69)

<400> 57
ttt aga aga atg aaa gag ttt gta agt aca gta atg gaa caa tta aag
48
Phe Arg Arg Met Lys Glu Phe Val Ser Thr Val Met Glu Gln Leu Lys
1 5 10 15

aaa agt aag aca tta ttc agt
69
Lys Ser Lys Thr Leu Phe Ser

20

<210> 58
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 58

Phe Arg Arg Met Lys Glu Phe Val Ser Thr Val Met Glu Gln Leu Lys
1 5 10 15

Lys Ser Lys Thr Leu Phe Ser
20

<210> 59
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(54)

<400> 59
gga aat agt ttt cca gca agt tta gta gta gca gca gaa gag gga gag
48
Gly Asn Ser Phe Pro Ala Ser Leu Val Val Ala Ala Glu Glu Gly Glu

1 5 10 15

aga gaa
54
Arg Glu

<210> 60
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 60

Gly Asn Ser Phe Pro Ala Ser Leu Val Val Ala Ala Glu Glu Gly Glu
1 5 10 15

Arg Glu

<210> 61
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(84)

<400> 61
aac gca caa atc gga att gca atg tta gta agt gta gga aat tta gag
48
Asn Ala Gln Ile Gly Ile Ala Met Leu Val Ser Val Gly Asn Leu Glu

1 5 10 15

gaa gca gga gaa agt gta agt ttt caa tta cag ata
84
Glu Ala Gly Glu Ser Val Ser Phe Gln Leu Gln Ile

20 25

<210> 62
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 62

Asn Ala Gln Ile Gly Ile Ala Met Leu Val Ser Val Gly Asn Leu Glu
1 5 10 15

Glu Ala Gly Glu Ser Val Ser Phe Gln Leu Gln Ile
20 25

<210> 63
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(54)

<400> 63
aca tta gga cca agt caa gaa gag aca gga gga gta ttt tta tgt cca
48
Thr Leu Gly Pro Ser Gln Glu Glu Thr Gly Gly Val Phe Leu Cys Pro
1 5 10 15

tgg aga
54
Trp Arg

<210> 64
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 64

Thr Leu Gly Pro Ser Gln Glu Glu Thr Gly Gly Val Phe Leu Cys Pro
1 5 10 15

Trp Arg

<210> 65
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(39)

<400> 65
gca gaa gga gga caa tgt cca agt tta tta ttt gat tta
39
Ala Glu Gly Gly Gln Cys Pro Ser Leu Leu Phe Asp Leu

1 5 10

<210> 66
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 66

Ala Glu Gly Gly Gln Cys Pro Ser Leu Leu Phe Asp Leu
1 5 10

<210> 67
<211> 117
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(117)

<400> 67
gcc atg gtc aca gta ttg gca ttt ctt tgg ctc cca agt cta tat cag
48
Ala Met Val Thr Val Leu Ala Phe Leu Trp Leu Pro Ser Leu Tyr Gln
1 5 10 15

aga cca ctg gat caa ttt gtg tta caa agt cat gct tgg ttc aat gtt
96
Arg Pro Leu Asp Gln Phe Val Leu Gln Ser His Ala Trp Phe Asn Val
20 25 30

agt agt tta cca tac gcg gta 1
17
Ser Ser Leu Pro Tyr Ala Val
35

<210> 68
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 68

Ala Met Val Thr Val Leu Ala Phe Leu Trp Leu Pro Ser Leu Tyr Gln
1 5 10 15

Arg Pro Leu Asp Gln Phe Val Leu Gln Ser His Ala Trp Phe Asn Val
20 25 30

Ser Ser Leu Pro Tyr Ala Val
35

<210> 69
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(36)

<400> 69
gga gca cat tat atg aga gca tta agt aat gta gaa
36
Gly Ala His Tyr Met Arg Ala Leu Ser Asn Val Glu

1 5 10

<210> 70
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 70

Gly Ala His Tyr Met Arg Ala Leu Ser Asn Val Glu
1 5 10

<210> 71
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(12)

<400> 71
gga gca cca tta
12
Gly Ala Pro Leu

1

<210> 72
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 72

Gly Ala Pro Leu
1

<210> 73
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(39)

<400> 73
gga gat gga aga cat gac tta tta gta gga gca cca tta
39
Gly Asp Gly Arg His Asp Leu Leu Val Gly Ala Pro Leu

1 5 10

<210> 74
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 74

Gly Asp Gly Arg His Asp Leu Leu Val Gly Ala Pro Leu
1 5 10

<210> 75
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(33)

<400> 75
aca gat gta aat gga gac gga aga cat gat tta
33
Thr Asp Val Asn Gly Asp Gly Arg His Asp Leu

1 5 10

<210> 76
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 76

Thr Asp Val Asn Gly Asp Gly Arg His Asp Leu
1 5 10

<210> 77
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(36)

<400> 77
gga gat gga aga cat gac tta tta gta gga gca cca
36
Gly Asp Gly Arg His Asp Leu Leu Val Gly Ala Pro

1 5 10

<210> 78
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 78

Gly Asp Gly Arg His Asp Leu Leu Val Gly Ala Pro
1 5 10

<210> 79
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(42)

<400> 79
gga gac gga aga cat gat tta tta gta gga gca cca tta tat
42
Gly Asp Gly Arg His Asp Leu Leu Val Gly Ala Pro Leu Tyr

1 5 10

<210> 80
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 80

Gly Asp Gly Arg His Asp Leu Leu Val Gly Ala Pro Leu Tyr
1 5 10

<210> 81
<211> 681
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(681)

<400> 81
gaa ttt gac ggt gat ctt aat acg act gag tac gtc gtc gga gca cca
48
Glu Phe Asp Gly Asp Leu Asn Thr Thr Glu Tyr Val Val Gly Ala Pro
1 5 10 15

act tgg tcg tgg aca tta ggc gca gtc gag ata ctc gac agt tat tat
96
Thr Trp Ser Trp Thr Leu Gly Ala Val Glu Ile Leu Asp Ser Tyr Tyr
20 25 30

cag agg tta cat aga tta cgt gca gaa cag atg gcg tcc tac ttt ggt 1
44
Gln Arg Leu His Arg Leu Arg Ala Glu Gln Met Ala Ser Tyr Phe Gly
35 40 45

cac agc gta gcg gta acg gat gtg aac gga gac ggc cgc cat gac ttg 1
92
His Ser Val Ala Val Thr Asp Val Asn Gly Asp Gly Arg His Asp Leu
50 55 60

cta gtt gga gct ccg ctc tac atg gag agt cga gca gat cgc aag ctt 2
40
Leu Val Gly Ala Pro Leu Tyr Met Glu Ser Arg Ala Asp Arg Lys Leu
65 70 75 80

gct gaa gtg ggc cga gta tat ctt ttc ctt caa cca cgg ggt ccc cac 2
88
Ala Glu Val Gly Arg Val Tyr Leu Phe Leu Gln Pro Arg Gly Pro His
85 90 95

gcc cta ggc gct cct agt tta ttg tta acc gga aca cag ttg tat ggt 3
36
Ala Leu Gly Ala Pro Ser Leu Leu Leu Thr Gly Thr Gln Leu Tyr Gly
100 105 110

aga ttc gga tct gca ata gcg cca ctc ggg gat ttg gat aga gat ggc 3
84
Arg Phe Gly Ser Ala Ile Ala Pro Leu Gly Asp Leu Asp Arg Asp Gly
115 120 125

tat aac gat ata gct gtg gcc gcc cct tac gga gga ccc tcc ggc aga 4
32
Tyr Asn Asp Ile Ala Val Ala Ala Pro Tyr Gly Gly Pro Ser Gly Arg
130 135 140

ggg cag gtt ctg gtt ttc cta ggg caa agt gaa ggg tta agg tca aga 4
80
Gly Gln Val Leu Val Phe Leu Gly Gln Ser Glu Gly Leu Arg Ser Arg
145 150 155 160

ccg tct caa gtc tta gac tcg cca ttt cca acc gga agt gcg ttt ggg 5
28
Pro Ser Gln Val Leu Asp Ser Pro Phe Pro Thr Gly Ser Ala Phe Gly
165 170 175

ttc agt ctc cgt ggt gca gtg gac atc gat gac aat ggt tac ccg gat 5
76
Phe Ser Leu Arg Gly Ala Val Asp Ile Asp Asp Asn Gly Tyr Pro Asp
180 185 190

cta att gtt gga gcc tac ggg gcc aat caa gta gca gta tat cgg gcg 6
24
Leu Ile Val Gly Ala Tyr Gly Ala Asn Gln Val Ala Val Tyr Arg Ala
195 200 205

cag ccc gta gtt aaa gct tca gtc caa ctg ctg ctg caa gac agc ctg 6
72
Gln Pro Val Val Lys Ala Ser Val Gln Leu Leu Leu Gln Asp Ser Leu
210 215 220

aac cct gca 6
81
Asn Pro Ala
225

<210> 82
<211> 227
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 82

Glu Phe Asp Gly Asp Leu Asn Thr Thr Glu Tyr Val Val Gly Ala Pro
1 5 10 15

Thr Trp Ser Trp Thr Leu Gly Ala Val Glu Ile Leu Asp Ser Tyr Tyr
20 25 30

Gln Arg Leu His Arg Leu Arg Ala Glu Gln Met Ala Ser Tyr Phe Gly
35 40 45

His Ser Val Ala Val Thr Asp Val Asn Gly Asp Gly Arg His Asp Leu
50 55 60

Leu Val Gly Ala Pro Leu Tyr Met Glu Ser Arg Ala Asp Arg Lys Leu
65 70 75 80

Ala Glu Val Gly Arg Val Tyr Leu Phe Leu Gln Pro Arg Gly Pro His

85 90 95

Ala Leu Gly Ala Pro Ser Leu Leu Leu Thr Gly Thr Gln Leu Tyr Gly
100 105 110

Arg Phe Gly Ser Ala Ile Ala Pro Leu Gly Asp Leu Asp Arg Asp Gly
115 120 125

Tyr Asn Asp Ile Ala Val Ala Ala Pro Tyr Gly Gly Pro Ser Gly Arg
130 135 140

Gly Gln Val Leu Val Phe Leu Gly Gln Ser Glu Gly Leu Arg Ser Arg
145 150 155 160

Pro Ser Gln Val Leu Asp Ser Pro Phe Pro Thr Gly Ser Ala Phe Gly
165 170 175

Phe Ser Leu Arg Gly Ala Val Asp Ile Asp Asp Asn Gly Tyr Pro Asp
180 185 190

Leu Ile Val Gly Ala Tyr Gly Ala Asn Gln Val Ala Val Tyr Arg Ala
195 200 205

Gln Pro Val Val Lys Ala Ser Val Gln Leu Leu Leu Gln Asp Ser Leu
210 215 220

Asn Pro Ala
225

<210> 83
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(60)

<400> 83
gca gta aca gat gta aat gga gac gga aga cat gat tta tta gta gga
48
Ala Val Thr Asp Val Asn Gly Asp Gly Arg His Asp Leu Leu Val Gly

1 5 10 15

gca cca tta tat
60
Ala Pro Leu Tyr

20

<210> 84
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 84

Ala Val Thr Asp Val Asn Gly Asp Gly Arg His Asp Leu Leu Val Gly
1 5 10 15

Ala Pro Leu Tyr
20

<210> 85
<211> 882
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>

<221> CDS
<222> (1)..(882)

<400> 85
ttt tcc tca gtc gtg aca caa gct ggc gag tta gta ttg ggg gct ccc
48
Phe Ser Ser Val Val Thr Gln Ala Gly Glu Leu Val Leu Gly Ala Pro

1 5 10 15

gga ggc tac tac ttc ctg ggg cta ctc gca cag gca ccc gtg gcg gac
96
Gly Gly Tyr Tyr Phe Leu Gly Leu Leu Ala Gln Ala Pro Val Ala Asp

20 25 30

ata ttc tcg tct tat aga cct ggg att ttg ttg tgg cac gtc tcc tct 1
44
Ile Phe Ser Ser Tyr Arg Pro Gly Ile Leu Leu Trp His Val Ser Ser

35 40 45

cag tct tta agt ttc gat agt agc aat cca gaa tat ttt gac gga tac 1
92
Gln Ser Leu Ser Phe Asp Ser Ser Asn Pro Glu Tyr Phe Asp Gly Tyr

50 55 60

tgg ggg tat tct gtg gca gtc ggt gag ttc gat ggt gat ctg aat act 2
40
Trp Gly Tyr Ser Val Ala Val Gly Glu Phe Asp Gly Asp Leu Asn Thr

65 70 75 80

aca gaa tat gtg gta ggg gct cct aca tgg agt tgg act tta ggc gcg 2
88
Thr Glu Tyr Val Val Gly Ala Pro Thr Trp Ser Trp Thr Leu Gly Ala

85 90 95

gtc gag ata tta gat agc tac tac caa cgc tta cac aga ttg cgt gct 3
36

Val Glu Ile Leu Asp Ser Tyr Tyr Gln Arg Leu His Arg Leu Arg Ala
100 105 110

gaa caa atg gcc tcc tac ttt ggt cat tca gtc gcc gtt acc gat gtg 384
Glu Gln Met Ala Ser Tyr Phe Gly His Ser Val Ala Val Thr Asp Val
115 120 125

aat ggt gat gga cgg cat gac ctc cta gtt gga gct cca ctt tac atg 432
Asn Gly Asp Gly Arg His Asp Leu Leu Val Gly Ala Pro Leu Tyr Met
130 135 140

gag agc aga gcg gac cga aag tta gct gaa gta gga aga gtt tat ttg 480
Glu Ser Arg Ala Asp Arg Lys Leu Ala Glu Val Gly Arg Val Tyr Leu
145 150 155 160

ttc cta caa ccg agg ggc ccg cat gcg ctt ggc gca cct tcc tta ctt 528
Phe Leu Gln Pro Arg Gly Pro His Ala Leu Gly Ala Pro Ser Leu Leu
165 170 175

ctg acc ggt acg caa ctt tac ggg cga ttt ggg tcg gcc att gcg cca 576
Leu Thr Gly Thr Gln Leu Tyr Gly Arg Phe Gly Ser Ala Ile Ala Pro
180 185 190

ctg ggg gac ctt gat cgc gac gga tat aac gac atc gca gtt gcc gcg 624
Leu Gly Asp Leu Asp Arg Asp Gly Tyr Asn Asp Ile Ala Val Ala Ala
195 200 205

cct tat gga ggc cca tcg ggt cgg gga cag gtt cta gtg ttc ctc ggt 672

72
Pro Tyr Gly Gly Pro Ser Gly Arg Gly Gln Val Leu Val Phe Leu Gly
210 215 220

caa agt gaa ggc ctc cgt agt aga ccg agc cag gta ctg gac agt ccg 7
20
Gln Ser Glu Gly Leu Arg Ser Arg Pro Ser Gln Val Leu Asp Ser Pro
225 230 235 240

ttt ccc acg ggc tcg gct ttt ggt ttt tca tta aga ggt gcg gta gac 7
68
Phe Pro Thr Gly Ser Ala Phe Gly Phe Ser Leu Arg Gly Ala Val Asp
245 250 255

atc gat gat aac gga tac ccc gat ctc ata gta ggg gcc tat ggc gcc 8
16
Ile Asp Asp Asn Gly Tyr Pro Asp Leu Ile Val Gly Ala Tyr Gly Ala
260 265 270

aac cag gtc gca gtt tat agg gcc cag cca gta gtg aaa gca tca gtc 8
64
Asn Gln Val Ala Val Tyr Arg Ala Gln Pro Val Val Lys Ala Ser Val
275 280 285

caa tta cta gtt cag gac 8
82
Gln Leu Leu Val Gln Asp
290

<210> 86
<211> 294
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Integrin

<400> 86

Phe Ser Ser Val Val Thr Gln Ala Gly Glu Leu Val Leu Gly Ala Pro
1 5 10 15

Gly Gly Tyr Tyr Phe Leu Gly Leu Leu Ala Gln Ala Pro Val Ala Asp
20 25 30

Ile Phe Ser Ser Tyr Arg Pro Gly Ile Leu Leu Trp His Val Ser Ser
35 40 45

Gln Ser Leu Ser Phe Asp Ser Ser Asn Pro Glu Tyr Phe Asp Gly Tyr
50 55 60

Trp Gly Tyr Ser Val Ala Val Gly Glu Phe Asp Gly Asp Leu Asn Thr
65 70 75 80

Thr Glu Tyr Val Val Gly Ala Pro Thr Trp Ser Trp Thr Leu Gly Ala
85 90 95

Val Glu Ile Leu Asp Ser Tyr Tyr Gln Arg Leu His Arg Leu Arg Ala
100 105 110

Glu Gln Met Ala Ser Tyr Phe Gly His Ser Val Ala Val Thr Asp Val
115 120 125

Asn Gly Asp Gly Arg His Asp Leu Leu Val Gly Ala Pro Leu Tyr Met
130 135 140

Glu Ser Arg Ala Asp Arg Lys Leu Ala Glu Val Gly Arg Val Tyr Leu
145 150 155 160

Phe Leu Gln Pro Arg Gly Pro His Ala Leu Gly Ala Pro Ser Leu Leu
165 170 175

Leu Thr Gly Thr Gln Leu Tyr Gly Arg Phe Gly Ser Ala Ile Ala Pro
180 185 190

Leu Gly Asp Leu Asp Arg Asp Gly Tyr Asn Asp Ile Ala Val Ala Ala
195 200 205

Pro Tyr Gly Gly Pro Ser Gly Arg Gly Gln Val Leu Val Phe Leu Gly
210 215 220

Gln Ser Glu Gly Leu Arg Ser Arg Pro Ser Gln Val Leu Asp Ser Pro
225 230 235 240

Phe Pro Thr Gly Ser Ala Phe Gly Phe Ser Leu Arg Gly Ala Val Asp
245 250 255

Ile Asp Asp Asn Gly Tyr Pro Asp Leu Ile Val Gly Ala Tyr Gly Ala
260 265 270

Asn Gln Val Ala Val Tyr Arg Ala Gln Pro Val Val Lys Ala Ser Val
275 280 285

Gln Leu Leu Val Gln Asp
290

<210> 87
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(21)

<400> 87
gta gaa aat gat ttt agt tgg
21

Val Glu Asn Asp Phe Ser Trp

1 5

<210> 88
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 88

Val Glu Asn Asp Phe Ser Trp
1 5

<210> 89
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(15)

<400> 89
gga gaa tta gta tta
15
Gly Glu Leu Val Leu

1 5

<210> 90
<211> 5
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Integrin

<400> 90

Gly Glu Leu Val Leu
1 5

<210> 91
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(39)

<400> 91
gat tta tat tat tta atg gac tta agt tac agt atg aaa
39
Asp Leu Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met Lys

1 5 10

<210> 92
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 92

Asp Leu Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met Lys
1 5 10

<210> 93
<211> 16
<212> PRT
<213> Artificial

<220>
<223> Integrin

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Integrin

<220>
<221> misc_feature
<222> (2)..(6)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (8)..(8)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (10)..(10)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (12)..(12)
<223> Xaa can be any naturally occurring amino acid

<400> 93

Asp Xaa Xaa Xaa Xaa Xaa Asp Xaa Ser Xaa Ser Xaa Lys Asp Asp Leu
1 5 10 15

<210> 94
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(324)

<400> 94
tac tgc cga aaa gaa aac tca tcg gaa ata tgt agt aac aat ggg gag 48
Tyr Cys Arg Lys Glu Asn Ser Ser Glu Ile Cys Ser Asn Asn Gly Glu
1 5 10 15

tgc gtc tgc ggc caa tgt gta tgc cgg aaa cgt gac aac aca aac gaa 96
Cys Val Cys Gly Gln Cys Val Cys Arg Lys Arg Asp Asn Thr Asn Glu
20 25 30

atc tat agt gga aag ttt tgt gag tgt gat aat ttc aac tgt gat cgc 144
Ile Tyr Ser Gly Lys Phe Cys Glu Cys Asp Asn Phe Asn Cys Asp Arg
35 40 45

agc aat ggc tta ata tgc ggt ggc aat gga gtt tgc aag tgt agg gtg 192
Ser Asn Gly Leu Ile Cys Gly Gly Asn Gly Val Cys Lys Cys Arg Val
50 55 60

tgt gaa tgc aat cca aat tat aca ggg agt gca tgc gat tgc tct tta 240
Cys Glu Cys Asn Pro Asn Tyr Thr Gly Ser Ala Cys Asp Cys Ser Leu
65 70 75 80

gac act agt acg tgc gag gca tcc aac ggg cag ata tgt aat gga aga 288
Asp Thr Ser Thr Cys Glu Ala Ser Asn Gly Gln Ile Cys Asn Gly Arg
85 90 95

ggt att tgt gag tgt ggt gta tgc aaa tgt acc gac 324
Gly Ile Cys Glu Cys Gly Val Cys Lys Cys Thr Asp

100 105

<210> 95
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 95

Tyr Cys Arg Lys Glu Asn Ser Ser Glu Ile Cys Ser Asn Asn Gly Glu
1 5 10 15

Cys Val Cys Gly Gln Cys Val Cys Arg Lys Arg Asp Asn Thr Asn Glu
20 25 30

Ile Tyr Ser Gly Lys Phe Cys Glu Cys Asp Asn Phe Asn Cys Asp Arg
35 40 45

Ser Asn Gly Leu Ile Cys Gly Gly Asn Gly Val Cys Lys Cys Arg Val
50 55 60

Cys Glu Cys Asn Pro Asn Tyr Thr Gly Ser Ala Cys Asp Cys Ser Leu
65 70 75 80

Asp Thr Ser Thr Cys Glu Ala Ser Asn Gly Gln Ile Cys Asn Gly Arg
85 90 95

Gly Ile Cys Glu Cys Gly Val Cys Lys Cys Thr Asp
100 105

<210> 96
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(21)

<400> 96
tgt aca agt gaa caa aat tgc
21
Cys Thr Ser Glu Gln Asn Cys

1 5

<210> 97
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 97

Cys Thr Ser Glu Gln Asn Cys
1 5

<210> 98
<211> 708
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(708)

<400> 98
tta cga tta cgc tcg ggc gaa ccc cag aca ttt acg ctt aag ttc aaa
48
Leu Arg Leu Arg Ser Gly Glu Pro Gln Thr Phe Thr Leu Lys Phe Lys

1 5 10 15

cgg gct gag gat tat cct atc gac ctt tac tat ctt atg gat ctc tca 96
Arg Ala Glu Asp Tyr Pro Ile Asp Leu Tyr Tyr Leu Met Asp Leu Ser
20 25 30

tat agt atg aaa gat gat ctg gag aat gtt aag tcc tta ggg acc gat 144
Tyr Ser Met Lys Asp Asp Leu Glu Asn Val Lys Ser Leu Gly Thr Asp
35 40 45

tta atg aac gag atg aga aga atc act tca gac ttc aga att gga ttt 192
Leu Met Asn Glu Met Arg Arg Ile Thr Ser Asp Phe Arg Ile Gly Phe
50 55 60

ggc tct ttt gtc gaa aaa acc gta atg cca tac ata agc aca acc cca 240
Gly Ser Phe Val Glu Lys Thr Val Met Pro Tyr Ile Ser Thr Thr Pro
65 70 75 80

gca aag ctg agg aat ccg tgt aca tcg gag caa aac tgc act act ccc 288
Ala Lys Leu Arg Asn Pro Cys Thr Ser Glu Gln Asn Cys Thr Thr Pro
85 90 95

ttc agt tat aag aat gtt ctc agt ctg acg aac aaa ggg gaa gta ttt 336
Phe Ser Tyr Lys Asn Val Leu Ser Leu Thr Asn Lys Gly Glu Val Phe
100 105 110

aac gag cta gtg gga aaa cag aga att agc ggt aac ctc gac tct cca 384
Asn Glu Leu Val Gly Lys Gln Arg Ile Ser Gly Asn Leu Asp Ser Pro

115 120 125

gaa ggt ggt ttt gat gca att atg caa gtt gca gtg tgt gga tct cta 4
32
Glu Gly Gly Phe Asp Ala Ile Met Gln Val Ala Val Cys Gly Ser Leu
130 135 140

ata ggg tgg cgt aat gta act aga cta ttg gtg ttt tcc acc gac gcc 4
80
Ile Gly Trp Arg Asn Val Thr Arg Leu Leu Val Phe Ser Thr Asp Ala
145 150 155 160

ggc ttc cac ttc gct gga gac ggc aag cta ggg gga atc gta ttg cct 5
28
Gly Phe His Phe Ala Gly Asp Gly Lys Leu Gly Gly Ile Val Leu Pro
165 170 175

aac gat ggt cag tgc cat ttg gaa aat aat atg tat acg atg tcg cac 5
76
Asn Asp Gly Gln Cys His Leu Glu Asn Asn Met Tyr Thr Met Ser His
180 185 190

tac tac gac tac cca tcc ata gcc cat tta gtc caa aag ctg agc gaa 6
24
Tyr Tyr Asp Tyr Pro Ser Ile Ala His Leu Val Gln Lys Leu Ser Glu
195 200 205

aac aat att caa aca ata ttt gcg gta acg gaa gag ttc cag cca gtc 6
72
Asn Asn Ile Gln Thr Ile Phe Ala Val Thr Glu Glu Phe Gln Pro Val
210 215 220

tat aag gag ctt aaa aat ctc atc ccg aaa tca gcg 7
08

Tyr Lys Glu Leu Lys Asn Leu Ile Pro Lys Ser Ala
225 230 235

<210> 99
<211> 236
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 99

Leu Arg Leu Arg Ser Gly Glu Pro Gln Thr Phe Thr Leu Lys Phe Lys
1 5 10 15

Arg Ala Glu Asp Tyr Pro Ile Asp Leu Tyr Tyr Leu Met Asp Leu Ser
20 25 30

Tyr Ser Met Lys Asp Asp Leu Glu Asn Val Lys Ser Leu Gly Thr Asp
35 40 45

Leu Met Asn Glu Met Arg Arg Ile Thr Ser Asp Phe Arg Ile Gly Phe
50 55 60

Gly Ser Phe Val Glu Lys Thr Val Met Pro Tyr Ile Ser Thr Thr Pro
65 70 75 80

Ala Lys Leu Arg Asn Pro Cys Thr Ser Glu Gln Asn Cys Thr Thr Pro
85 90 95

Phe Ser Tyr Lys Asn Val Leu Ser Leu Thr Asn Lys Gly Glu Val Phe
100 105 110

Asn Glu Leu Val Gly Lys Gln Arg Ile Ser Gly Asn Leu Asp Ser Pro
115 120 125

Glu Gly Gly Phe Asp Ala Ile Met Gln Val Ala Val Cys Gly Ser Leu
130 135 140

Ile Gly Trp Arg Asn Val Thr Arg Leu Leu Val Phe Ser Thr Asp Ala
145 150 155 160

Gly Phe His Phe Ala Gly Asp Gly Lys Leu Gly Gly Ile Val Leu Pro
165 170 175

Asn Asp Gly Gln Cys His Leu Glu Asn Asn Met Tyr Thr Met Ser His
180 185 190

Tyr Tyr Asp Tyr Pro Ser Ile Ala His Leu Val Gln Lys Leu Ser Glu
195 200 205

Asn Asn Ile Gln Thr Ile Phe Ala Val Thr Glu Glu Phe Gln Pro Val
210 215 220

Tyr Lys Glu Leu Lys Asn Leu Ile Pro Lys Ser Ala
225 230 235

<210> 100
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(36)

<400> 100
aac aag gga gaa gta ttt aat gag tta gta gga aaa
36
Asn Lys Gly Glu Val Phe Asn Glu Leu Val Gly Lys
1 5 10

<210> 101
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 101

Asn Lys Gly Glu Val Phe Asn Glu Leu Val Gly Lys
1 5 10

<210> 102
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(15)

<400> 102
aca gca gaa aaa tta
15
Thr Ala Glu Lys Leu

1 5

<210> 103
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 103

Thr Ala Glu Lys Leu
1 5

<210> 104
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(78)

<400> 104
gat tac cca ata gac tta tac tat tta atg gac tta agt tat agt atg
48
Asp Tyr Pro Ile Asp Leu Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met

1 5 10 15

aag gat gat tta gaa gta aaa agt tta gga
78
Lys Asp Asp Leu Glu Val Lys Ser Leu Gly

20 25

<210> 105
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 105

Asp Tyr Pro Ile Asp Leu Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met
1 5 10 15

Lys Asp Asp Leu Glu Val Lys Ser Leu Gly

20 25

<210> 106
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(60)

<400> 106
aat gta aag agt tta gga aca gca tta atg aga gag atg gaa aaa ata
48
Asn Val Lys Ser Leu Gly Thr Ala Leu Met Arg Glu Met Glu Lys Ile

1 5 10 15

aca agt gat ttt
60
Thr Ser Asp Phe

20

<210> 107
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 107

Asn Val Lys Ser Leu Gly Thr Ala Leu Met Arg Glu Met Glu Lys Ile
1 5 10 15

Thr Ser Asp Phe
20

<210> 108
<211> 744
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(744)

<400> 108
gga caa aaa cag tta agt ccg cag aag gtc act cta tac ttg cgt ccc
48
Gly Gln Lys Gln Leu Ser Pro Gln Lys Val Thr Leu Tyr Leu Arg Pro

1 5 10 15

ggg caa gca gcc gcg ttc aac gta acg ttt cgt cgc gca aaa gga tac
96
Gly Gln Ala Ala Ala Phe Asn Val Thr Phe Arg Arg Ala Lys Gly Tyr

20 25 30

cca ata gac ctt tat tat tta atg gat tta tcc tac tca atg ctc gat 1
44
Pro Ile Asp Leu Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met Leu Asp

35 40 45

gat tta aga aac gtt aag aag tta ggc ggg gat ctg ctc aga gct ctc 1
92
Asp Leu Arg Asn Val Lys Lys Leu Gly Gly Asp Leu Leu Arg Ala Leu

50 55 60

aat gag ata act gaa agt ggt cgg ata ggt ttc ggt tcg ttc gtt gat 2
40
Asn Glu Ile Thr Glu Ser Gly Arg Ile Gly Phe Gly Ser Phe Val Asp

65 70 75 80

aag acg gtg ctg ccc ttt gta aat aca cac cca gac aaa ctg agg aac 2
88
Lys Thr Val Leu Pro Phe Val Asn Thr His Pro Asp Lys Leu Arg Asn
85 90 95

ccc tgc cca aat aag gag aaa gaa tgc cag ccg cct ttc gct ttt cgc 3
36
Pro Cys Pro Asn Lys Glu Lys Glu Cys Gln Pro Pro Phe Ala Phe Arg
100 105 110

cat gtc cta aaa tta aca aat aat agc aat caa ttt cag acc gag gta 3
84
His Val Leu Lys Leu Thr Asn Asn Ser Asn Gln Phe Gln Thr Glu Val
115 120 125

gga aaa caa ctt att agt gga aac tta gac gcc cca gag ggc ggc tta 4
32
Gly Lys Gln Leu Ile Ser Gly Asn Leu Asp Ala Pro Glu Gly Gly Leu
130 135 140

gac gca atg atg caa gta gca gcc tgt ccg gag gaa att ggt tgg cgg 4
80
Asp Ala Met Met Gln Val Ala Ala Cys Pro Glu Glu Ile Gly Trp Arg
145 150 155 160

aat gtc acc agg ttg ttg gta ttt gcc act gac gat gga ttc cat ttt 5
28
Asn Val Thr Arg Leu Leu Val Phe Ala Thr Asp Asp Gly Phe His Phe
165 170 175

gct gga gat ggc aag cta ggg gcg att ctt acc cct aac gac ggg cga 5
76
Ala Gly Asp Gly Lys Leu Gly Ala Ile Leu Thr Pro Asn Asp Gly Arg

180 185 190

tgt cac ctc gaa gac aac cta tat aag aga agt aat gaa ttc gat tat 624
Cys His Leu Glu Asp Asn Leu Tyr Lys Arg Ser Asn Glu Phe Asp Tyr
195 200 205

cca tct gtg gga caa ctg gcg cat aag ttg gct gag aac aac ata cag 672
Pro Ser Val Gly Gln Leu Ala His Lys Leu Ala Glu Asn Asn Ile Gln
210 215 220

cca atc ttt gca gtt aca agt cga atg gtg aaa aca tac gaa aaa ctt 720
Pro Ile Phe Ala Val Thr Ser Arg Met Val Lys Thr Tyr Glu Lys Leu
225 230 235 240

acg gaa atc atc cct aaa agt gcg 744
Thr Glu Ile Ile Pro Lys Ser Ala
245

<210> 109
<211> 248
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 109

Gly Gln Lys Gln Leu Ser Pro Gln Lys Val Thr Leu Tyr Leu Arg Pro
1 5 10 15

Gly Gln Ala Ala Ala Phe Asn Val Thr Phe Arg Arg Ala Lys Gly Tyr

20 25 30

Pro Ile Asp Leu Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met Leu Asp
35 40 45

Asp Leu Arg Asn Val Lys Lys Leu Gly Gly Asp Leu Leu Arg Ala Leu
50 55 60

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

Lys Thr Val Leu Pro Phe Val Asn Thr His Pro Asp Lys Leu Arg Asn
85 90 95

Pro Cys Pro Asn Lys Glu Lys Glu Cys Gln Pro Pro Phe Ala Phe Arg
100 105 110

His Val Leu Lys Leu Thr Asn Asn Ser Asn Gln Phe Gln Thr Glu Val
115 120 125

Gly Lys Gln Leu Ile Ser Gly Asn Leu Asp Ala Pro Glu Gly Gly Leu
130 135 140

Asp Ala Met Met Gln Val Ala Ala Cys Pro Glu Glu Ile Gly Trp Arg
145 150 155 160

Asn Val Thr Arg Leu Leu Val Phe Ala Thr Asp Asp Gly Phe His Phe
165 170 175

Ala Gly Asp Gly Lys Leu Gly Ala Ile Leu Thr Pro Asn Asp Gly Arg
180 185 190

Cys His Leu Glu Asp Asn Leu Tyr Lys Arg Ser Asn Glu Phe Asp Tyr
195 200 205

Pro Ser Val Gly Gln Leu Ala His Lys Leu Ala Glu Asn Asn Ile Gln

210 215 220

Pro Ile Phe Ala Val Thr Ser Arg Met Val Lys Thr Tyr Glu Lys Leu
225 230 235 240

Thr Glu Ile Ile Pro Lys Ser Ala
245

<210> 110
<211> 783
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(783)

<400> 110
tac cca ata gat ctc tac tac ctg atg gat cta tcc tat tca atg ctg
48
Tyr Pro Ile Asp Leu Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met Leu

1 5 10 15

gac gat cta cgt aac gtt aag aaa ctt gga ggt gat tta cta aga gct
96
Asp Asp Leu Arg Asn Val Lys Lys Leu Gly Gly Asp Leu Leu Arg Ala

20 25 30

ctt aac gaa atc acg gag agt ggg cga atc ggc ttc ggc tca ttc gtc 1
44
Leu Asn Glu Ile Thr Glu Ser Gly Arg Ile Gly Phe Gly Ser Phe Val

35 40 45

gac aag aca gta ttg ccc ttc gta aac acg cac cca gac aag ctt aga 1
92

Asp Lys Thr Val Leu Pro Phe Val Asn Thr His Pro Asp Lys Leu Arg
50 55 60

aac ccc tgc cca aat aaa gag aaa gag tgt caa ccc ccg ttt gcc ttt 2
40
Asn Pro Cys Pro Asn Lys Glu Lys Glu Cys Gln Pro Pro Phe Ala Phe
65 70 75 80

aga cat gtc tta aag ctc acg aat aac agc aat cag ttt cag aca gaa 2
88
Arg His Val Leu Lys Leu Thr Asn Asn Ser Asn Gln Phe Gln Thr Glu
85 90 95

gtt gga aaa caa ctg ata tcg ggt aat cta gac gca cca gag ggg gga 3
36
Val Gly Lys Gln Leu Ile Ser Gly Asn Leu Asp Ala Pro Glu Gly Gly
100 105 110

ctt gat gcc atg atg cag gtg gca gcc tgc ccg gag gaa att ggg tgg 3
84
Leu Asp Ala Met Met Gln Val Ala Ala Cys Pro Glu Glu Ile Gly Trp
115 120 125

agg aat gtc aca aga ctg cta gtt ttc gca act gat gac ggg ttt cat 4
32
Arg Asn Val Thr Arg Leu Leu Val Phe Ala Thr Asp Asp Gly Phe His
130 135 140

ttt gct gga gat ggt aaa ctg ggc gca att ttg act cct aac gat gga 4
80
Phe Ala Gly Asp Gly Lys Leu Gly Ala Ile Leu Thr Pro Asn Asp Gly
145 150 155 160

cgg tgt cat ttg gaa gac aac ctc tat aaa aga agc aat gaa ttc gac 5

28
Arg Cys His Leu Glu Asp Asn Leu Tyr Lys Arg Ser Asn Glu Phe Asp
165 170 175

tat cct agt gta ggt caa tta gcg cac aag tta gca gaa aac aat ata 5
76
Tyr Pro Ser Val Gly Gln Leu Ala His Lys Leu Ala Glu Asn Asn Ile
180 185 190

caa ccg ata ttt gcg gtt acc agt cgc atg gtg aaa aca tac gaa aag 6
24
Gln Pro Ile Phe Ala Val Thr Ser Arg Met Val Lys Thr Tyr Glu Lys
195 200 205

tta acc gag ata att cca aaa tct gct gtg ggc gag ctc tcc gaa gat 6
72
Leu Thr Glu Ile Ile Pro Lys Ser Ala Val Gly Glu Leu Ser Glu Asp
210 215 220

agt agt aat gtc gta cac ttg atc aag aat gca tat aac aaa tta tct 7
20
Ser Ser Asn Val Val His Leu Ile Lys Asn Ala Tyr Asn Lys Leu Ser
225 230 235 240

agt aga gta ttt ttg gac cat aat gcg ctt cct gat act ctc aag gtg 7
68
Ser Arg Val Phe Leu Asp His Asn Ala Leu Pro Asp Thr Leu Lys Val
245 250 255

acc tat gac tcg ttc 7
83
Thr Tyr Asp Ser Phe
260

<210> 111
<211> 261
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 111

Tyr Pro Ile Asp Leu Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met Leu
1 5 10 15

Asp Asp Leu Arg Asn Val Lys Lys Leu Gly Gly Asp Leu Leu Arg Ala
20 25 30

Leu Asn Glu Ile Thr Glu Ser Gly Arg Ile Gly Phe Gly Ser Phe Val
35 40 45

Asp Lys Thr Val Leu Pro Phe Val Asn Thr His Pro Asp Lys Leu Arg
50 55 60

Asn Pro Cys Pro Asn Lys Glu Lys Glu Cys Gln Pro Pro Phe Ala Phe
65 70 75 80

Arg His Val Leu Lys Leu Thr Asn Asn Ser Asn Gln Phe Gln Thr Glu
85 90 95

Val Gly Lys Gln Leu Ile Ser Gly Asn Leu Asp Ala Pro Glu Gly Gly
100 105 110

Leu Asp Ala Met Met Gln Val Ala Ala Cys Pro Glu Glu Ile Gly Trp
115 120 125

Arg Asn Val Thr Arg Leu Leu Val Phe Ala Thr Asp Asp Gly Phe His
130 135 140

Phe Ala Gly Asp Gly Lys Leu Gly Ala Ile Leu Thr Pro Asn Asp Gly

145 150 155 160

Arg Cys His Leu Glu Asp Asn Leu Tyr Lys Arg Ser Asn Glu Phe Asp
165 170 175

Tyr Pro Ser Val Gly Gln Leu Ala His Lys Leu Ala Glu Asn Asn Ile
180 185 190

Gln Pro Ile Phe Ala Val Thr Ser Arg Met Val Lys Thr Tyr Glu Lys
195 200 205

Leu Thr Glu Ile Ile Pro Lys Ser Ala Val Gly Glu Leu Ser Glu Asp
210 215 220

Ser Ser Asn Val Val His Leu Ile Lys Asn Ala Tyr Asn Lys Leu Ser
225 230 235 240

Ser Arg Val Phe Leu Asp His Asn Ala Leu Pro Asp Thr Leu Lys Val
245 250 255

Thr Tyr Asp Ser Phe
260

<210> 112
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(15)

<400> 112
aga aat gta aaa aag
15
Arg Asn Val Lys Lys

1 5

<210> 113
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 113

Arg Asn Val Lys Lys
1 5

<210> 114
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(15)

<400> 114
caa cca cca ttt gca
15
Gln Pro Pro Phe Ala

1 5

<210> 115
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 115

Gln Pro Pro Phe Ala
1 5

<210> 116
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(18)

<400> 116
tta ata agt gga aat tta
18
Leu Ile Ser Gly Asn Leu

1 5

<210> 117
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 117

Leu Ile Ser Gly Asn Leu
1 5

<210> 118
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(15)

<400> 118
gga caa tta gca cat
15
Gly Gln Leu Ala His

1 5

<210> 119
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 119

Gly Gln Leu Ala His
1 5

<210> 120
<211> 267
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(267)

<400> 120
gag ctc tca gaa gat tct agt aat gtc gtc cat tta atc aaa aac gcc
48
Glu Leu Ser Glu Asp Ser Ser Asn Val Val His Leu Ile Lys Asn Ala

1 5 10 15

tat aac aaa cta agt tcg aga gtt ttc tta gac cac aat gca ctg cca
96
Tyr Asn Lys Leu Ser Ser Arg Val Phe Leu Asp His Asn Ala Leu Pro

20 25 30

gat acg ttg aag gta aca tac gac agc ttt tgc tcc aat ggg gtg acc 1
44
Asp Thr Leu Lys Val Thr Tyr Asp Ser Phe Cys Ser Asn Gly Val Thr

35 40 45

cat aga aac cag cca aga ggc gat tgt gac gga gta caa ata aat gta 1
92
His Arg Asn Gln Pro Arg Gly Asp Cys Asp Gly Val Gln Ile Asn Val

50 55 60

cca ata aca ttc cag gtt aag gtg aca gct act gag tgt ata caa gaa 2
40
Pro Ile Thr Phe Gln Val Lys Val Thr Ala Thr Glu Cys Ile Gln Glu

65 70 75 80

caa agt ttt gta att aga gcg ctt ggt 2
67
Gln Ser Phe Val Ile Arg Ala Leu Gly

85

<210> 121
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 121

Glu Leu Ser Glu Asp Ser Ser Asn Val Val His Leu Ile Lys Asn Ala
1 5 10 15

Tyr Asn Lys Leu Ser Ser Arg Val Phe Leu Asp His Asn Ala Leu Pro
20 25 30

Asp Thr Leu Lys Val Thr Tyr Asp Ser Phe Cys Ser Asn Gly Val Thr
35 40 45

His Arg Asn Gln Pro Arg Gly Asp Cys Asp Gly Val Gln Ile Asn Val
50 55 60

Pro Ile Thr Phe Gln Val Lys Val Thr Ala Thr Glu Cys Ile Gln Glu
65 70 75 80

Gln Ser Phe Val Ile Arg Ala Leu Gly
85

<210> 122
<211> 168
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(168)

<400> 122
ggt ttc acc gac att gta aca gta cag gta tta cca caa tgc gaa tgc
48
Gly Phe Thr Asp Ile Val Thr Val Gln Val Leu Pro Gln Cys Glu Cys

1 5 10 15

aga tgt aga gat caa agt aga gac aga agt tta tgc cat gga aag ggc

96
Arg Cys Arg Asp Gln Ser Arg Asp Arg Ser Leu Cys His Gly Lys Gly
20 25 30

ttt tta gaa tgt gga atc tgt aga tgc gat acg gga tat ata gga aaa 1
44
Phe Leu Glu Cys Gly Ile Cys Arg Cys Asp Thr Gly Tyr Ile Gly Lys
35 40 45

aat tgt gag tgt cag act caa ggg 1
68
Asn Cys Glu Cys Gln Thr Gln Gly
50 55

<210> 123
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 123

Gly Phe Thr Asp Ile Val Thr Val Gln Val Leu Pro Gln Cys Glu Cys
1 5 10 15

Arg Cys Arg Asp Gln Ser Arg Asp Arg Ser Leu Cys His Gly Lys Gly
20 25 30

Phe Leu Glu Cys Gly Ile Cys Arg Cys Asp Thr Gly Tyr Ile Gly Lys
35 40 45

Asn Cys Glu Cys Gln Thr Gln Gly
50 55

<210> 124

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

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(45)

<400> 124
tgt aat gca ttt aag ata tta gta gta ata aca gat gga gaa aaa
45
Cys Asn Ala Phe Lys Ile Leu Val Val Ile Thr Asp Gly Glu Lys

1 5 10 15

<210> 125
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 125

Cys Asn Ala Phe Lys Ile Leu Val Val Ile Thr Asp Gly Glu Lys
1 5 10 15

<210> 126
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(60)

<400> 126
aca gga ata aga aag gta gta aga gaa tta ttt aat ata aca aac gga
48
Thr Gly Ile Arg Lys Val Val Arg Glu Leu Phe Asn Ile Thr Asn Gly

1 5 10 15

gca aga aaa aat
60
Ala Arg Lys Asn

20

<210> 127
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 127

Thr Gly Ile Arg Lys Val Val Arg Glu Leu Phe Asn Ile Thr Asn Gly
1 5 10 15

Ala Arg Lys Asn
20

<210> 128
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(75)

<400> 128

gat tta agt tat agt ctc gac gat ctg aga aat gta aag aaa ctt gga
48
Asp Leu Ser Tyr Ser Leu Asp Asp Leu Arg Asn Val Lys Lys Leu Gly

1 5 10 15

gga gac cta tta aga gca ttg aac gaa
75
Gly Asp Leu Leu Arg Ala Leu Asn Glu

20 25

<210> 129
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 129

Asp Leu Ser Tyr Ser Leu Asp Asp Leu Arg Asn Val Lys Lys Leu Gly
1 5 10 15

Gly Asp Leu Leu Arg Ala Leu Asn Glu
20 25

<210> 130
<211> 189
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(189)

<400> 130
gac tat ccc gta gac ata tac tac ctt atg gat tta agt tac tcc atg

48
Asp Tyr Pro Val Asp Ile Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met
1 5 10 15

aag gac gat ctc tgg tca att cag aac ttg gga aca aaa cta gca aca
96
Lys Asp Asp Leu Trp Ser Ile Gln Asn Leu Gly Thr Lys Leu Ala Thr
20 25 30

caa atg aga aag ctg aca tcg aat tta aga ata gga ttt gga gca ttc 1
44
Gln Met Arg Lys Leu Thr Ser Asn Leu Arg Ile Gly Phe Gly Ala Phe
35 40 45

gta gat aaa cca gta agc cct tat atg tat atc tct cca ccg gaa 1
89
Val Asp Lys Pro Val Ser Pro Tyr Met Tyr Ile Ser Pro Pro Glu
50 55 60

<210> 131
<211> 63
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 131

Asp Tyr Pro Val Asp Ile Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met
1 5 10 15

Lys Asp Asp Leu Trp Ser Ile Gln Asn Leu Gly Thr Lys Leu Ala Thr
20 25 30

Gln Met Arg Lys Leu Thr Ser Asn Leu Arg Ile Gly Phe Gly Ala Phe
35 40 45

Val Asp Lys Pro Val Ser Pro Tyr Met Tyr Ile Ser Pro Pro Glu
50 55 60

<210> 132
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(45)

<400> 132
gac gca cca gaa gga gga ttt gat gca ata atg caa gca aca gta
45
Asp Ala Pro Glu Gly Gly Phe Asp Ala Ile Met Gln Ala Thr Val

1 5 10 15

<210> 133
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 133

Asp Ala Pro Glu Gly Gly Phe Asp Ala Ile Met Gln Ala Thr Val
1 5 10 15

<210> 134
<211> 363
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(363)

<400> 134

ttt tcc ata cag gtt cga cag gta gag gat tat cca gta gac atc tat
48
Phe Ser Ile Gln Val Arg Gln Val Glu Asp Tyr Pro Val Asp Ile Tyr
1 5 10 15

tac tta atg gac tta agc tat agt atg aag gac gat ctc tgg agt ata
96
Tyr Leu Met Asp Leu Ser Tyr Ser Met Lys Asp Asp Leu Trp Ser Ile
20 25 30

caa aat tta ggt acc aag ttg gcc acc caa atg cgt aaa tta act tca 1
44
Gln Asn Leu Gly Thr Lys Leu Ala Thr Gln Met Arg Lys Leu Thr Ser
35 40 45

aat tta cgg ata gga ttc ggg gca ttt gtg gat aaa ccc gta tcg ccg 1
92
Asn Leu Arg Ile Gly Phe Gly Ala Phe Val Asp Lys Pro Val Ser Pro
50 55 60

tac atg tat att agt cca cct gag gcg ctt gaa aac ccc tgc tac gac 2
40
Tyr Met Tyr Ile Ser Pro Pro Glu Ala Leu Glu Asn Pro Cys Tyr Asp
65 70 75 80

atg aaa aca acg tgt ctg cct atg ttt ggc tac aag cat gtc cta aca 2
88
Met Lys Thr Thr Cys Leu Pro Met Phe Gly Tyr Lys His Val Leu Thr
85 90 95

tta acg gat caa gtc act agg ttc aac gag gaa gtt aaa aag cag agt 3
36
Leu Thr Asp Gln Val Thr Arg Phe Asn Glu Glu Val Lys Lys Gln Ser
100 105 110

gtg tct cgc aat aga gat gct ccg gaa 3
63
Val Ser Arg Asn Arg Asp Ala Pro Glu
115 120

<210> 135
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 135

Phe Ser Ile Gln Val Arg Gln Val Glu Asp Tyr Pro Val Asp Ile Tyr
1 5 10 15

Tyr Leu Met Asp Leu Ser Tyr Ser Met Lys Asp Asp Leu Trp Ser Ile
20 25 30

Gln Asn Leu Gly Thr Lys Leu Ala Thr Gln Met Arg Lys Leu Thr Ser
35 40 45

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

Tyr Met Tyr Ile Ser Pro Pro Glu Ala Leu Glu Asn Pro Cys Tyr Asp
65 70 75 80

Met Lys Thr Thr Cys Leu Pro Met Phe Gly Tyr Lys His Val Leu Thr

85 90 95

Leu Thr Asp Gln Val Thr Arg Phe Asn Glu Glu Val Lys Lys Gln Ser
100 105 110

Val Ser Arg Asn Arg Asp Ala Pro Glu
115 120

<210> 136
<211> 87
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(87)

<400> 136
gga gta agt agt tgc cag caa tgt tta gca gta agt cca atg tgt gca
48
Gly Val Ser Ser Cys Gln Gln Cys Leu Ala Val Ser Pro Met Cys Ala

1 5 10 15

tgg tgc agt gat gaa gca tta cca tta gga agt cca aga
87
Trp Cys Ser Asp Glu Ala Leu Pro Leu Gly Ser Pro Arg

20 25

<210> 137
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 137

Gly Val Ser Ser Cys Gln Gln Cys Leu Ala Val Ser Pro Met Cys Ala
1 5 10 15

Trp Cys Ser Asp Glu Ala Leu Pro Leu Gly Ser Pro Arg
20 25

<210> 138
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(63)

<400> 138
gta tta gaa gac aga cca tta agt gat aaa gga agt gga gat agt agt
48
Val Leu Glu Asp Arg Pro Leu Ser Asp Lys Gly Ser Gly Asp Ser Ser
1 5 10 15

caa gta aca cag gta
63
Gln Val Thr Gln Val
20

<210> 139
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 139

Val Leu Glu Asp Arg Pro Leu Ser Asp Lys Gly Ser Gly Asp Ser Ser
1 5 10 15

Gln Val Thr Gln Val
20

<210> 140
<211> 153
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(153)

<400> 140
aac atc aat tta ata ttt gca gtc aca gaa aac gta gtg aat ctt tac
48
Asn Ile Asn Leu Ile Phe Ala Val Thr Glu Asn Val Val Asn Leu Tyr
1 5 10 15

cag aac tat agt gag cta ata cca gga aca aca gta gga gtt ctc agt
96
Gln Asn Tyr Ser Glu Leu Ile Pro Gly Thr Thr Val Gly Val Leu Ser
20 25 30

atg gat agt agt aat gta ctg caa ttg att gta gac gca tat gga aaa 1
44
Met Asp Ser Ser Asn Val Leu Gln Leu Ile Val Asp Ala Tyr Gly Lys
35 40 45

ata aga agt 1
53
Ile Arg Ser

50

<210> 141
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 141

Asn Ile Asn Leu Ile Phe Ala Val Thr Glu Asn Val Val Asn Leu Tyr
1 5 10 15

Gln Asn Tyr Ser Glu Leu Ile Pro Gly Thr Thr Val Gly Val Leu Ser
20 25 30

Met Asp Ser Ser Asn Val Leu Gln Leu Ile Val Asp Ala Tyr Gly Lys
35 40 45

Ile Arg Ser
50

<210> 142
<211> 123
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(123)

<400> 142
ata gga ttt gga gca ttc gta gac aaa cca gta agt cct tac atg tat
48
Ile Gly Phe Gly Ala Phe Val Asp Lys Pro Val Ser Pro Tyr Met Tyr

1 5 10 15

ata agt cca ccc gaa gca tta gag aat cca tgc tac gat atg aag aca
96
Ile Ser Pro Pro Glu Ala Leu Glu Asn Pro Cys Tyr Asp Met Lys Thr

20 25 30

aca tgt tta ccg atg ttt gga tat aaa 1
23
Thr Cys Leu Pro Met Phe Gly Tyr Lys

35 40

<210> 143
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 143

Ile Gly Phe Gly Ala Phe Val Asp Lys Pro Val Ser Pro Tyr Met Tyr
1 5 10 15

Ile Ser Pro Pro Glu Ala Leu Glu Asn Pro Cys Tyr Asp Met Lys Thr
20 25 30

Thr Cys Leu Pro Met Phe Gly Tyr Lys
35 40

<210> 144
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(36)

<400> 144
agt gta agt aga aat aga gat gca cca gaa gga gga
36
Ser Val Ser Arg Asn Arg Asp Ala Pro Glu Gly Gly

1 5 10

<210> 145
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 145

Ser Val Ser Arg Asn Arg Asp Ala Pro Glu Gly Gly
1 5 10

<210> 146
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(33)

<400> 146
agt gat agt aga aat aga gat gca cca gaa gga
33
Ser Asp Ser Arg Asn Arg Asp Ala Pro Glu Gly

1 5 10

<210> 147
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 147

Ser Asp Ser Arg Asn Arg Asp Ala Pro Glu Gly
1 5 10

<210> 148
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(15)

<400> 148
aga aat aga gat gca
15
Arg Asn Arg Asp Ala

1 5

<210> 149
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 149

Arg Asn Arg Asp Ala
1 5

<210> 150
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(45)

<400> 150
gat gca cca gaa gga gga ttt gac gca ata atg caa gca aca gta
45
Asp Ala Pro Glu Gly Gly Phe Asp Ala Ile Met Gln Ala Thr Val
1 5 10 15

<210> 151
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 151

Asp Ala Pro Glu Gly Gly Phe Asp Ala Ile Met Gln Ala Thr Val
1 5 10 15

<210> 152
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(45)

<400> 152
gat gca cca gaa gga gga ttt gac gca ata atg caa gca aca gta
45
Asp Ala Pro Glu Gly Gly Phe Asp Ala Ile Met Gln Ala Thr Val

1 5 10 15

<210> 153
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 153

Asp Ala Pro Glu Gly Gly Phe Asp Ala Ile Met Gln Ala Thr Val
1 5 10 15

<210> 154
<211> 258
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(258)

<400> 154
gat gcg cca gaa ggt ggg ttt gac gcg atc atg caa gct aca gtg tgc
48
Asp Ala Pro Glu Gly Gly Phe Asp Ala Ile Met Gln Ala Thr Val Cys

1 5 10 15

gac gaa aaa ata ggc tgg aga aac gat gca agt cac ctc ctt gtc ttc
96
Asp Glu Lys Ile Gly Trp Arg Asn Asp Ala Ser His Leu Leu Val Phe
20 25 30

aca acc gat gca aaa aca cat att gcc ctg gac ggg aga ttg gcc ggc 1
44
Thr Thr Asp Ala Lys Thr His Ile Ala Leu Asp Gly Arg Leu Ala Gly
35 40 45

ata gtt caa cca aat gat ggt cag tgt cat gta gga tca gac aat cac 1
92
Ile Val Gln Pro Asn Asp Gly Gln Cys His Val Gly Ser Asp Asn His
50 55 60

tat tct gct agc act acg atg gat tac cca tcc tta gga tta atg aca 2
40
Tyr Ser Ala Ser Thr Thr Met Asp Tyr Pro Ser Leu Gly Leu Met Thr
65 70 75 80

gag aag cta tcg cag aag 2
58
Glu Lys Leu Ser Gln Lys
85

<210> 155
<211> 86
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 155

Asp Ala Pro Glu Gly Gly Phe Asp Ala Ile Met Gln Ala Thr Val Cys

1 5 10 15

Asp Glu Lys Ile Gly Trp Arg Asn Asp Ala Ser His Leu Leu Val Phe
20 25 30

Thr Thr Asp Ala Lys Thr His Ile Ala Leu Asp Gly Arg Leu Ala Gly
35 40 45

Ile Val Gln Pro Asn Asp Gly Gln Cys His Val Gly Ser Asp Asn His
50 55 60

Tyr Ser Ala Ser Thr Thr Met Asp Tyr Pro Ser Leu Gly Leu Met Thr
65 70 75 80

Glu Lys Leu Ser Gln Lys
85

<210> 156
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(42)

<400> 156
atg gac tta agt tat agt atg aaa gat gat tta tgg agt ata
42
Met Asp Leu Ser Tyr Ser Met Lys Asp Asp Leu Trp Ser Ile

1 5 10

<210> 157
<211> 14
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 157

Met Asp Leu Ser Tyr Ser Met Lys Asp Asp Leu Trp Ser Ile
1 5 10

<210> 158
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(18)

<400> 158
gga cca aat ata tgt aca
18
Gly Pro Asn Ile Cys Thr

1 5

<210> 159
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 159

Gly Pro Asn Ile Cys Thr
1 5

<210> 160

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

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(39)

<400> 160
gga cca aat ata tgt aca aca aga gga gta agt agt tgc
39
Gly Pro Asn Ile Cys Thr Thr Arg Gly Val Ser Ser Cys

1 5 10

<210> 161
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 161

Gly Pro Asn Ile Cys Thr Thr Arg Gly Val Ser Ser Cys
1 5 10

<210> 162
<211> 207
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(207)

<400> 162
aaa gat tct tta ata gta cag gta aca ttt gac tgt gac tgt gca tgt
48
Lys Asp Ser Leu Ile Val Gln Val Thr Phe Asp Cys Asp Cys Ala Cys

1 5 10 15

cag gca caa gca gaa ccc aac tcg cat aga tgc aac aat gga aat ggc
96
Gln Ala Gln Ala Glu Pro Asn Ser His Arg Cys Asn Asn Gly Asn Gly

20 25 30

aca ttc gaa tgc gga gta tgc aga tgc gga ccg ggt tgg tta ggg agt 1
44
Thr Phe Glu Cys Gly Val Cys Arg Cys Gly Pro Gly Trp Leu Gly Ser

35 40 45

cag tgt gaa tgc tca gag gaa gat tat aga cct tcc caa caa gat gag 1
92
Gln Cys Glu Cys Ser Glu Glu Asp Tyr Arg Pro Ser Gln Gln Asp Glu

50 55 60

tgt agc cca aga gag 2
07
Cys Ser Pro Arg Glu

65

<210> 163
<211> 69
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 163

Lys Asp Ser Leu Ile Val Gln Val Thr Phe Asp Cys Asp Cys Ala Cys

1 5 10 15

Gln Ala Gln Ala Glu Pro Asn Ser His Arg Cys Asn Asn Gly Asn Gly
20 25 30

Thr Phe Glu Cys Gly Val Cys Arg Cys Gly Pro Gly Trp Leu Gly Ser
35 40 45

Gln Cys Glu Cys Ser Glu Glu Asp Tyr Arg Pro Ser Gln Gln Asp Glu
50 55 60

Cys Ser Pro Arg Glu
65

<210> 164
<211> 267
<212> DNA
<213> Artificial Sequence

<220>
<223> Integrin

<220>
<221> CDS
<222> (1)..(267)

<400> 164
cct act tgc ccg gat gct tgc act ttt aaa aaa gaa tgt gta gaa tgc 48
Pro Thr Cys Pro Asp Ala Cys Thr Phe Lys Lys Glu Cys Val Glu Cys
1 5 10 15

aaa aaa ttt gac cgt gag ccc tat atg aca gaa aat act tgc aac agg 96
Lys Lys Phe Asp Arg Glu Pro Tyr Met Thr Glu Asn Thr Cys Asn Arg
20 25 30

tat tgt aga gat gaa ata gag agc gtt aaa gag tta aaa gat aca ggt 1

44
Tyr Cys Arg Asp Glu Ile Glu Ser Val Lys Glu Leu Lys Asp Thr Gly
35 40 45

aaa gat gca gtt aac tgt aca tat aaa aat gag gac gat tgt gtg gta 1
92
Lys Asp Ala Val Asn Cys Thr Tyr Lys Asn Glu Asp Asp Cys Val Val
50 55 60

cga ttc caa tat tat gaa gac agt tca gga aaa tct ata ttg tat gta 2
40
Arg Phe Gln Tyr Tyr Glu Asp Ser Ser Gly Lys Ser Ile Leu Tyr Val
65 70 75 80

gtg gaa gag cca gaa tgt cca aaa ggg 2
67
Val Glu Glu Pro Glu Cys Pro Lys Gly
85

<210> 165
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Integrin

<400> 165

Pro Thr Cys Pro Asp Ala Cys Thr Phe Lys Lys Glu Cys Val Glu Cys
1 5 10 15

Lys Lys Phe Asp Arg Glu Pro Tyr Met Thr Glu Asn Thr Cys Asn Arg
20 25 30

Tyr Cys Arg Asp Glu Ile Glu Ser Val Lys Glu Leu Lys Asp Thr Gly
35 40 45

Lys Asp Ala Val Asn Cys Thr Tyr Lys Asn Glu Asp Asp Cys Val Val
50 55 60

Arg Phe Gln Tyr Tyr Glu Asp Ser Ser Gly Lys Ser Ile Leu Tyr Val
65 70 75 80

Val Glu Glu Pro Glu Cys Pro Lys Gly
85

<210> 166
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(15)

<400> 166
aaa gat gac tta tgg
15
Lys Asp Asp Leu Trp

1 5

<210> 167
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 167

Lys Asp Asp Leu Trp
1 5

<210> 168
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(39)

<400> 168
agt gta agt aga aat aga gat gca cca gaa gga gga ttt
39
Ser Val Ser Arg Asn Arg Asp Ala Pro Glu Gly Gly Phe

1 5 10

<210> 169
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 169

Ser Val Ser Arg Asn Arg Asp Ala Pro Glu Gly Gly Phe
1 5 10

<210> 170
<211> 270
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>

<221> CDS
<222> (1)..(270)

<400> 170
cac gtg ggg agt gac aac cat tat tcc gca tct aca act atg gac tat
48
His Val Gly Ser Asp Asn His Tyr Ser Ala Ser Thr Thr Met Asp Tyr
1 5 10 15

cca agt ctg ggc tta atg aca gag aag tta agc caa aag aat tta aac
96
Pro Ser Leu Gly Leu Met Thr Glu Lys Leu Ser Gln Lys Asn Leu Asn
20 25 30

ttg atc ttt gca gtt aca gag aac gta gtc aat ctt tac cag aat tac 1
44
Leu Ile Phe Ala Val Thr Glu Asn Val Val Asn Leu Tyr Gln Asn Tyr
35 40 45

agt gag cta att cca gga acg acc gta gga gta ttg tcg atg gat agt 1
92
Ser Glu Leu Ile Pro Gly Thr Thr Val Gly Val Leu Ser Met Asp Ser
50 55 60

tca aat gtc ctc caa cta ata gtg gat gca tat ggt aaa ata aga agt 2
40
Ser Asn Val Leu Gln Leu Ile Val Asp Ala Tyr Gly Lys Ile Arg Ser
65 70 75 80

aaa gtt gaa tta gaa gta aga gat ctc cca 2
70
Lys Val Glu Leu Glu Val Arg Asp Leu Pro
85 90

<210> 171

<211> 90
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 171

His Val Gly Ser Asp Asn His Tyr Ser Ala Ser Thr Thr Met Asp Tyr
1 5 10 15

Pro Ser Leu Gly Leu Met Thr Glu Lys Leu Ser Gln Lys Asn Leu Asn
20 25 30

Leu Ile Phe Ala Val Thr Glu Asn Val Val Asn Leu Tyr Gln Asn Tyr
35 40 45

Ser Glu Leu Ile Pro Gly Thr Thr Val Gly Val Leu Ser Met Asp Ser
50 55 60

Ser Asn Val Leu Gln Leu Ile Val Asp Ala Tyr Gly Lys Ile Arg Ser
65 70 75 80

Lys Val Glu Leu Glu Val Arg Asp Leu Pro
85 90

<210> 172
<211> 417
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(417)

<400> 172
gac gat agt aaa aat ttc agt att caa gta cga caa gta gaa gac tat

48
Asp Asp Ser Lys Asn Phe Ser Ile Gln Val Arg Gln Val Glu Asp Tyr
1 5 10 15

ccc gtt gac atc tac tat cta atg gat tta agt tac agt atg aaa gat
96
Pro Val Asp Ile Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met Lys Asp
20 25 30

gat tta tgg agt ata cag aat ttg ggg acc aag ctt gca acc caa atg 1
44
Asp Leu Trp Ser Ile Gln Asn Leu Gly Thr Lys Leu Ala Thr Gln Met
35 40 45

aga aag ctg aca tcg aac tta agg att gga ttt gga gca ttc gtt gat 1
92
Arg Lys Leu Thr Ser Asn Leu Arg Ile Gly Phe Gly Ala Phe Val Asp
50 55 60

aag cct gtg tca ccg tat atg tac atc tct ccc cca gag gct tta gaa 2
40
Lys Pro Val Ser Pro Tyr Met Tyr Ile Ser Pro Pro Glu Ala Leu Glu
65 70 75 80

aat ccg tgt tac gac atg aaa acg aca tgt tta cct atg ttt ggt tat 2
88
Asn Pro Cys Tyr Asp Met Lys Thr Thr Cys Leu Pro Met Phe Gly Tyr
85 90 95

aaa cat gta tta acg ctc act gac cag gta aca cgt ttt aac gaa gag 3
36
Lys His Val Leu Thr Leu Thr Asp Gln Val Thr Arg Phe Asn Glu Glu
100 105 110

gtc aag aaa cag agc gtg tcc cgg aac cgc gat gcg cca gag ggc gga 3
84
Val Lys Lys Gln Ser Val Ser Arg Asn Arg Asp Ala Pro Glu Gly Gly
115 120 125

ttc gac gcc ata atg caa gca act gtc tgc gat 4
17
Phe Asp Ala Ile Met Gln Ala Thr Val Cys Asp
130 135

<210> 173
<211> 139
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 173

Asp Asp Ser Lys Asn Phe Ser Ile Gln Val Arg Gln Val Glu Asp Tyr
1 5 10 15

Pro Val Asp Ile Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met Lys Asp
20 25 30

Asp Leu Trp Ser Ile Gln Asn Leu Gly Thr Lys Leu Ala Thr Gln Met
35 40 45

Arg Lys Leu Thr Ser Asn Leu Arg Ile Gly Phe Gly Ala Phe Val Asp
50 55 60

Lys Pro Val Ser Pro Tyr Met Tyr Ile Ser Pro Pro Glu Ala Leu Glu
65 70 75 80

Asn Pro Cys Tyr Asp Met Lys Thr Thr Cys Leu Pro Met Phe Gly Tyr
85 90 95

Lys His Val Leu Thr Leu Thr Asp Gln Val Thr Arg Phe Asn Glu Glu
100 105 110

Val Lys Lys Gln Ser Val Ser Arg Asn Arg Asp Ala Pro Glu Gly Gly
115 120 125

Phe Asp Ala Ile Met Gln Ala Thr Val Cys Asp
130 135

<210> 174
<211> 117
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(117)

<400> 174
tat atg tac ata agt ccc ccg gaa gca tta gag aat cct tgt tac gat
48
Tyr Met Tyr Ile Ser Pro Pro Glu Ala Leu Glu Asn Pro Cys Tyr Asp
1 5 10 15

atg aaa act acc tgc tta cca atg ttt gga tat aag cat gta tta aca
96
Met Lys Thr Thr Cys Leu Pro Met Phe Gly Tyr Lys His Val Leu Thr
20 25 30

tta acg gac caa gta aca aga 1
17
Leu Thr Asp Gln Val Thr Arg
35

<210> 175
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 175

Tyr Met Tyr Ile Ser Pro Pro Glu Ala Leu Glu Asn Pro Cys Tyr Asp
1 5 10 15

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

Leu Thr Asp Gln Val Thr Arg
35

<210> 176
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(18)

<400> 176
aga aat aga gat gca tat
18
Arg Asn Arg Asp Ala Tyr

1 5

<210> 177
<211> 6
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 177

Arg Asn Arg Asp Ala Tyr
1 5

<210> 178
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(48)

<400> 178
gac gca cca gaa gga gga ttt gat gca ata atg caa gca aca gta tat
48
Asp Ala Pro Glu Gly Gly Phe Asp Ala Ile Met Gln Ala Thr Val Tyr
1 5 10 15

<210> 179
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 179

Asp Ala Pro Glu Gly Gly Phe Asp Ala Ile Met Gln Ala Thr Val Tyr
1 5 10 15

<210> 180

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

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(24)

<400> 180
tgc tat gat atg aaa aca aca tgt
24
Cys Tyr Asp Met Lys Thr Thr Cys

1 5

<210> 181
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 181

Cys Tyr Asp Met Lys Thr Thr Cys
1 5

<210> 182
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(60)

<400> 182
aat ttt agt ata cag gta aga caa gta gaa gac tat cca gta gat ata
48
Asn Phe Ser Ile Gln Val Arg Gln Val Glu Asp Tyr Pro Val Asp Ile

1 5 10 15

tat tac tta atg
60
Tyr Tyr Leu Met

20

<210> 183
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 183

Asn Phe Ser Ile Gln Val Arg Gln Val Glu Asp Tyr Pro Val Asp Ile
1 5 10 15

Tyr Tyr Leu Met
20

<210> 184
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(15)

<400> 184

gat atg aaa aca aca
15
Asp Met Lys Thr Thr

1 5

<210> 185
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 185

Asp Met Lys Thr Thr
1 5

<210> 186
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(15)

<400> 186
ata agt cca cca gca
15
Ile Ser Pro Pro Ala

1 5

<210> 187
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 187

Ile Ser Pro Pro Ala
1 5

<210> 188
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(36)

<400> 188
aaa caa agt gta agt aga aat aga gat gca cca gaa
36
Lys Gln Ser Val Ser Arg Asn Arg Asp Ala Pro Glu

1 5 10

<210> 189
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 189

Lys Gln Ser Val Ser Arg Asn Arg Asp Ala Pro Glu
1 5 10

<210> 190
<211> 837

130588.00025.ST25.txt

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(837)

<400> 190
gat gac agt aaa aat ttt agt atc cag gta aga cag gta gaa gat tat
48
Asp Asp Ser Lys Asn Phe Ser Ile Gln Val Arg Gln Val Glu Asp Tyr

1 5 10 15

cca gtc gac ata tat tac ctc atg gac ctg agt tac agt atg aag gat
96
Pro Val Asp Ile Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met Lys Asp

20 25 30

gat ctc tgg tca att caa aat cta ggg act aag ctt gcg acg caa atg 1
44
Asp Leu Trp Ser Ile Gln Asn Leu Gly Thr Lys Leu Ala Thr Gln Met

35 40 45

aga aaa ttg aca agc aat tta cga att gga ttt gga gca ttc gtc gat 1
92
Arg Lys Leu Thr Ser Asn Leu Arg Ile Gly Phe Gly Ala Phe Val Asp

50 55 60

aag cct gtt agt cct tac atg tac atc tca ccc cct gaa gcc tta gag 2
40
Lys Pro Val Ser Pro Tyr Met Tyr Ile Ser Pro Pro Glu Ala Leu Glu

65 70 75 80

aac ccc tgc tat gac atg aaa acc aca tgt tta ccg atg ttt ggt tat 2

88
Asn Pro Cys Tyr Asp Met Lys Thr Thr Cys Leu Pro Met Phe Gly Tyr
85 90 95

aaa cat gtg ctc acg ctt acg gac caa gtg act cgg ttc aat gag gaa 3
36
Lys His Val Leu Thr Leu Thr Asp Gln Val Thr Arg Phe Asn Glu Glu
100 105 110

gta aaa aag cag tct gtc agt agg aac cgt gat gca ccg gaa gga gga 3
84
Val Lys Lys Gln Ser Val Ser Arg Asn Arg Asp Ala Pro Glu Gly Gly
115 120 125

ttt gac gcg ata atg caa gcc aca gta tgt gac gag aaa ata ggc tgg 4
32
Phe Asp Ala Ile Met Gln Ala Thr Val Cys Asp Glu Lys Ile Gly Trp
130 135 140

cgc aac gat gca tcc cat tta ctg gtg ttc acc act gat gcg aaa aca 4
80
Arg Asn Asp Ala Ser His Leu Leu Val Phe Thr Thr Asp Ala Lys Thr
145 150 155 160

cac atc gca ttg gat ggt aga ttg gct gga ata gta cag cca aat gat 5
28
His Ile Ala Leu Asp Gly Arg Leu Ala Gly Ile Val Gln Pro Asn Asp
165 170 175

ggc caa tgc cat gtc ggg agc gac aac cac tat tcg gca agt acc acg 5
76
Gly Gln Cys His Val Gly Ser Asp Asn His Tyr Ser Ala Ser Thr Thr
180 185 190

atg gac tac ccc agc tta ggt cta atg act gag aag tta tcg cag aag 6
24
Met Asp Tyr Pro Ser Leu Gly Leu Met Thr Glu Lys Leu Ser Gln Lys
195 200 205

aac ctt aac cta atc ttc gct gta aca gaa aat gta gtt aat tta tat 6
72
Asn Leu Asn Leu Ile Phe Ala Val Thr Glu Asn Val Val Asn Leu Tyr
210 215 220

caa aac tac tcg gaa ctg ata ccg gga aca aca gtt ggg gtc ttg tcc 7
20
Gln Asn Tyr Ser Glu Leu Ile Pro Gly Thr Thr Val Gly Val Leu Ser
225 230 235 240

atg gac tca agt aat gtt tta cag cta att gtg gac gct tat ggc aag 7
68
Met Asp Ser Ser Asn Val Leu Gln Leu Ile Val Asp Ala Tyr Gly Lys
245 250 255

att aga tcc aaa gtg gag tta gaa gtt aga gat ctt cca gag gag ctc 8
16
Ile Arg Ser Lys Val Glu Leu Glu Val Arg Asp Leu Pro Glu Glu Leu
260 265 270

tct ctg tct ttt aac gcc acc 8
37
Ser Leu Ser Phe Asn Ala Thr
275

<210> 191
<211> 279
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 191

Asp Asp Ser Lys Asn Phe Ser Ile Gln Val Arg Gln Val Glu Asp Tyr
1 5 10 15

Pro Val Asp Ile Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met Lys Asp
20 25 30

Asp Leu Trp Ser Ile Gln Asn Leu Gly Thr Lys Leu Ala Thr Gln Met
35 40 45

Arg Lys Leu Thr Ser Asn Leu Arg Ile Gly Phe Gly Ala Phe Val Asp
50 55 60

Lys Pro Val Ser Pro Tyr Met Tyr Ile Ser Pro Pro Glu Ala Leu Glu
65 70 75 80

Asn Pro Cys Tyr Asp Met Lys Thr Thr Cys Leu Pro Met Phe Gly Tyr
85 90 95

Lys His Val Leu Thr Leu Thr Asp Gln Val Thr Arg Phe Asn Glu Glu
100 105 110

Val Lys Lys Gln Ser Val Ser Arg Asn Arg Asp Ala Pro Glu Gly Gly
115 120 125

Phe Asp Ala Ile Met Gln Ala Thr Val Cys Asp Glu Lys Ile Gly Trp
130 135 140

Arg Asn Asp Ala Ser His Leu Leu Val Phe Thr Thr Asp Ala Lys Thr
145 150 155 160

His Ile Ala Leu Asp Gly Arg Leu Ala Gly Ile Val Gln Pro Asn Asp
165 170 175

Gly Gln Cys His Val Gly Ser Asp Asn His Tyr Ser Ala Ser Thr Thr
180 185 190

Met Asp Tyr Pro Ser Leu Gly Leu Met Thr Glu Lys Leu Ser Gln Lys
195 200 205

Asn Leu Asn Leu Ile Phe Ala Val Thr Glu Asn Val Val Asn Leu Tyr
210 215 220

Gln Asn Tyr Ser Glu Leu Ile Pro Gly Thr Thr Val Gly Val Leu Ser
225 230 235 240

Met Asp Ser Ser Asn Val Leu Gln Leu Ile Val Asp Ala Tyr Gly Lys
245 250 255

Ile Arg Ser Lys Val Glu Leu Glu Val Arg Asp Leu Pro Glu Glu Leu
260 265 270

Ser Leu Ser Phe Asn Ala Thr
275

<210> 192
<211> 621
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(621)

<400> 192
gat gat tct aag aat ttt tcc atc cag gtt cga cag gtc gaa gat tac
48
Asp Asp Ser Lys Asn Phe Ser Ile Gln Val Arg Gln Val Glu Asp Tyr
1 5 10 15

cca gta gac ata tat tac cta atg gat ctc agt tat agt atg aag gac
96
Pro Val Asp Ile Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met Lys Asp
20 25 30

gat cta tgg agt atc caa aac ctg ggc acg aaa ctt gcc act caa atg 1
44
Asp Leu Trp Ser Ile Gln Asn Leu Gly Thr Lys Leu Ala Thr Gln Met
35 40 45

cgg aaa tta aca tca aac ttg agg att ggc ttt ggg gca ttc gtg gat 1
92
Arg Lys Leu Thr Ser Asn Leu Arg Ile Gly Phe Gly Ala Phe Val Asp
50 55 60

aaa ccc gta tcc cca tat atg tac atc tct cca ccg gag gca ctc gaa 2
40
Lys Pro Val Ser Pro Tyr Met Tyr Ile Ser Pro Pro Glu Ala Leu Glu
65 70 75 80

aac cct tgc tac gac atg aag acc aca tgc ctt cct atg ttt ggg tat 2
88
Asn Pro Cys Tyr Asp Met Lys Thr Thr Cys Leu Pro Met Phe Gly Tyr
85 90 95

aaa cac gtg ctt act tta acc gac cag gtt acg aga ttc aat gaa gag 3
36
Lys His Val Leu Thr Leu Thr Asp Gln Val Thr Arg Phe Asn Glu Glu
100 105 110

gta aaa aag caa agt gta agc cgt aac aga gac gca ccg gag gga ggg 3
84
Val Lys Lys Gln Ser Val Ser Arg Asn Arg Asp Ala Pro Glu Gly Gly

115 120 125

ttc gac gca ata atg caa gct act gtc tgt gac gag aag att gga tgg 4
32
Phe Asp Ala Ile Met Gln Ala Thr Val Cys Asp Glu Lys Ile Gly Trp
130 135 140

aga aat gat gcg tcg cat ttg tta gtc ttt aca aca gat gcc aaa aca 4
80
Arg Asn Asp Ala Ser His Leu Leu Val Phe Thr Thr Asp Ala Lys Thr
145 150 155 160

cac att gcg ctg gac ggt cgc ctc gca ggc ata gtt cag cca aat gat 5
28
His Ile Ala Leu Asp Gly Arg Leu Ala Gly Ile Val Gln Pro Asn Asp
165 170 175

ggt cag tgt cat gtg ggt agt gat aat cat tat agc gct tca aca acc 5
76
Gly Gln Cys His Val Gly Ser Asp Asn His Tyr Ser Ala Ser Thr Thr
180 185 190

atg gac tac ccc agt cta gga ctg atg acg gaa aag ttg tcg caa 6
21
Met Asp Tyr Pro Ser Leu Gly Leu Met Thr Glu Lys Leu Ser Gln
195 200 205

<210> 193
<211> 207
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 193

Asp Asp Ser Lys Asn Phe Ser Ile Gln Val Arg Gln Val Glu Asp Tyr
1 5 10 15

Pro Val Asp Ile Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met Lys Asp
20 25 30

Asp Leu Trp Ser Ile Gln Asn Leu Gly Thr Lys Leu Ala Thr Gln Met
35 40 45

Arg Lys Leu Thr Ser Asn Leu Arg Ile Gly Phe Gly Ala Phe Val Asp
50 55 60

Lys Pro Val Ser Pro Tyr Met Tyr Ile Ser Pro Pro Glu Ala Leu Glu
65 70 75 80

Asn Pro Cys Tyr Asp Met Lys Thr Thr Cys Leu Pro Met Phe Gly Tyr
85 90 95

Lys His Val Leu Thr Leu Thr Asp Gln Val Thr Arg Phe Asn Glu Glu
100 105 110

Val Lys Lys Gln Ser Val Ser Arg Asn Arg Asp Ala Pro Glu Gly Gly
115 120 125

Phe Asp Ala Ile Met Gln Ala Thr Val Cys Asp Glu Lys Ile Gly Trp
130 135 140

Arg Asn Asp Ala Ser His Leu Leu Val Phe Thr Thr Asp Ala Lys Thr
145 150 155 160

His Ile Ala Leu Asp Gly Arg Leu Ala Gly Ile Val Gln Pro Asn Asp
165 170 175

Gly Gln Cys His Val Gly Ser Asp Asn His Tyr Ser Ala Ser Thr Thr
180 185 190

Met Asp Tyr Pro Ser Leu Gly Leu Met Thr Glu Lys Leu Ser Gln
195 200 205

<210> 194
<211> 1053
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(1053)

<400> 194
aag caa ctg aat ttc acg gcc tct gga gag gca gag gcc cgc aga tgc 48
Lys Gln Leu Asn Phe Thr Ala Ser Gly Glu Ala Glu Ala Arg Arg Cys
1 5 10 15

gca cgg agg gaa gag ctc cta gct agg gga tgc ccc ctg gag gag cta 96
Ala Arg Arg Glu Glu Leu Leu Ala Arg Gly Cys Pro Leu Glu Glu Leu
20 25 30

gaa gag cca cgt gga cag caa gag gta cta cag gat cag ccg ctg tcg 144
Glu Glu Pro Arg Gly Gln Gln Glu Val Leu Gln Asp Gln Pro Leu Ser
35 40 45

caa gga gcc cga ggt gag ggt gcg acc cag cta gca cca caa cgc gta 192
Gln Gly Ala Arg Gly Glu Gly Ala Thr Gln Leu Ala Pro Gln Arg Val
50 55 60

cgc gtt aca tta cgg cca ggc gaa cca caa caa tta cag gta aga ttt 2

40
Arg Val Thr Leu Arg Pro Gly Glu Pro Gln Gln Leu Gln Val Arg Phe
65 70 75 80

ttg cgt gct gaa ggg tat ccg gtg gat tta tac tat ctc atg gat ctt 2
88
Leu Arg Ala Glu Gly Tyr Pro Val Asp Leu Tyr Tyr Leu Met Asp Leu
85 90 95

agt tac tcc atg aag gat gat cta gaa agg gta cgc caa ctg ggt cat 3
36
Ser Tyr Ser Met Lys Asp Asp Leu Glu Arg Val Arg Gln Leu Gly His
100 105 110

gcc tta ttg gta aga tta caa gaa gta aca cat agc gta cgt atc ggg 3
84
Ala Leu Leu Val Arg Leu Gln Glu Val Thr His Ser Val Arg Ile Gly
115 120 125

ttt gga tct ttc gta gac aaa acc gtt tta cct ttc gtg agt acc gtg 4
32
Phe Gly Ser Phe Val Asp Lys Thr Val Leu Pro Phe Val Ser Thr Val
130 135 140

cct agc aaa ttg cgt cac cct tgt cca act agg ctt gag cga tgc cag 4
80
Pro Ser Lys Leu Arg His Pro Cys Pro Thr Arg Leu Glu Arg Cys Gln
145 150 155 160

agt ccg ttc tca ttc cac cat gtt ttg agt tta act gga gat gcc cag 5
28
Ser Pro Phe Ser Phe His His Val Leu Ser Leu Thr Gly Asp Ala Gln
165 170 175

gcc ttc gag cga gaa gtc ggc cgg caa tcc gtt tct ggg aat tta gac 5
76
Ala Phe Glu Arg Glu Val Gly Arg Gln Ser Val Ser Gly Asn Leu Asp
180 185 190

agt ccc gag gga ggg ttt gac gcg ata ctt caa gca gcg ctc tgt cag 6
24
Ser Pro Glu Gly Gly Phe Asp Ala Ile Leu Gln Ala Ala Leu Cys Gln
195 200 205

gaa cag att ggc tgg cga aac gtc agc aga cta tta gtc ttt acg agt 6
72
Glu Gln Ile Gly Trp Arg Asn Val Ser Arg Leu Leu Val Phe Thr Ser
210 215 220

gac gat act ttt cac aca gca ggg gac gga aag ctt ggc ggt att ttt 7
20
Asp Asp Thr Phe His Thr Ala Gly Asp Gly Lys Leu Gly Gly Ile Phe
225 230 235 240

atg ccc agc gac ggt cat tgt cac ctc gat tca aat gga ttg tac agt 7
68
Met Pro Ser Asp Gly His Cys His Leu Asp Ser Asn Gly Leu Tyr Ser
245 250 255

cgg tcc aca gaa ttc gat tat cct tcg gtg ggc cag gtg gcg cag gca 8
16
Arg Ser Thr Glu Phe Asp Tyr Pro Ser Val Gly Gln Val Ala Gln Ala
260 265 270

ctg agt gct gca aac atc cag cca ata ttt gct gtt aca tcg gcg gcg 8
64
Leu Ser Ala Ala Asn Ile Gln Pro Ile Phe Ala Val Thr Ser Ala Ala
275 280 285

ttg ccg gtt tac caa gaa ctc tca aaa tta ata ccc aaa tcc gct gtc 9
12
Leu Pro Val Tyr Gln Glu Leu Ser Lys Leu Ile Pro Lys Ser Ala Val
290 295 300

ggc gaa tta tct gag gac tcc tca aac gtg gtc caa ctc atc atg gac 9
60
Gly Glu Leu Ser Glu Asp Ser Ser Asn Val Val Gln Leu Ile Met Asp
305 310 315 320

gct tat aat tcg ctt agt agc acg gta aca ctg gaa cac tca tcg ctt 10
08
Ala Tyr Asn Ser Leu Ser Ser Thr Val Thr Leu Glu His Ser Ser Leu
325 330 335

ccg ccc ggt gtc cat att tct tat gag agt caa tgt gaa ggg cct 10
53
Pro Pro Gly Val His Ile Ser Tyr Glu Ser Gln Cys Glu Gly Pro
340 345 350

<210> 195
<211> 351
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 195

Lys Gln Leu Asn Phe Thr Ala Ser Gly Glu Ala Glu Ala Arg Arg Cys
1 5 10 15

Ala Arg Arg Glu Glu Leu Leu Ala Arg Gly Cys Pro Leu Glu Glu Leu
20 25 30

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

Gln Gly Ala Arg Gly Glu Gly Ala Thr Gln Leu Ala Pro Gln Arg Val
50 55 60

Arg Val Thr Leu Arg Pro Gly Glu Pro Gln Gln Leu Gln Val Arg Phe
65 70 75 80

Leu Arg Ala Glu Gly Tyr Pro Val Asp Leu Tyr Tyr Leu Met Asp Leu
85 90 95

Ser Tyr Ser Met Lys Asp Asp Leu Glu Arg Val Arg Gln Leu Gly His
100 105 110

Ala Leu Leu Val Arg Leu Gln Glu Val Thr His Ser Val Arg Ile Gly
115 120 125

Phe Gly Ser Phe Val Asp Lys Thr Val Leu Pro Phe Val Ser Thr Val
130 135 140

Pro Ser Lys Leu Arg His Pro Cys Pro Thr Arg Leu Glu Arg Cys Gln
145 150 155 160

Ser Pro Phe Ser Phe His His Val Leu Ser Leu Thr Gly Asp Ala Gln
165 170 175

Ala Phe Glu Arg Glu Val Gly Arg Gln Ser Val Ser Gly Asn Leu Asp
180 185 190

Ser Pro Glu Gly Gly Phe Asp Ala Ile Leu Gln Ala Ala Leu Cys Gln
195 200 205

Glu Gln Ile Gly Trp Arg Asn Val Ser Arg Leu Leu Val Phe Thr Ser
210 215 220

Asp Asp Thr Phe His Thr Ala Gly Asp Gly Lys Leu Gly Gly Ile Phe
225 230 235 240

Met Pro Ser Asp Gly His Cys His Leu Asp Ser Asn Gly Leu Tyr Ser
245 250 255

Arg Ser Thr Glu Phe Asp Tyr Pro Ser Val Gly Gln Val Ala Gln Ala
260 265 270

Leu Ser Ala Ala Asn Ile Gln Pro Ile Phe Ala Val Thr Ser Ala Ala
275 280 285

Leu Pro Val Tyr Gln Glu Leu Ser Lys Leu Ile Pro Lys Ser Ala Val
290 295 300

Gly Glu Leu Ser Glu Asp Ser Ser Asn Val Val Gln Leu Ile Met Asp,
305 310 315 320

Ala Tyr Asn Ser Leu Ser Ser Thr Val Thr Leu Glu His Ser Ser Leu
325 330 335

Pro Pro Gly Val His Ile Ser Tyr Glu Ser Gln Cys Glu Gly Pro
340 345 350

<210> 196
<211> 273
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(273)

<400> 196
agt ttt gtt gat aaa aca gtc ctg ccg ttc gta agt acc gta cca agt
48

Ser Phe Val Asp Lys Thr Val Leu Pro Phe Val Ser Thr Val Pro Ser
1 5 10 15

aag tta cgc cat cca tgt cca acg agg ttg gag aga tgc cag tct cct
96
Lys Leu Arg His Pro Cys Pro Thr Arg Leu Glu Arg Cys Gln Ser Pro
20 25 30

ttt tcc ttc cac cat gtc tta agc cta act ggt gac gct caa gcc ttt 1
44
Phe Ser Phe His His Val Leu Ser Leu Thr Gly Asp Ala Gln Ala Phe
35 40 45

gaa cgg gaa gta gga aga caa tcg gtg agt ggg aac ctt gat tca ccc 1
92
Glu Arg Glu Val Gly Arg Gln Ser Val Ser Gly Asn Leu Asp Ser Pro
50 55 60

gaa gga ggc ttc gac gca ata tta cag gcg gca ctc tgt cag gag caa 2
40
Glu Gly Gly Phe Asp Ala Ile Leu Gln Ala Ala Leu Cys Gln Glu Gln
65 70 75 80

ata gga tgg cga aat gtt agt cgt tta tta gtg 2
73
Ile Gly Trp Arg Asn Val Ser Arg Leu Leu Val
85 90

<210> 197
<211> 91
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 197

Ser Phe Val Asp Lys Thr Val Leu Pro Phe Val Ser Thr Val Pro Ser
1 5 10 15

Lys Leu Arg His Pro Cys Pro Thr Arg Leu Glu Arg Cys Gln Ser Pro
20 25 30

Phe Ser Phe His His Val Leu Ser Leu Thr Gly Asp Ala Gln Ala Phe
35 40 45

Glu Arg Glu Val Gly Arg Gln Ser Val Ser Gly Asn Leu Asp Ser Pro
50 55 60

Glu Gly Gly Phe Asp Ala Ile Leu Gln Ala Ala Leu Cys Gln Glu Gln
65 70 75 80

Ile Gly Trp Arg Asn Val Ser Arg Leu Leu Val
85 90

<210> 198
<211> 312
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(312)

<400> 198
aaa caa ctc aat ttc aca gct agt ggc gaa gca gag gct agg aga tgc
48
Lys Gln Leu Asn Phe Thr Ala Ser Gly Glu Ala Glu Ala Arg Arg Cys
1 5 10 15

gcc agg cga gaa gaa tta ttg gca cgc ggg tgt ccc ctg gag gag ctt
96
Ala Arg Arg Glu Glu Leu Leu Ala Arg Gly Cys Pro Leu Glu Glu Leu

20 25 30

gaa gag cca cgg ggt cag cag gaa gtt tta caa gat caa cca tta agt 1
44
Glu Glu Pro Arg Gly Gln Gln Glu Val Leu Gln Asp Gln Pro Leu Ser

35 40 45

cag gga gca cgc ggc gaa ggg gcg aca caa tta gcg cca cag cgt gtc 1
92
Gln Gly Ala Arg Gly Glu Gly Ala Thr Gln Leu Ala Pro Gln Arg Val

50 55 60

aga gtg aca ttg cga cca gga gag cct caa cag tta caa gta cgt ttt 2
40
Arg Val Thr Leu Arg Pro Gly Glu Pro Gln Gln Leu Gln Val Arg Phe

65 70 75 80

ctt cgg gcc gag ggt tac ccg gta gat ctg tac tac cta atg gac ctc 2
88
Leu Arg Ala Glu Gly Tyr Pro Val Asp Leu Tyr Tyr Leu Met Asp Leu

85 90 95

agt tat agt atg aag gac gat cta 3
12
Ser Tyr Ser Met Lys Asp Asp Leu

100

<210> 199
<211> 104
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 199

Lys Gln Leu Asn Phe Thr Ala Ser Gly Glu Ala Glu Ala Arg Arg Cys
1 5 10 15

Ala Arg Arg Glu Glu Leu Leu Ala Arg Gly Cys Pro Leu Glu Glu Leu
20 25 30

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

Gln Gly Ala Arg Gly Glu Gly Ala Thr Gln Leu Ala Pro Gln Arg Val
50 55 60

Arg Val Thr Leu Arg Pro Gly Glu Pro Gln Gln Leu Gln Val Arg Phe
65 70 75 80

Leu Arg Ala Glu Gly Tyr Pro Val Asp Leu Tyr Tyr Leu Met Asp Leu
85 90 95

Ser Tyr Ser Met Lys Asp Asp Leu
100

<210> 200
<211> 1017
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(1017)

<400> 200
gaa aaa cgt gag gga aaa gcc gaa gac aga ggc cag tgt aac cac gtg

48
Glu Lys Arg Glu Gly Lys Ala Glu Asp Arg Gly Gln Cys Asn His Val
1 5 10 15

agg ata aac caa acc gta acc ttc tgg gtc tcg ctt cag gca act cat
96
Arg Ile Asn Gln Thr Val Thr Phe Trp Val Ser Leu Gln Ala Thr His
20 25 30

tgt tta ccc gaa cca cat ttg cta cgc ctc cgg gct tta ggg ttt tct 1
44
Cys Leu Pro Glu Pro His Leu Leu Arg Leu Arg Ala Leu Gly Phe Ser
35 40 45

gag gag ctc ata gtt gag cta cac acg tta tgt gac tgc aat tgc tca 1
92
Glu Glu Leu Ile Val Glu Leu His Thr Leu Cys Asp Cys Asn Cys Ser
50 55 60

gac acg caa cca caa gcg cca cac tgt tcc gat ggg cag ggg cac ctt 2
40
Asp Thr Gln Pro Gln Ala Pro His Cys Ser Asp Gly Gln Gly His Leu
65 70 75 80

caa tgt gga gtc tgt agt tgc gct cct ggt aga ttg ggt agg ctg tgc 2
88
Gln Cys Gly Val Cys Ser Cys Ala Pro Gly Arg Leu Gly Arg Leu Cys
85 90 95

gag tgc agt gta gct gag tta tcg agt cct gat ctc gaa agc gga tgt 3
36
Glu Cys Ser Val Ala Glu Leu Ser Ser Pro Asp Leu Glu Ser Gly Cys
100 105 110

cgc gcg ccg aat ggg act gga cct ctg tgt tcc gga aaa ggg cat tgc 3
84
Arg Ala Pro Asn Gly Thr Gly Pro Leu Cys Ser Gly Lys Gly His Cys
115 120 125

cag tgt ggt cgg tgc tct tgc tcg ggt cag tca agt ggc cat ttg tgc 4
32
Gln Cys Gly Arg Cys Ser Cys Ser Gly Gln Ser Ser Gly His Leu Cys
130 135 140

gaa tgt gac gac gcc agc tgt gaa cgg cat gag ggc att ttg tgc ggg 4
80
Glu Cys Asp Asp Ala Ser Cys Glu Arg His Glu Gly Ile Leu Cys Gly
145 150 155 160

ggt ttc ggc agg tgc cag tgt ggg gtg tgt cac tgt cat gca aac cga 5
28
Gly Phe Gly Arg Cys Gln Cys Gly Val Cys His Cys His Ala Asn Arg
165 170 175

aca ggt cga gca tgc gag tgt tcc ggc gac atg gat tct tgt ata agt 5
76
Thr Gly Arg Ala Cys Glu Cys Ser Gly Asp Met Asp Ser Cys Ile Ser
180 185 190

ccg gag gga ggt tta tgc agt ggt cat gga aga tgc aag tgc aat cgc 6
24
Pro Glu Gly Gly Leu Cys Ser Gly His Gly Arg Cys Lys Cys Asn Arg
195 200 205

tgc caa tgc tta gat ggt tac tac ggc gcc cta tgt gat cag tgc cca 6
72
Cys Gln Cys Leu Asp Gly Tyr Tyr Gly Ala Leu Cys Asp Gln Cys Pro
210 215 220

ggc tgt aag act cca tgt gaa aga cac cga gac tgc gca gag tgc ggt 7
20
Gly Cys Lys Thr Pro Cys Glu Arg His Arg Asp Cys Ala Glu Cys Gly
225 230 235 240

gcg ttt aga aca ggc ccc ctg gcc acc aat tgc agc aca gct tgt gct 7
68
Ala Phe Arg Thr Gly Pro Leu Ala Thr Asn Cys Ser Thr Ala Cys Ala
245 250 255

cac act aat gtg acg ctt gca ctt gcg ccc ata tta gat gac ggc tgg 8
16
His Thr Asn Val Thr Leu Ala Leu Ala Pro Ile Leu Asp Asp Gly Trp
260 265 270

tgt aaa gaa aga aca ttg gat aac caa ctg ttt ttt ttc cta gta gaa 8
64
Cys Lys Glu Arg Thr Leu Asp Asn Gln Leu Phe Phe Phe Leu Val Glu
275 280 285

gac gat gcc aga ggc acg gta gtt ctc cgt gtt aga ccg caa gaa aag 9
12
Asp Asp Ala Arg Gly Thr Val Val Leu Arg Val Arg Pro Gln Glu Lys
290 295 300

gga gca gat cat acc caa gca att gta ctg ggg tgt gtt ggg gga atc 9
60
Gly Ala Asp His Thr Gln Ala Ile Val Leu Gly Cys Val Gly Gly Ile
305 310 315 320

gtc gca gtg ggg cta ggg ctc gta ctt gcg tat cgt tta tca gtc gaa 10
08
Val Ala Val Gly Leu Gly Leu Val Leu Ala Tyr Arg Leu Ser Val Glu
325 330 335

10

atc tat gat
17
Ile Tyr Asp

<210> 201
<211> 339
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 201

Glu Lys Arg Glu Gly Lys Ala Glu Asp Arg Gly Gln Cys Asn His Val
1 5 10 15

Arg Ile Asn Gln Thr Val Thr Phe Trp Val Ser Leu Gln Ala Thr His
20 25 30

Cys Leu Pro Glu Pro His Leu Leu Arg Leu Arg Ala Leu Gly Phe Ser
35 40 45

Glu Glu Leu Ile Val Glu Leu His Thr Leu Cys Asp Cys Asn Cys Ser
50 55 60

Asp Thr Gln Pro Gln Ala Pro His Cys Ser Asp Gly Gln Gly His Leu
65 70 75 80

Gln Cys Gly Val Cys Ser Cys Ala Pro Gly Arg Leu Gly Arg Leu Cys
85 90 95

Glu Cys Ser Val Ala Glu Leu Ser Ser Pro Asp Leu Glu Ser Gly Cys
100 105 110

Arg Ala Pro Asn Gly Thr Gly Pro Leu Cys Ser Gly Lys Gly His Cys
115 120 125

Gln Cys Gly Arg Cys Ser Cys Ser Gly Gln Ser Ser Gly His Leu Cys
130 135 140

Glu Cys Asp Asp Ala Ser Cys Glu Arg His Glu Gly Ile Leu Cys Gly
145 150 155 160

Gly Phe Gly Arg Cys Gln Cys Gly Val Cys His Cys His Ala Asn Arg
165 170 175

Thr Gly Arg Ala Cys Glu Cys Ser Gly Asp Met Asp Ser Cys Ile Ser
180 185 190

Pro Glu Gly Gly Leu Cys Ser Gly His Gly Arg Cys Lys Cys Asn Arg
195 200 205

Cys Gln Cys Leu Asp Gly Tyr Tyr Gly Ala Leu Cys Asp Gln Cys Pro
210 215 220

Gly Cys Lys Thr Pro Cys Glu Arg His Arg Asp Cys Ala Glu Cys Gly
225 230 235 240

Ala Phe Arg Thr Gly Pro Leu Ala Thr Asn Cys Ser Thr Ala Cys Ala
245 250 255

His Thr Asn Val Thr Leu Ala Leu Ala Pro Ile Leu Asp Asp Gly Trp
260 265 270

Cys Lys Glu Arg Thr Leu Asp Asn Gln Leu Phe Phe Phe Leu Val Glu
275 280 285

Asp Asp Ala Arg Gly Thr Val Val Leu Arg Val Arg Pro Gln Glu Lys
290 295 300

Gly Ala Asp His Thr Gln Ala Ile Val Leu Gly Cys Val Gly Gly Ile
305 310 315 320

Val Ala Val Gly Leu Gly Leu Val Leu Ala Tyr Arg Leu Ser Val Glu
325 330 335

Ile Tyr Asp

<210> 202
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(15)

<400> 202
gaa cat ata cca gca
15
Glu His Ile Pro Ala

1 5

<210> 203
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 203

Glu His Ile Pro Ala
1 5

<210> 204
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(60)

<400> 204
ata cca tgt aat aac aaa gga gca cat agt gta gga tta atg tgg tgg
48
Ile Pro Cys Asn Asn Lys Gly Ala His Ser Val Gly Leu Met Trp Trp
1 5 10 15

atg tta gca aga
60
Met Leu Ala Arg
20

<210> 205
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 205

Ile Pro Cys Asn Asn Lys Gly Ala His Ser Val Gly Leu Met Trp Trp
1 5 10 15

Met Leu Ala Arg
20

<210> 206

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

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(39)

<400> 206
aaa gta ata tta gat aga gga agt gta tta gta aca tgt
39
Lys Val Ile Leu Asp Arg Gly Ser Val Leu Val Thr Cys

1 5 10

<210> 207
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 207

Lys Val Ile Leu Asp Arg Gly Ser Val Leu Val Thr Cys
1 5 10

<210> 208
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(24)

<400> 208
tgc tgg gac gat gga tgg tta tgt
24
Cys Trp Asp Asp Gly Trp Leu Cys

1 5

<210> 209
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 209

Cys Trp Asp Asp Gly Trp Leu Cys
1 5

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

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(24)

<400> 210
tgc tgg gat gac tta tgg tta tgt
24
Cys Trp Asp Asp Leu Trp Leu Cys

1 5

<210> 211
<211> 8
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 211

Cys Trp Asp Asp Leu Trp Leu Cys
1 5

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

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(27)

<400> 212
tgc tta tta aga atg aga agt ata tgt
27
Cys Leu Leu Arg Met Arg Ser Ile Cys

1 5

<210> 213
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 213

Cys Leu Leu Arg Met Arg Ser Ile Cys
1 5

<210> 214

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

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(60)

<400> 214
cca gat aca aga ccc gcc cct gga agt aca gca ccg cca gcg cat gga
48
Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly
1 5 10 15

gta aca agt gct
60
Val Thr Ser Ala
20

<210> 215
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 215

Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly
1 5 10 15

Val Thr Ser Ala
20

<210> 216
<211> 42

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(42)

<400> 216
gag tgg tgt gaa tat tta gga gga tat tta aga tgc tac gca
42
Glu Trp Cys Glu Tyr Leu Gly Gly Tyr Leu Arg Cys Tyr Ala

1 5 10

<210> 217
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 217

Glu Trp Cys Glu Tyr Leu Gly Gly Tyr Leu Arg Cys Tyr Ala
1 5 10

<210> 218
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<220>
<221> CDS
<222> (1)..(18)

<400> 218

gaa tgg cca gag tat tta
18
Glu Trp Pro Glu Tyr Leu

1 5

<210> 219
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Integrin

<400> 219

Glu Trp Pro Glu Tyr Leu
1 5