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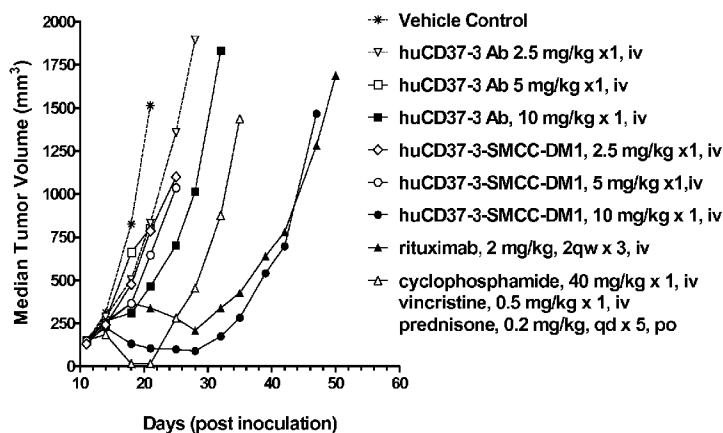
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Figure 9.



(57) Abstract: Methods to improve the success of cancer therapies that target CD37 are provided. Kits comprising reagent useful in the methods are further provided.

METHODS FOR INCREASING EFFICACY OF CD37-BASED THERAPY

FIELD OF THE INVENTION

[0001] The field of invention generally relates to increasing the efficacy of the treatment of B-cell diseases characterized by the overexpression of human CD37. More specifically, the invention concerns more effective treatment of patients susceptible to or diagnosed with B-cell diseases, for example cancer or autoimmune disease, in which the cells express CD37 as determined by a gene expression assay, with a CD37 antagonist, e.g., a CD37 immunoconjugate.

BACKGROUND OF THE INVENTION

[0002] Cancer is one of the leading causes of death in the developed world, with over one million people diagnosed with cancer and 500,000 deaths per year in the United States alone. Overall it is estimated that more than 1 in 3 people will develop some form of cancer during their lifetime.

[0003] Leukocyte antigen CD37 ("CD37"), also known as GP52-40, tetraspanin-26, or TSPAN26, is a transmembrane protein of the tetraspanin superfamily (Maecker et al., 1997 FASEB J. 11:428-442). It is a heavily glycosylated protein with four transmembrane domains that is expressed on B cells during the pre-B to peripheral mature B-cell stages, but is absent on terminal differentiation to plasma cells. (Link et al., 1987, J Pathol. 152:12-21). The CD37 antigen is only weakly expressed on T-cells, myeloid cells and granulocytes (Schwartz-Albiez et al. 1988, J. Immunol., 140(3)905-914). However, CD37 is also expressed on malignant B-cells such as those founding non-Hodgkin's lymphoma (NHL) and chronic lymphoid leukemia (CLL) (Moore et al. 1986, J Immunol. 137(9):3013-8). This expression profile suggests that CD37 represents a promising therapeutic target for B-cell malignancies, and currently, there is a clear unmet medical need for more effective therapeutics for B-cell malignancies.

SUMMARY OF THE INVENTION

[0004] The present invention is based on the discovery of a dynamic range of expression of CD37 in cancer and the discovery that cancers with increased levels of CD37 expression are more responsive to treatment with anti-CD37 antibodies or anti-CD37 immunoconjugates. The present invention advantageously permits treatment of patients who have a greater likelihood of

responding to treatment by administering therapeutic agents, i.e., anti-CD37 antibodies or anti-CD37 immunoconjugates, to patients who are found to have an increased expression level of CD37.

[0005] In one embodiment, the invention provides a method for increasing the efficacy of cancer therapy with an anti-CD37 antibody, or anti-CD37 immunoconjugate, wherein the method comprises administering to a subject having cancer an anti-CD37 antibody, or anti-CD37 immunoconjugate, wherein an increased expression of CD37 gene or protein in a cancerous sample from the subject has been detected using a detection method that distinguishes between staining intensity or staining uniformity in a CD37 expressing cancerous sample as compared to staining intensity or staining uniformity in one or more reference sample.

[0006] In another embodiment, the invention provides a method of identifying a cancer as likely sensitive to treatment with an anti-CD37 antibody, or anti-CD37 immunoconjugate comprising (a) measuring the level of CD37 expression in a cancerous sample obtained from the subject cancer, wherein the measuring comprises the use of a detection method that distinguishes between staining intensity or staining uniformity in a CD37 expressing cancerous sample as compared to staining intensity or staining uniformity in one or more reference samples; (b) determining a CD37 staining intensity or staining uniformity score for the cancerous sample; and (c) comparing the CD37 staining intensity or staining uniformity score determined in step (b) to a relative value determined by measuring CD37 protein expression in at least one reference sample, wherein the at least one reference sample is a tissue, cell, or cell pellet sample which is not sensitive to treatment with an anti-CD37 antibody, or anti-CD37 immunoconjugate, and wherein a CD37 staining intensity score for the sample determined in step (b) that is higher than the relative value identifies the cancer as sensitive to treatment with an anti-CD37 antibody, or anti-CD37 immunoconjugate.

[0007] In another embodiment, the invention provides a method for identifying a cancer likely to respond to an anti-CD37 antibody, or anti-CD37 immunoconjugate comprising (a) contacting a biological sample comprising cells from the cancer with an agent that binds CD37 protein on the cell surface; (b) detecting binding of the agent that binds CD37 protein on the cell surface of the biological sample of (a); (c) assigning a score to the binding of step (b), wherein the score is assigned based on comparison to one or more reference samples; and (d) comparing the score in step (c) to the score of a reference tissue or cell, wherein a score for the cancer CD37 level that is greater than the score for a negative or low CD37 expressing reference sample or a score for the cancer CD37 level that is equal to or greater than the score for a high

CD37 expressing reference sample identifies the cancer as likely to respond to an anti-CD37 antibody or anti-CD immunoconjugate.

[0008] In another embodiment, the invention provides a method of identifying a subject having a cancer as likely to respond to a low dose anti-CD37 antibody or anti-CD37 immunoconjugate treatment regimen comprising: (a) contacting a biological sample comprising cells from the cancer with an agent that binds cell surface CD37 protein; (b) detecting binding of the agent to the biological sample of (a); (c) assigning a score to the binding of step (b), wherein the score is assigned based on comparison to one or more reference samples; and (d) comparing the score in step (c) to the score of a reference tissue or cell, wherein a score for the cancer CD37 level that is greater than the score for a negative or low CD37 expressing reference sample or a score for the cancer CD37 level that is equal to or greater than the score for a high CD37 expressing reference sample identifies the cancer as likely to respond to a low dose anti-CD37 antibody or anti-CD37 immunoconjugate.

[0009] In another embodiment, the invention provides a method of optimizing a therapeutic regimen with an anti-CD37 antibody or an anti-CD37 immunoconjugate for a subject having cancer comprising: (a) detecting the level of CD37 expression in a cancerous sample obtained from the subject; (b) comparing the level of CD37 expression in the cancerous sample to the CD37 expression in a reference sample; (c) determining a CD37 staining intensity score for the cancerous sample; and (d) administering an increased dose of an anti-CD37 antibody or an anti-CD37 immunoconjugate to the subject if the score is low or administering a decreased dose of an anti-CD37 antibody or an anti-CD37 immunoconjugate to the subject if the score is high.

[0010] In another embodiment, the invention provides a method of detecting the expression of cell surface CD37 on cancer cells in a cancerous sample from a subject comprising: (a) obtaining a cancerous sample, wherein the sample is formalin-fixed paraffin embedded; (b) contacting the cancerous sample with an antibody that specifically binds cell surface CD37; (c) measuring the binding of the antibody in (b) to the cell surface CD37 in the cancerous sample using a detection method that can distinguish between staining intensity or staining uniformity in a CD37 expressing sample as compared to staining intensity or staining uniformity in one or more reference samples; and (d) assigning a CD37 expression score to the CD37 after comparing the level of cell surface CD37 staining intensity or staining uniformity in the cancerous sample to one or more reference samples.

[0011] In some embodiments, detection is by immunohistochemistry (IHC). The IHC can be calibrated IHC that can distinguish different levels of CD37 expression.

[0012] In some embodiments, the detection method produces a range of staining intensity for samples having low cell surface CD37 expression, intermediate CD37 cell surface expression, or high CD37 cell surface expression.

[0013] In some embodiments, the detection method distinguishes between staining intensity and staining uniformity in a CD37 expressing cancerous sample as compared to a reference sample.

[0014] In some embodiments, the cancerous sample or biological sample has a staining intensity score greater than 1 for CD37 expression by immunohistochemistry. In some embodiments, the cancerous sample or biological sample has a staining intensity score of 2, 3, or 3+ for CD37 expression by immunohistochemistry. In some embodiments, the cancerous sample or biological sample has a staining intensity score of 2, 3, or 3+ for CD37 expression by immunohistochemistry on a formalin fixed paraffin embedded sample. In some embodiments, the cancerous sample or biological sample has a staining uniformity for CD37 expression that is homogenous. In some embodiments, the cancerous sample or biological sample has a staining intensity score of 2, 3, or 3+ for CD37 and a staining uniformity that is heterogeneous or homogenous.

[0015] In some embodiments, the immunohistochemistry is performed manually. In some embodiments, the immunohistochemistry is performed using an automated system.

[0016] In some embodiments, the reference sample is a positive reference sample or a negative reference sample. In some embodiments, the reference sample comprises cells, cell pellets, or tissue.

[0017] In some embodiments, the detection comprises detecting CD37 expression with an antibody that specifically binds cell surface CD37. In some embodiments, the antibody further comprises a detection reagent selected from the group consisting of: an enzyme, a fluorophore, a radioactive label, and a luminophore. In some embodiments, the detection reagent is selected from the group consisting of: biotin, digoxigenin, fluorescein, tritium, and rhodamine. In some embodiments, the antibody is clone CT1.

[0018] In some embodiments, the concentration of the antibody is about 1 to about 10 $\mu\text{g/mL}$ or about 2.1 to about 8.4 $\mu\text{g/mL}$, about 4 to about 5 $\mu\text{g/mL}$, or 2.1, 4.2, or 8.4 $\mu\text{g/mL}$. In one embodiment the concentration of the antibody (e.g., clone CT1) is 4.2 $\mu\text{g/mL}$.

[0019] In some embodiments, the cancer is selected from the group consisting of B cell lymphomas, NHL, precursor B cell lymphoblastic leukemia/lymphoma and mature B cell neoplasms, B cell chronic lymphocytic leukemia (CLL)/small lymphocytic lymphoma (SLL), B cell prolymphocytic leukemia, lymphoplasmacytic lymphoma, mantle cell lymphoma (MCL),

follicular lymphoma (FL), low grade, intermediate-grade and high-grade (FL), cutaneous follicle center lymphoma, marginal zone B cell lymphoma, MALT type marginal zone B cell lymphoma, nodal marginal zone B cell lymphoma, splenic type marginal zone B cell lymphoma, hairy cell leukemia, diffuse large B cell lymphoma (DLBCL), Burkitt's lymphoma (BL), plasmacytoma, plasma cell myeloma, post-transplant lymphoproliferative disorder, Waldenstrom's macroglobulinemia, and anaplastic large-cell lymphoma (ALCL).

[0020] The present invention also provides articles of manufacture comprising an anti-CD37 antibody or an anti-CD37 immunoconjugate, a container, and a package insert or label indicating that the antibody or immunoconjugate can be used to treat a cancer characterized by the expression of CD37 at a level of 2, 3, or 3+ measured by IHC.

[0021] The present invention also provides combination diagnostic and pharmaceutical kits comprising a murine anti-CD37 antibody for use in diagnosis and an anti-CD37 antibody or an anti-CD37 immunoconjugate for use in therapy. In some embodiments, the diagnostic antibody is a detection antibody that is able to detect CD37 expression by IHC.

[0022] The present invention also provides diagnostic kits comprising a detection antibody that can specifically bind to cell surface CD37, a reagent for immunohistochemistry (IHC), and one or more standardized reference samples, wherein the standardized reference samples comprise formalin fixed paraffin embedded cells, cell pellets, or tissue samples, and wherein the one or more standardized referenced samples are from non-CD37 expressing, low-CD37 expressing, intermediate-CD37 expressing, or high CD37 expressing cells, cell pellets, or tissues. Examples of such reference samples are described herein in the Examples.

[0023] In some embodiments, the article or kit is one in which the IHC is calibrated IHC that can distinguish different levels of CD37 expression. In some embodiments, the calibrated IHC produces a range of staining intensity for samples having low cell surface CD37 expression, intermediate cell surface CD37 expression, or high cell surface CD37 expression. In some embodiments, the IHC distinguishes between staining intensity and staining uniformity in a CD37 expressing sample as compared to a reference sample. In some embodiments, the IHC is performed on a formalin fixed paraffin embedded sample. The IHC can be performed manually or performed using an automated system.

[0024] In some embodiments, the article or kit comprises a CD37 immunoconjugate comprising an anti-CD37 antibody, a linker, and a cytotoxin. In some embodiments, the anti-CD37 antibody is chimeric, or humanized CD37-3, CD37-38, or CD37-50. In some embodiments, the anti-CD37 antibody is an antibody selected from the group consisting of: an antibody comprising the polypeptide of SEQ ID NO:56 and the polypeptide of SEQ ID NO:73,

an antibody comprising the polypeptide of SEQ ID NO:57 and the polypeptide of SEQ ID NO:74, an antibody comprising the polypeptide of SEQ ID NO:58 and the polypeptide of SEQ ID NO:74, an antibody comprising the polypeptide of SEQ ID NO:62 and the polypeptide of SEQ ID NO:78, an antibody comprising the polypeptide of SEQ ID NO:63 and the polypeptide of SEQ ID NO:79, and an antibody comprising the polypeptide of SEQ ID NO:65 and the polypeptide of SEQ ID NO:81.

[0025] In some embodiments, the linker is selected from the group consisting of a cleavable linker, a non-cleavable linker, a hydrophilic linker, and a dicarboxylic acid based linker. In some embodiments, the linker is selected from the group consisting: N-succinimidyl 4-(2-pyridyldithio)pentanoate (SPP) or N-succinimidyl 4-(2-pyridyldithio)-2-sulfopentanoate (sulfo-SPP); N-succinimidyl 4-(2-pyridyldithio)butanoate (SPDB) or N-succinimidyl 4-(2-pyridyldithio)-2-sulfobutanoate (sulfo-SPDB); N-succinimidyl 4-(maleimidomethyl)cyclohexanecarboxylate (SMCC); N-sulfosuccinimidyl 4-(maleimidomethyl)cyclohexanecarboxylate (sulfoSMCC); N-succinimidyl-4-(iodoacetyl)-aminobenzoate (SIAB); and N-succinimidyl-[(N-maleimidopropionamido)-tetraethyleneglycol] ester (NHS-PEG4-maleimide). In some embodiments, the linker is N-succinimidyl 4-(maleimidomethyl)cyclohexanecarboxylate (SMCC). In some embodiments, the cytotoxin is selected from the group consisting of a maytansinoid, maytansinoid analog, benzodiazepine, taxoid, CC-1065, CC-1065 analog, duocarmycin, duocarmycin analog, calicheamicin, dolastatin, dolastatin analog, auristatin, tomaymycin derivative, and leptomycin derivative or a prodrug of the cytotoxin. In some embodiments, the cytotoxin is a maytansinoid. In some embodiments, the maytansinoid is N(2')-deacetyl-N(2')-(3-mercapto-1-oxopropyl)-maytansine or N(2')-deacetyl-N2-(4-mercapto-4-methyl-1-oxopentyl)-maytansine. In some embodiments, the maytansinoid is N(2')-deacetyl-N(2')-(3-mercapto-1-oxopropyl)-maytansine (DM1). In some embodiments, the immunoconjugate comprises the antibody huCD37-3, SMCC, and DM1.

[0026] In some embodiments, a combination diagnostic and pharmaceutical kit further comprises one or more reference samples. In some embodiments, the reference sample is a positive reference sample or a negative reference sample. In some embodiments, the reference sample comprises cells, cell pellets, or tissue.

[0027] In some embodiments, a detection antibody for use in kit as provided herein further comprises a detection reagent selected from the group consisting of: an enzyme, a fluorophore, a radioactive label, and a luminophore. In some embodiments, the detection reagent is selected from the group consisting of: biotin, digoxigenin, fluorescein, tritium, and rhodamine. The

concentration of antibody in a kit can be about 1 to about 10 $\mu\text{g/mL}$ or about 2.1 to about 8.4 $\mu\text{g/mL}$, about 4 to about 5 $\mu\text{g/mL}$, or 2.1, 4.2, or 8.4 $\mu\text{g/mL}$ or 4.2 $\mu\text{g/mL}$.

[0028] In some embodiments, a kit comprises a low-CD37 expressing control, and the low-CD37 expressing control is Namalwa or RL tumor cells. In some embodiments, a kit comprises a high-CD37 expressing control, and the high-CD37 expressing control is selected from the group consisting of: Daudi, and Ramos cell lines, and a cell line stably or transiently transfected with CD37. In some embodiments, the cell line stably or transiently transfected with CD37 is 300-19/CD37.

[0029] In some embodiments, the anti-CD37 antibody or immunoconjugate is an antibody or immunoconjugate as described in International Published Application Nos. WO 2011/112978 or WO 2012/135740, each of which is herein incorporated by reference in its entirety.

BRIEF DESCRIPTIONS OF THE DRAWINGS

[0030] Figure 1. Immunohistochemical (IHC) staining of CD37 on non-transfected 300-19 cells (left) and 300-19 cells transfected with human CD37 (huCD37).

[0031] Figure 2. IHC staining of CD37 in white pulp of human spleen tissue at 10x (left) and 40x (right) magnification.

[0032] Figure 3. IHC staining results for CD37 obtained with the optimized manual method for Daudi, Ramos and RL cells. CD37 expression levels obtained by quantitative flow cytometry are given below each image.

[0033] Figure 4. Flow cytometry histograms obtained after staining with a PE-labeled anti-CD37 antibody (bold lines) in comparison to unstained samples (thin lines) using Daudi, Ramos and RL cells.

[0034] Figure 5. IHC staining results for CD37 on Daudi cells and for CD20 on RL cells obtained with the optimized manual method. Cells expressing similar CD37 and CD20 antigen levels show a similar staining pattern.

[0035] Figure 6. Summary of staining scores for CD37 obtained with the optimized manual method for lymphoma samples in comparison to staining scores for CD20.

[0036] Figure 7. Representative pictures of NHL patient samples stained for CD37 using the optimized manual method.

[0037] Figure 8. Anti-tumor activity (median tumor volume, mm^3) of huCD37-3-SMCC-DM1 in female CB.17 SCID mice bearing SU-DHL-4 xenografts.

[0038] Figure 9. Anti-tumor activity (median tumor volume, mm³) of huCD37-3 antibody, huCD37-3-SMCC-DM1, and standard chemotherapeutics in SCID mice bearing DoHH2 human tumor xenografts.

[0039] Figure 10. Anti-tumor activity (median tumor volume, mm³) huCD37-3-SMCC-DM1 in SCID mice bearing DoHH2 human tumor xenografts.

[0040] Figure 11. Anti-tumor activity (median tumor volume, mm³) of huCD37-3 antibody, huCD37-3-SMCC-DM1, Ofatumumab, and Bendamustine in SCID mice bearing JVM-3 human tumor xenografts.

[0041] Figure 12. Anti-tumor activity (median tumor volume, mm³) of huCD37-3-SMCC-DM1 in SCID mice bearing JVM-3 human tumor xenografts.

[0042] Figure 13. Scoring distribution in large cell lymphoma (DLBCL) using automated staining methods.

[0043] Figure 14. Scoring distribution in small cell lymphoma including follicular lymphoma (FL), Mantle cell lymphoma (MCL), MALT type marginal zone B cell lymphoma, marginal zone B cell lymphoma, unclassified small cell lymphoma, and unclassified non-Hodgkin's lymphoma (NHL) samples using automated staining methods.

DETAILED DESCRIPTION OF THE INVENTION

[0044] The present invention provides methods for treating B-cell diseases such as cancer and autoimmune diseases and for increasing the efficacy of or the likelihood of response to the treatment diseases characterized by the overexpression of CD37. The present invention is based on the discovery of methods of detecting a dynamic range of expression of CD37 in a cancer and autoimmune diseases as compared to negative normal tissue and the discovery that B-cells with high levels of CD37 expression are more responsive to treatment with anti-CD37 antibodies or anti-CD37 immunoconjugates. Kits comprising one or more reagents useful for practicing the methods of the invention are further provided.

I. Definitions

[0045] To facilitate an understanding of the present invention, a number of terms and phrases are defined below.

[0046] The term CD37 as used herein, refers to any native CD37, unless otherwise indicated. CD37 is also referred to as GP52-40, leukocyte antigen CD37, and Tetraspanin-26. The term "CD37" encompasses "full-length," unprocessed CD37 as well as any form of CD37

that results from processing in the cell. The term also encompasses naturally occurring variants of CD37, e.g., splice variants, allelic variants, and isoforms. The CD37 polypeptides described herein can be isolated from a variety of sources, such as from human biological samples or from another source, or prepared by recombinant or synthetic methods.

[0047] The term "increased expression" or "high expression" of CD37 refers to a sample which contains elevated levels of CD37 expression as compared to a negative or low reference control or as compared to a healthy or non-diseased sample of the same tissue or cell type. In one example, the CD37 expression is measured by IHC and given a staining intensity score or a staining uniformity score by comparison to calibrated controls exhibiting defined scores (e.g., an intensity score of 3 is given to the test sample if the intensity is comparable to the level 3 calibrated control or an intensity of 2 is given to the test sample if the intensity is comparable to the level 2 calibrated control). For example, a score of 1, 2, 3, or 3+ or greater, preferably a score of 2, 3, 3+, or greater, by immunohistochemistry indicates increased expression of CD37. A staining uniformity that is heterogeneous or homogeneous is also indicative of increased CD37 expression. The staining intensity and staining uniformity scores can be used alone or in combination (e.g., 2 homo, 2 hetero, 3 homo, 3 hetero, etc.). In another example, an increase in CD37 expression can be determined by detection of an increase of at least 2-fold, at least 3-fold, or at least 5-fold relative to control values (e.g., expression level in a biological sample, tissue, or cell from a subject without cancer or with a cancer that does not have elevated CD37 values).

[0048] The term "overexpression" of CD37 in a particular tumor, tissue, or cell sample refers to CD37 (a CD37 polypeptide or a nucleic acid encoding such a polypeptide) that is present at a level higher than that which is present in non-diseased tissue or cells of the same type or origin or other cells in the proximity of a tumor or cancer. Such overexpression can be caused, for example, by mutation, gene amplification, increased transcription, or increased translation.

[0049] A "reference sample" can be used to correlate and compare the results obtained in the methods of the invention from a test sample. Reference samples can be cells (e.g., cell lines, cell pellets) or tissue. The CD37 levels in the "reference sample" can be an absolute or relative amount, a range of amount, a minimum and/or maximum amount, a mean amount, and/or a median amount of CD37. The diagnostic methods of the invention involve a comparison between expression levels of CD37 in a test sample and a "reference value." In some embodiments, the reference value is the expression level of the CD37 in a reference sample. A reference value can be a predetermined value and can also be determined from reference samples (e.g., control biological samples) tested in parallel with the test samples. A reference value can be a single cut-off value, such as a median or mean or a range of values, such as a

confidence interval. Reference values can be established for various subgroups of individuals, such as individuals predisposed to cancer, individuals having early or late stage cancer, male and/or female individuals, or individuals undergoing cancer therapy. Examples of negative reference samples or values and positive reference samples or values are described herein.

[0050] In some embodiments, the reference sample is a sample from a healthy tissue, in particular a corresponding tissue which is not affected by cancer. These types of reference samples are referred to as negative control samples or reference samples. In other embodiments, the reference sample is a sample from a tumor that expresses CD37. These types of reference samples are referred to as positive control samples. Positive control samples can also be used as a comparative indicator for the type (hetero versus homo) and/or degree (0, 1, 2, 3, 3+) of staining intensity, which correlates with the level of CD37 expression. Positive control comparative samples are also referred to as calibrated reference samples. As shown in the Examples, low or non-CD37 references include the red pulp of the spleen (e.g., monocytes and red blood cells) and T-cells and high CD37-expressing references include white pulp of the spleen (e.g., B lymphocytes). For cell lines, exemplary non-expressors include 300-19 cells, and high expressors include Daudi, Ramos, and RL cells. Another positive high CD37 reference is a cell line stably or transiently transfected with CD37 (e.g., 300-19/CD37). Appropriate positive and negative reference levels of CD37 for a particular cancer can be determined by measuring levels of CD37 in one or more appropriate subjects, and such reference levels may be tailored to specific populations of subjects (e.g., a reference level may be age-matched so that comparisons may be made between CD37 levels in samples from subjects of a certain age and reference levels for a particular disease state, phenotype, or lack thereof in a certain age group). Such reference levels may also be tailored to specific techniques that are used to measure levels of CD37 in biological samples (e.g., immunoassays, etc.), where the levels of CD37 may differ based on the specific technique that is used.

[0051] The term "primary antibody" herein refers to an antibody that binds specifically to the target protein antigen in a sample. A primary antibody is generally the first antibody used in an immunohistochemical (IHC) procedure. In one embodiment, the primary antibody is the only antibody used in an IHC procedure. The term "secondary antibody" herein refers to an antibody that binds specifically to a primary antibody, thereby forming a bridge between the primary antibody and a subsequent reagent, if any. The secondary antibody is generally the second antibody used in an immunohistochemical procedure. The term "tertiary antibody" herein refers to an antibody that binds specifically to a secondary antibody, thereby forming a bridge between the secondary antibody and a subsequent reagent, if any.

[0052] A "sample" of the present invention is of biological origin, in specific embodiments, such as from eukaryotic organisms. In preferred embodiments, the sample is a human sample, but animal samples may also be used in the practice of the invention. Non-limiting sources of a sample for use in the present invention include solid tissue, biopsy aspirates, fluidic extracts, blood, plasma, serum, spinal fluid, lymph fluid, the external sections of the skin, respiratory, intestinal, and genitourinary tracts, tears, saliva, milk, tumors, organs, cell cultures and/or cell culture constituents, for example. A "cancerous sample" is a sample that contains a cancerous cell. The present invention is useful for solid tissue samples where the amount of available material is small. The method can be used to examine an aspect of expression of CD37 or a state of a sample, including, but not limited to, comparing different types of cells or tissues, comparing different developmental stages, and detecting or determining the presence and/or type of disease or abnormality.

[0053] For the purposes herein, a "section" of a tissue sample refers to a single part or piece of a tissue sample, e.g., a thin slice of tissue or cells cut from a tissue sample. It is understood that multiple sections of tissue samples may be taken and subjected to analysis according to the present invention. In some cases, the selected portion or section of tissue comprises a homogeneous population of cells. In other cases, the selected portion comprises a region of tissue, e.g., the lumen as a non-limiting example. The selected portion can be as small as one cell or two cells, or could represent many thousands of cells, for example. In most cases, the collection of cells is important, and while the invention has been described for use in the detection of cellular components, the method may also be used for detecting non-cellular components of an organism (e.g., soluble components in the blood as a non-limiting example).

[0054] By "correlate" or "correlating" is meant comparing, in any way, the performance and/or results of a first analysis with the performance and/or results of a second analysis. For example, one may use the results of a first analysis in carrying out the second analysis and/or one may use the results of a first analysis to determine whether a second analysis should be performed and/or one may compare the results of a first analysis with the results of a second analysis. In one embodiment, increased expression of CD37 correlates with increased likelihood of effectiveness of a CD37-targeting anti-cancer therapy.

[0055] The term "antibody" means an immunoglobulin molecule that recognizes and specifically binds to a target, such as a protein, polypeptide, peptide, carbohydrate, polynucleotide, lipid, or combinations of the foregoing through at least one antigen recognition site within the variable region of the immunoglobulin molecule. As used herein, the term "antibody" encompasses intact polyclonal antibodies, intact monoclonal antibodies, antibody

fragments (such as Fab, Fab', F(ab')₂, and Fv fragments), single chain Fv (scFv) mutants, multispecific antibodies such as bispecific antibodies generated from at least two intact antibodies, chimeric antibodies, humanized antibodies, human antibodies, fusion proteins comprising an antigen determination portion of an antibody, and any other modified immunoglobulin molecule comprising an antigen recognition site so long as the antibodies exhibit the desired biological activity. An antibody can be of any the five major classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, or subclasses (isotypes) thereof (e.g., IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2), based on the identity of their heavy-chain constant domains referred to as alpha, delta, epsilon, gamma, and mu, respectively. The different classes of immunoglobulins have different and well known subunit structures and three-dimensional configurations. Antibodies can be naked or conjugated to other molecules such as toxins, radioisotopes, etc.

[0056] A "blocking" antibody or an "antagonist" antibody is one which inhibits or reduces biological activity of the antigen it binds, such as CD37. In a certain embodiment blocking antibodies or antagonist antibodies substantially or completely inhibit the biological activity of the antigen. Desirably, the biological activity is reduced by 10%, 20%, 30%, 50%, 70%, 80%, 90%, 95%, or even 100%.

[0057] The term "anti-CD37 antibody" or "an antibody that binds to CD37" refers to an antibody that is capable of binding CD37 with sufficient affinity such that the antibody is useful as a diagnostic and/or therapeutic agent in targeting CD37. The extent of binding of an anti-CD37 antibody to an unrelated, non-CD37 protein is less than about 10% of the binding of the antibody to CD37 as measured, e.g., by a radioimmunoassay (RIA). In certain embodiments, an antibody that binds to CD37 has a dissociation constant (K_d) of $\leq 1 \mu\text{M}$, $\leq 100 \text{ nM}$, $\leq 10 \text{ nM}$, $\leq 1 \text{ nM}$, or $\leq 0.1 \text{ nM}$. Examples of anti-CD37 antibodies are known in the art and are disclosed in U.S. Published Application No. 2011/0256153, which is herein incorporated by reference.

[0058] The term "antibody fragment" refers to a portion of an intact antibody and refers to the antigenic determining variable regions of an intact antibody. Examples of antibody fragments include, but are not limited to Fab, Fab', F(ab')₂, and Fv fragments, linear antibodies, single chain antibodies, and multispecific antibodies formed from antibody fragments.

[0059] A "monoclonal antibody" refers to a homogeneous antibody population involved in the highly specific recognition and binding of a single antigenic determinant, or epitope. This is in contrast to polyclonal antibodies that typically include different antibodies directed against different antigenic determinants. The term "monoclonal antibody" encompasses both intact and full-length monoclonal antibodies as well as antibody fragments (such as Fab, Fab', F(ab')₂, Fv),

single chain (scFv) mutants, fusion proteins comprising an antibody portion, and any other modified immunoglobulin molecule comprising an antigen recognition site. Furthermore, "monoclonal antibody" refers to such antibodies made in any number of manners including but not limited to by hybridoma, phage selection, recombinant expression, and transgenic animals.

[0060] The term "epitope" or "antigenic determinant" are used interchangeably herein and refer to that portion of an antigen capable of being recognized and specifically bound by a particular antibody. When the antigen is a polypeptide, epitopes can be formed both from contiguous amino acids and noncontiguous amino acids juxtaposed by tertiary folding of a protein. Epitopes formed from contiguous amino acids are typically retained upon protein denaturing, whereas epitopes formed by tertiary folding are typically lost upon protein denaturing. An epitope typically includes at least 3, and more usually, at least 5 or 8-10 amino acids in a unique spatial conformation.

[0061] "Binding affinity" generally refers to the strength of the sum total of noncovalent interactions between a single binding site of a molecule (e.g., an antibody) and its binding partner (e.g., an antigen). Unless indicated otherwise, as used herein, "binding affinity" refers to intrinsic binding affinity which reflects a 1:1 interaction between members of a binding pair (e.g., antibody and antigen). The affinity of a molecule X for its partner Y can generally be represented by the dissociation constant (K_d). Affinity can be measured by common methods known in the art, including those described herein. Low-affinity antibodies generally bind antigen slowly and tend to dissociate readily, whereas high-affinity antibodies generally bind antigen faster and tend to remain bound longer. A variety of methods of measuring binding affinity are known in the art, any of which can be used for purposes of the present invention. Specific illustrative embodiments are described in the following.

[0062] "Or better" when used herein to refer to binding affinity refers to a stronger binding between a molecule and its binding partner. "Or better" when used herein refers to a stronger binding, represented by a smaller numerical K_d value. For example, an antibody which has an affinity for an antigen of "0.6 nM or better", the antibody's affinity for the antigen is <0.6 nM, i.e., 0.59 nM, 0.58 nM, 0.57 nM etc. or any value less than 0.6 nM.

[0063] The phrase "substantially similar," or "substantially the same", as used herein, denotes a sufficiently high degree of similarity between two numeric values (generally one associated with an antibody of the invention and the other associated with a reference/comparator antibody) such that one of skill in the art would consider the difference between the two values to be of little or no biological and/or statistical significance within the context of the biological characteristics measured by said values (e.g., K_d values). The

difference between said two values is less than about 50%, less than about 40%, less than about 30%, less than about 20%, or less than about 10% as a function of the value for the reference/comparator antibody.

[0064] A polypeptide, antibody, polynucleotide, vector, cell, or composition which is "isolated" is a polypeptide, antibody, polynucleotide, vector, cell, or composition which is in a form not found in nature. Isolated polypeptides, antibodies, polynucleotides, vectors, cell or compositions include those which have been purified to a degree that they are no longer in a form in which they are found in nature. In some embodiments, an antibody, polynucleotide, vector, cell, or composition which is isolated is substantially pure.

[0065] As used herein, "substantially pure" refers to material which is at least 50% pure (i.e., free from contaminants), at least 90% pure, at least 95% pure, at least 98% pure, or at least 99% pure.

[0066] The term "immunoconjugate" or "conjugate" as used herein refers to a compound or a derivative thereof that is linked to a cell binding agent (i.e., an anti-CD37 antibody or fragment thereof) and is defined by a generic formula: C-L-A, wherein C = cytotoxin, L = linker, and A = cell binding agent or anti-CD37 antibody or antibody fragment. Immunoconjugates can also be defined by the generic formula in reverse order: A-L-C.

[0067] A "linker" is any chemical moiety that is capable of linking a compound, usually a drug, such as a maytansinoid, to a cell-binding agent such as an anti CD37 antibody or a fragment thereof in a stable, covalent manner. Linkers can be susceptible to or be substantially resistant to acid-induced cleavage, light-induced cleavage, peptidase-induced cleavage, esterase-induced cleavage, and disulfide bond cleavage, at conditions under which the compound or the antibody remains active. Suitable linkers are well known in the art and include, for example, disulfide groups, thioether groups, acid labile groups, photolabile groups, peptidase labile groups and esterase labile groups. Linkers also include charged linkers, and hydrophilic forms thereof as described herein and known in the art.

[0068] The terms "cancer" and "cancerous" refer to or describe the physiological condition in mammals in which a population of cells are characterized by unregulated cell growth. Examples of cancer include, but are not limited to, carcinoma, lymphoma, blastoma, sarcoma, and leukemia. More particular examples of "cancer" or "tumorigenic" diseases include B-cell lymphomas including NHL, precursor B-cell lymphoblastic leukemia/lymphoma and mature B-cell neoplasms, such as B-cell chronic lymphocytic leukemia (CLL)/small lymphocytic lymphoma (SLL), B-cell prolymphocytic leukemia, lymphoplasmacytic lymphoma, mantle cell lymphoma (MCL), follicular lymphoma (FL), including low-grade, intermediate-

grade and high-grade FL, cutaneous follicle center lymphoma, marginal zone B-cell lymphoma (MALT type, nodal and splenic type), hairy cell leukemia, diffuse large B-cell lymphoma (DLBCL), Burkitt's lymphoma (BL), plasmacytoma, plasma cell myeloma, post-transplant lymphoproliferative disorder, and anaplastic large-cell lymphoma (ALCL).

[0069] "Tumor" and "neoplasm" refer to any mass that result from excessive cell growth or proliferation, either benign (noncancerous) or malignant (cancerous) including pre-cancerous lesions.

[0070] The terms "cancer cell," "tumor cell," and grammatical equivalents refer to the total population of cells derived from a tumor or a pre-cancerous lesion, including both non-tumorigenic cells, which comprise the bulk of the tumor cell population, and tumorigenic stem cells (cancer stem cells). As used herein, the term "tumor cell" will be modified by the term "non-tumorigenic" when referring solely to those tumor cells lacking the capacity to renew and differentiate to distinguish those tumor cells from cancer stem cells.

[0071] The term "subject" refers to any animal (e.g., a mammal), including, but not limited to humans, non-human primates, rodents, and the like, which is to be the recipient of a particular treatment. Typically, the terms "subject" and "patient" are used interchangeably herein in reference to a human subject.

[0072] Administration "in combination with" one or more further therapeutic agents includes simultaneous (concurrent) and consecutive administration in any order.

[0073] The term "pharmaceutical formulation" refers to a preparation which is in such form as to permit the biological activity of the active ingredient to be effective, and which contains no additional components which are unacceptably toxic to a subject to which the formulation would be administered. Such formulation can be sterile.

[0074] An "effective amount" of an antibody as disclosed herein is an amount sufficient to carry out a specifically stated purpose. An "effective amount" can be determined empirically and in a routine manner, in relation to the stated purpose.

[0075] The term "therapeutically effective amount" refers to an amount of an antibody or other drug effective to "treat" a disease or disorder in a subject or mammal. In the case of cancer, the therapeutically effective amount of the drug can reduce the number of cancer cells; reduce the tumor size; inhibit (i.e., slow to some extent or stop) cancer cell infiltration into peripheral organs; inhibit (i.e., slow to some extent or stop) tumor metastasis; inhibit, to some extent, tumor growth; and/or relieve to some extent one or more of the symptoms associated with the cancer. See the definition herein of "treating." To the extent the drug can prevent growth and/or kill existing cancer cells, it can be cytostatic and/or cytotoxic. A "prophylactically effective amount"

refers to an amount effective, at dosages and for periods of time necessary, to achieve the desired prophylactic result. Typically but not necessarily, since a prophylactic dose is used in subjects prior to or at an earlier stage of disease, the prophylactically effective amount will be less than the therapeutically effective amount.

[0076] The term "respond favorably" generally refers to causing a beneficial state in a subject. With respect to cancer treatment, the term refers to providing a therapeutic effect on the subject. Positive therapeutic effects in cancer can be measured in a number of ways (*See*, W.A. Weber, J. Nucl. Med. 50:1S-10S (2009)). For example, tumor growth inhibition, molecular marker expression, serum marker expression, and molecular imaging techniques can all be used to assess therapeutic efficacy of an anti-cancer therapeutic. With respect to tumor growth inhibition, according to NCI standards, a $T/C \leq 42\%$ is the minimum level of anti-tumor activity. A $T/C < 10\%$ is considered a high anti-tumor activity level, with $T/C (\%) = \text{Median tumor volume of the treated} / \text{Median tumor volume of the control} \times 100$. Progression-free survival (PFS), disease-free survival (DFS), or overall survival (OS) can also be used to assess the therapeutic efficacy of an anti-cancer therapeutic.

[0077] PFS, DFS, and OS can be measured by standards set by the National Cancer Institute and the U.S. Food and Drug Administration for the approval of new drugs. *See* Johnson et al, (2003) J. Clin. Oncol. 21(7):1404-1411. "Progression free survival" (PFS), also referred to as or "Time to Tumor Progression" (TTP) indicates the length of time during and after treatment that the cancer does not grow. Progression-free survival includes the amount of time patients have experienced a complete response or a partial response, as well as the amount of time patients have experienced stable disease. "Disease free survival" (DFS) refers to the length of time during and after treatment that the patient remains free of disease. "Overall Survival" (OS) refers to a prolongation in life expectancy as compared to naive or untreated individuals or patients.

[0078] The word "label" when used herein refers to a detectable compound or composition which is conjugated directly or indirectly to the antibody so as to generate a "labeled" antibody. The label can be detectable by itself (e.g., radioisotope labels or fluorescent labels) or, in the case of an enzymatic label, can catalyze chemical alteration of a substrate compound or composition which is detectable.

[0079] A "chemotherapeutic agent" is a chemical compound useful in the treatment of cancer, regardless of mechanism of action. Classes of chemotherapeutic agents include, but are not limited to: alkylating agents, antimetabolites, spindle poison plant alkaloids, cytotoxic/antitumor antibiotics, topoisomerase inhibitors, antibodies, photosensitizers, and kinase

inhibitors. Chemotherapeutic agents include compounds used in "targeted therapy" and conventional chemotherapy.

[0080] Terms such as "treating" or "treatment" or "to treat" or "alleviating" or "to alleviate" refer to therapeutic measures that cure, slow down, lessen symptoms of, and/or halt progression of a diagnosed pathologic condition or disorder. Thus, those in need of treatment include those already diagnosed with or suspected of having the disorder. Prophylactic or preventative measures refer to therapeutic measures that prevent and/or slow the development of a targeted pathologic condition or disorder. Thus, those in need of prophylactic or preventative measures include those prone to have the disorder and those in whom the disorder is to be prevented. In certain embodiments, a subject is successfully "treated" for cancer according to the methods of the present invention if the patient shows one or more of the following: a reduction in the number of or complete absence of cancer cells; a reduction in the tumor size; inhibition of or an absence of cancer cell infiltration into peripheral organs including, for example, the spread of cancer into soft tissue and bone; inhibition of or an absence of tumor metastasis; inhibition or an absence of tumor growth; relief of one or more symptoms associated with the specific cancer; reduced morbidity and mortality; improvement in quality of life; reduction in tumorigenicity, tumorigenic frequency, or tumorigenic capacity, of a tumor; reduction in the number or frequency of cancer stem cells in a tumor; differentiation of tumorigenic cells to a non-tumorigenic state; or some combination of effects.

[0081] As used in the present disclosure and claims, the singular forms "a," "an," and "the" include plural forms unless the context clearly dictates otherwise.

[0082] It is understood that wherever embodiments are described herein with the language "comprising," otherwise analogous embodiments described in terms of "consisting of" and/or "consisting essentially of" are also provided.

[0083] The term "and/or" as used in a phrase such as "A and/or B" herein is intended to include both "A and B," "A or B," "A," and "B." Likewise, the term "and/or" as used in a phrase such as "A, B, and/or C" is intended to encompass each of the following embodiments: A, B, and C; A, B, or C; A or C; A or B; B or C; A and C; A and B; B and C; A (alone); B (alone); and C (alone).

II. Biological samples

[0084] Biological samples are often fixed with a fixative. Aldehyde fixatives such as formalin (formaldehyde) and glutaraldehyde are typically used. Samples fixed using other fixation techniques such as alcohol immersion (Battifora and Kopinski, J. Histochem.

Cytochem. (1986) 34:1095) are also suitable. The samples used may also be embedded in paraffin. In one embodiment, the samples are both formalin-fixed and paraffin-embedded (FFPE). In another embodiment, the FFPE block is hematoxylin and eosin stained prior to selecting one or more portions for analysis in order to select specific area(s) for the FFPE core sample. Methods of preparing tissue blocks from these particulate specimens have been used in previous IHC studies of various prognostic factors, and/or is well known to those of skill in the art (see, for example, Abbondanzo et al., Am J Clin Pathol. 1990 May;93(5):698-702; Allred et al., Arch Surg. 1990 Jan;125(1):107-13).

[0085] Briefly, any intact organ or tissue may be cut into fairly small pieces and incubated in various fixatives (e.g., formalin, alcohol, etc.) for varying periods of time until the tissue is "fixed". The samples may be virtually any intact tissue surgically removed from the body. The samples may be cut into reasonably small piece(s) that fit on the equipment routinely used in histopathology laboratories. The size of the cut pieces typically ranges from a few millimeters to a few centimeters. The biological sample can also be fluidic extracts, blood, plasma, serum, spinal fluid, bone marrow aspirate, bone marrow biopsy, lymph fluid, or splenic preparations.

III. Detection Antibody Conjugates

[0086] The present invention further provides antibodies against CD37, generally of the monoclonal type, that are linked to at least one agent to form a detection antibody conjugate. In order to increase the efficacy of antibody molecules as diagnostic it is conventional to link or covalently bind or complex at least one desired molecule or moiety. Such a molecule or moiety may be, but is not limited to, at least one reporter molecule. A reporter molecule is defined as any moiety that may be detected using an assay. Non-limiting examples of reporter molecules that have been conjugated to antibodies include enzymes, radiolabels, haptens, fluorescent labels, phosphorescent molecules, chemiluminescent molecules, chromophores, luminescent molecules, photoaffinity molecules, colored particles and/or ligands, such as biotin.

[0087] Any antibody of sufficient selectivity, specificity or affinity may be employed as the basis for a detection antibody conjugate. Such properties may be evaluated using conventional immunological screening methodology known to those of skill in the art. Sites for binding to biological active molecules in the antibody molecule, in addition to the canonical antigen binding sites, include sites that reside in the variable domain that can bind the antigen. In addition, the variable domain is involved in antibody self-binding (Kang et al., 1988) and contains epitopes (idiotypes) recognized by anti-antibodies (Kohler et al., 1989).

[0088] Certain examples of antibody conjugates are those conjugates in which the antibody is linked to a detectable label. "Detectable labels" are compounds and/or elements that can be detected due to their specific functional properties, and/or chemical characteristics, the use of which allows the antibody to which they are attached to be detected, and/or further quantified if desired.

[0089] Many appropriate imaging agents are known in the art, as are methods for their attachment to antibodies (see, for e.g., U.S. Pat. Nos. 5,021,236; 4,938,948; and 4,472,509, each incorporated herein by reference). The imaging moieties used can be paramagnetic ions; radioactive isotopes; fluorochromes; NMR-detectable substances; and/or X-ray imaging, for example.

[0090] Exemplary fluorescent labels contemplated for use as conjugates include Alexa 350, Alexa 430, Alexa 488, AMCA, BODIPY 630/650, BODIPY 650/665, BODIPY-FL, BODIPY-R6G, BODIPY-TMR, BODIPY-TRX, Cascade Blue, Cy3, Cy5, 6-FAM, Dylight 488, Fluorescein Isothiocyanate (FITC), Green fluorescent protein (GFP), HEX, 6-JOE, Oregon Green 488, Oregon Green 500, Oregon Green 514, Pacific Blue, Phycoerythrin, REG, Rhodamine Green, Rhodamine Red, tetramethyl rhodamine (TMR), Renographin, ROX, TAMRA, TET, Tetramethylrhodamine, Texas Red, and derivatives of these labels (i.e., halogenated analogues, modified with isothiocyanate or other linker for conjugating, etc.), for example.

[0091] Detection antibody conjugates contemplated in the present invention include those for use *in vitro*, where the antibody is linked to a secondary binding ligand and/or to an enzyme (an enzyme tag) that will generate a colored product upon contact with a chromogenic substrate. Examples of suitable enzymes include urease, alkaline phosphatase, (horseradish) hydrogen peroxidase and/or glucose oxidase. Preferred secondary binding ligands are biotin and/or avidin and streptavidin compounds. The use of such labels is well known to those of skill in the art and are described, for example, in U.S. Pat. Nos. 3,817,837; 3,850,752; 3,939,350; 3,996,345; 4,277,437; 4,275,149 and 4,366,241; each incorporated herein by reference.

[0092] Molecules containing azido groups may also be used to form covalent bonds to proteins through reactive nitrene intermediates that are generated by low intensity ultraviolet light (Potter & Haley, 1983). In particular, 2- and 8-azido analogues of purine nucleotides have been used as site-directed photoprobes to identify nucleotide binding proteins in crude cell extracts (Owens & Haley, 1987; Atherton et al., 1985). The 2- and 8-azido nucleotides have also been used to map nucleotide binding domains of purified proteins (Khatoon et al., 1989; King et al., 1989; and Dholakia et al., 1989) and may be used as antibody binding agents.

[0093] Several methods are known in the art for the attachment or conjugation of an antibody to its conjugate moiety. Some attachment methods involve the use of a metal chelate complex employing, for example, an organic chelating agent such as diethylenetriaminepentaacetic acid anhydride (DTPA); ethylenetriaminetetraacetic acid; N-chloro-p-toluenesulfonamide; and/or tetrachloro-3 α -6 α -diphenylglycouril-3 attached to the antibody (U.S. Pat. Nos. 4,472,509 and 4,938,948, each incorporated herein by reference). Monoclonal antibodies may also be reacted with an enzyme in the presence of a coupling agent such as glutaraldehyde or periodate. Conjugates with fluorescein markers are prepared in the presence of these coupling agents or by reaction with an isothiocyanate. In U.S. Pat. No. 4,938,948, imaging of breast tumors, for example, is achieved using monoclonal antibodies, and the detectable imaging moieties are bound to the antibody using linkers such as methyl-p-hydroxybenzimidate or N-succinimidyl-3-(4-hydroxyphenyl)propionate.

[0094] In other embodiments, derivatization of immunoglobulins by selectively introducing sulfhydryl groups in the Fc region of an immunoglobulin using reaction conditions that do not alter the antibody combining site are contemplated. Antibody conjugates produced according to this methodology are disclosed to exhibit improved longevity, specificity and sensitivity (U.S. Pat. No. 5,196,066, incorporated herein by reference). Site-specific attachment of effector or reporter molecules, wherein the reporter or effector molecule is conjugated to a carbohydrate residue in the Fc region, have also been disclosed in the literature (O'Shannessy et al., 1987).

[0095] In other embodiments of the invention, immunoglobulins are radiolabeled with nuclides such as tritium. In additional embodiments, nanogold particles (such as sizes from about 0.5 nm-40 nm) and/or Quantum Dots (Hayward, Calif.) are employed.

IV. Enzymes and Substrates (Chromagens)

[0096] The use of substrates and indicators is contemplated for detection of CD37, such as the exemplary embodiments provided below, for example.

[0097] Horseradish peroxidase (HRP) is an enzyme that first forms a complex with hydrogen peroxide and then causes it to decompose, resulting in water and atomic oxygen. Like many other enzymes, HRP and some HRP-like activities can be inhibited by excess substrate. The complex formed between HRP and excess hydrogen peroxide is catalytically inactive and in the absence of an electron donor (e.g. chromogenic substance) is reversibly inhibited. It is the excess hydrogen peroxide and the absence of an electron donor that brings about quenching of endogenous HRP activities.

[0098] When used in assays systems, HRP can also be used to convert a defined substrate into its activated chromagen, thus causing a color change. The HRP enzyme may be conjugated to an antibody, protein, peptide, polymer, or other molecule by a number of methods. Such methods are known in the art. Adding glutaraldehyde to a solution containing an admixture of HRP and antibody will result in more antibody molecules being conjugated to each other than to the enzyme. In the two-step procedure, HRP reacts with the bifunctional reagents first. In the second stage, only activated HRP is admixed with the antibody, resulting in much more efficient labelling and no polymerization. HRP is also conjugated to (strept)avidin using the two-step glutaraldehyde procedure. This form is used in procedures where LAB and LSAB are substrate, for example. Conjugation with biotin also involves two steps, as biotin must first be derivatized to the biotinyl-N-hydroxysuccinimide ester or to biotin hydrazide before it can be reacted with the epsilonamino groups of the HRP enzyme.

[0099] 3,3'-diaminobenzidine (DAB) is a substrate for enzymes such as HRP that produces a brown end product that is highly insoluble in alcohol and other organic solvents. Oxidation of DAB also causes polymerization, resulting in the ability to react with osmium tetroxide, and thus increasing its staining intensity and electron density. Of the several metals and methods used to intensify the optical density of polymerized DAB, gold chloride in combination with silver sulfide appears to be the most successful.

[00100] 3-Amino-9-ethylcarbazole (AEC), is a substrate for enzymes such as HRP, and upon oxidation, forms a rose-red end product that is alcohol soluble. Therefore, specimens processed with AEC must not be immersed in alcohol or alcoholic solutions (e.g., Harris' hematoxylin). Instead, an aqueous counterstain and mounting medium should be used. AEC is unfortunately susceptible to further oxidation and, when exposed to excessive light, will fade in intensity. Storage in the dark is therefore recommended.

[00101] 4-Chloro-1-naphthol (CN) is a substrate for enzymes such as HRP that precipitates as a blue end product. Because CN is soluble in alcohol and other organic solvents, the specimen must not be dehydrated, exposed to alcoholic counterstains, or coverslipped with mounting media containing organic solvents. Unlike DAB, CN tends to diffuse from the site of precipitation.

[0100] p-Phenylenediamine dihydrochloride/pyrocatechol (Hanker-Yates reagent) is a substrate for enzymes such as HRP that gives a blue-black reaction product that is insoluble in alcohol and other organic solvents. Like polymerized DAB, this reaction product can be osmicated. Varying results have been achieved with Hanker-Yates reagent in immunoperoxidase techniques.

[0101] Calf intestine alkaline phosphatase (AP) (molecular weight 100 kD) removes (by hydrolysis) and transfers phosphate groups from organic esters by breaking the P-O bond; an intermediate enzyme-substrate bond is briefly formed. The chief metal activators for AP are Mg^{++} , Mn^{++} and Ca^{++} .

[0102] AP had not been used extensively in immunohistochemistry until publication of the unlabeled alkaline phosphatase/alkaline phosphatase (APAAP) procedure. The soluble immune complexes utilized in this procedure have molecular weights of approximately 560 kD. The major advantage of the APAAP procedure compared to the PAP technique is the lack of interference posed by endogenous peroxidase activity. Because of the potential distraction of endogenous peroxidase activity on PAP staining, the APAAP technique is recommended for use on blood and bone marrow smears. Endogenous alkaline phosphatase activity from bone, kidney, liver and some white cells can be inhibited by the addition of 1 mM levamisole to the substrate solution, although 5 mM has been found to be more effective. Intestinal alkaline phosphatases are not adequately inhibited by levamisole.

[0103] In the immunoalkaline phosphatase staining method, the enzyme hydrolyzes naphthol phosphate esters (substrate) to phenolic compounds and phosphates. The phenols couple to colorless diazonium salts (chromogen) to produce insoluble, colored azo dyes. Several different combinations of substrates and chromogens have been used successfully.

[0104] Naphthol AS-MX phosphate AP substrate can be used in its acid form or as the sodium salt. The chromogen substrate Fast Red TR and Fast Blue BB produce a bright red or blue end product, respectively. Both are soluble in alcoholic and other organic solvents, so aqueous mounting media must be used. Fast Red TR is preferred when staining cell smears.

[0105] Additional exemplary substrates include naphthol AS-BI phosphate, naphthol AS-TR phosphate and 5-bromo-4-chloro-3-indoxyl phosphate (BCIP). Other possible chromogens include Fast Red LB, Fast Garnet GBC, Nitro Blue Tetrazolium (NBT) and iodonitrotetrazolium Violet (INT), for example.

V. Immunodetection Methods

[0106] In still further embodiments, the present invention concerns immunodetection methods for binding, purifying, removing, quantifying and/or otherwise generally detecting biological components such as CD37 as contemplated by the present invention. The antibodies prepared in accordance with the present invention may be employed to detect CD37. Some immunodetection methods include immunohistochemistry, flow cytometry, enzyme linked immunosorbent assay (ELISA), radioimmunoassay (RIA), immunoradiometric assay,

fluoroimmunoassay, chemiluminescent assay, bioluminescent assay, and Western blot to mention a few. The steps of various useful immunodetection methods have been described in the scientific literature, such as, e.g., Doolittle M H and Ben-Zeev O, *Methods Mol Biol.* 1999;109:215-37; Gulbis B and Galand P, *Hum Pathol.* 1993 Dec;24(12):1271-85; and De Jager R et al., *Semin Nucl Med.* 1993 Apr;23(2):165-79, each incorporated herein by reference.

[0107] In general, the immunobinding methods include obtaining a sample suspected of comprising ligand protein, polypeptide and/or peptide, and contacting the sample with a first anti-ligand antibody in accordance with the present invention, as the case may be, under conditions effective to allow the formation of immunocomplexes.

[0108] In terms of antigen detection, the biological sample analyzed may be any sample in which it is desirable to detect CD37, such as a fluidic extract, blood, plasma, serum, spinal fluid, lymph fluid, tissue section or specimen, homogenized tissue extract, biopsy aspirates, a cell, separated and/or purified forms of CD37-containing compositions, or any biological fluid. In some embodiments, blood, plasma, tissue or lymph samples or extracts are used.

[0109] Contacting the chosen biological sample with the antibody under effective conditions and for a period of time sufficient to allow the formation of immune complexes (primary immune complexes) is generally a matter of simply adding the antibody composition to the sample and incubating the mixture for a period of time long enough for the antibodies to form immune complexes with, i.e., to bind to, any ligand protein antigens present. After this time, the sample-antibody composition, such as a tissue section, ELISA plate, dot blot or western blot, will generally be washed to remove any non-specifically bound antibody species, allowing only those antibodies specifically bound within the primary immune complexes to be detected.

[0110] In general, the detection of immunocomplex formation is well known in the art and may be achieved through the application of numerous approaches. These methods are generally based upon the detection of a label or marker, such as any of those radioactive, fluorescent, biological and enzymatic tags. U.S. Patents concerning the use of such labels include U.S. Pat. Nos. 3,817,837; 3,850,752; 3,939,350; 3,996,345; 4,277,437; 4,275,149 and 4,366,241, each incorporated herein by reference. Of course, one may find additional advantages through the use of a secondary binding ligand such as a second antibody and/or a biotin/avidin ligand binding arrangement, as is known in the art.

[0111] The anti-ligand antibody employed in the detection may itself be linked to a detectable label, wherein one would then simply detect this label, thereby allowing the amount of the primary immune complexes in the composition to be determined. Alternatively, the first

antibody that becomes bound within the primary immune complexes may be detected by means of a second binding agent that has binding affinity for the antibody. In these cases, the second binding agent may be linked to a detectable label. The second binding agent is itself often an antibody, which may thus be termed a "secondary" antibody. The primary immune complexes are contacted with the labeled, secondary binding agent, or antibody, under effective conditions and for a period of time sufficient to allow the formation of secondary immune complexes. The secondary immune complexes are then generally washed to remove any non-specifically bound labeled secondary antibodies or ligands, and the remaining label in the secondary immune complexes is then detected.

[0112] Further methods include the detection of primary immune complexes by a two-step approach. A second binding agent, such as an antibody, that has binding affinity for the antibody is used to form secondary immune complexes, as described above. After washing, the secondary immune complexes are contacted with a third binding agent or antibody that has binding affinity for the second antibody, again under effective conditions and for a period of time sufficient to allow the formation of immune complexes (tertiary immune complexes). The third ligand or antibody is linked to a detectable label, allowing detection of the tertiary immune complexes thus formed. This system may provide for signal amplification if this is desired.

[0113] In another embodiment, a biotinylated monoclonal or polyclonal antibody is used to detect the target antigen(s), and a second step antibody is then used to detect the biotin attached to the complexed biotin. In that method the sample to be tested is first incubated in a solution comprising the first step antibody. If the target antigen is present, some of the antibody binds to the antigen to form a biotinylated antibody/antigen complex. The antibody/antigen complex is then amplified by incubation in successive solutions of streptavidin (or avidin), biotinylated DNA, and/or complementary biotinylated DNA, with each step adding additional biotin sites to the antibody/antigen complex. The amplification steps are repeated until a suitable level of amplification is achieved, at which point the sample is incubated in a solution comprising the second step antibody against biotin. This second step antibody is labeled, as for example with an enzyme that can be used to detect the presence of the antibody/antigen complex by histoenzymology using a chromogen substrate. With suitable amplification, a conjugate can be produced that is macroscopically visible.

[0114] In one embodiment, immunohistochemistry (IHC) is used for immunological detection. Using IHC, detection of CD37 in a sample can be achieved by targeting a sample with a probe, e.g., an anti-CD37 antibody. The probe can be linked, either directly or indirectly

to a detectable label or can be detected by another probe that is linked, either directly or indirectly to a detectable label.

[0115] In some embodiments, the IHC can distinguish between different levels of protein expression, e.g., calibrated IHC. In some embodiments, the IHC can distinguish staining intensity for samples having low cell surface CD37 expression, intermediate CD37 cell surface expression, or high CD37 cell surface expression.

[0116] In some embodiments, the IHC can distinguish between staining intensity and staining uniformity. In one embodiment, immunological detection (by immunohistochemistry) of CD37 is scored for both intensity and uniformity (percent of stained cells – membrane only). Comparative scales for CD37 expression for intensity correlate as 0 – Negative, 0-1 - Very Weak, 1 – Weak, 1-2 - Weak to Moderate, 2 – Moderate, 2-3 - Moderate to Strong, 3 – Strong, 3+ - Very Strong. Quantitatively, Score 0 represents that no staining is observed or membrane staining is observed in less than 10% of tumor cells. Score 1 represents that a faint/barely perceptible membrane staining is detected in more than 10% of the tumor cells. The cells are only stained in part of their membrane. For Score 2, a moderate complete membrane staining is observed in more than 10% of the tumor cells. Lastly, Score 3 represents that a strong complete membrane staining is observed in more than 10% of the tumor cells. Those samples with 0 or 1 score for CD37 expression can be characterized as not overexpressing CD37, whereas those samples with 2 or 3 scores can be characterized as overexpressing CD37. Samples overexpressing CD37 can also be rated by immunohistochemical scores corresponding to the number of copies of CD37 molecules expressed per cell, or antibodies bound per cell (ABC), and can be determined biochemically. Comparative scales for CD37 percent cell membrane staining uniformity correlate as follows: 0 – Negative, Focal - <25%, heterogeneous (hetero) - 25-75%, and homogeneous (homo) - >75%.

[0117] IHC can be performed manually or using an automated system (e.g., using an automated stainer). Thus, IHC can be performed on cells, cell pellets, tissues, preparations from blood, plasma, serum, or lymph fluid, etc. In some embodiments, the samples are fixed samples. In some embodiments, the samples are paraffin embedded samples. In some embodiments, the samples are formalin fixed and paraffin embedded samples.

[0118] Another known method of immunodetection takes advantage of the immuno-PCR (Polymerase Chain Reaction) methodology. The PCR method uses a DNA/biotin/streptavidin/antibody complex that is washed out with a low pH or high salt buffer that releases the antibody. The resulting wash solution is then used to carry out a PCR reaction with suitable primers with appropriate controls. In specific embodiments, the enormous

amplification capability and specificity of PCR can be utilized to detect a single antigen molecule. Such detection may take place in real-time. For example, the use of quantitative real-time PCR is contemplated.

[0119] In one embodiment, flow cytometry is used for immunological detection. Thus, for example, the number of antibodies bound per cell (ABC) can be assessed using flow cytometry. A high number of anti-CD37 antibodies bound per cell can indicate high CD37 expression levels and a high likelihood to be susceptible to treatment with an anti-CD37 antibody or immunoconjugate thereof.

VI. Nucleic Acid Hybridization

[0120] In situ hybridization is generally carried out on cells or tissue sections fixed to slides. In situ hybridization may be performed by several conventional methodologies (See for e.g., Leitch et al. *In situ Hybridization: a practical guide*, Oxford BIOS Scientific Publishers, Microscopy handbooks v. 27 (1994)). In one in situ procedure, fluorescent dyes (such as fluorescein isothiocyanate (FITC) that fluoresces green when excited by an Argon ion laser) are used to label a nucleic acid sequence probe that is complementary to a target nucleotide sequence in the cell. Each cell comprising the target nucleotide sequence will bind the labeled probe, producing a fluorescent signal upon exposure of the cells to a light source of a wavelength appropriate for excitation of the specific fluorochrome used.

[0121] Various degrees of hybridization stringency can be employed. As the hybridization conditions become more stringent, a greater degree of complementarity is required between the probe and target to form and maintain a stable duplex. Stringency is increased by raising temperature, lowering salt concentration, or raising formamide concentration. Adding dextran sulfate or raising its concentration may also increase the effective concentration of labeled probe to increase the rate of hybridization and ultimate signal intensity. After hybridization, slides are washed in a solution generally comprising reagents similar to those found in the hybridization solution with washing time varying from minutes to hours depending on required stringency. Longer or more stringent washes typically lower nonspecific background but run the risk of decreasing overall sensitivity.

[0122] Probes used in nucleic hybridization analysis may be either RNA or DNA oligonucleotides or polynucleotides and may contain not only naturally-occurring nucleotides but their analogs, like digoxigenin dCTP, biotin dCTP 7-azaguanosine, azidothymidine, inosine, or uridine, for example. Other useful probes include peptide probes and analogues thereof, branched gene DNA, peptidomimetics, peptide nucleic acid (PNA) and/or antibodies, for example.

[0123] Probes should have sufficient complementarity to the target nucleic acid sequence of interest so that stable and specific binding occurs between the target nucleic acid sequence and the probe. The degree of homology required for stable hybridization varies with the stringency of the hybridization medium and/or wash medium. Preferably, completely homologous probes are employed in the present invention, but persons of skill in the art will readily appreciate that probes exhibiting lesser but sufficient homology can be used in the present invention (see for e.g., Sambrook, J., Fritsch, E. F., Maniatis, T., *Molecular Cloning A Laboratory Manual*, Cold Spring Harbor Press, (1989)).

[0124] Probes may also be generated and chosen by several means including, but not limited to, mapping by in situ hybridization, somatic cell hybrid panels, or spot blots of sorted chromosomes; chromosomal linkage analysis; or cloned and isolated from sorted chromosome libraries from human cell lines or somatic cell hybrids with human chromosomes, radiation somatic cell hybrids, microdissection of a chromosome region, or from yeast artificial chromosomes (YACs) identified by PCR primers specific for a unique chromosome locus or other suitable means like an adjacent YAC clone. Probes may be genomic DNA, cDNA, or RNA cloned in a plasmid, phage, cosmid, YAC, Bacterial Artificial Chromosomes (BACs), viral vector, or any other suitable vector. Probes may be cloned or synthesized chemically by conventional methods. When cloned, the isolated probe nucleic acid fragments are typically inserted into a vector, such as lambda phage, pBR322, M13, or vectors containing the SP6 or T7 promoter and cloned as a library in a bacterial host. [See for e.g., Sambrook, J., Fritsch, E. F., Maniatis, T., *Molecular Cloning A Laboratory Manual*, Cold Spring Harbor Press, (1989)].

[0125] Probes are preferably labeled, such as with a fluorophor, for example. Examples of fluorophores include, but are not limited to, rare earth chelates (europium chelates), Texas Red, rhodamine, fluorescein, dansyl, Lissamine, umbelliferone, phycocrytherin, phycocyanin, or commercially available fluorophors such SPECTRUM ORANGE™ and SPECTRUM GREEN™ and/or derivatives of any one or more of the above. Multiple probes used in the assay may be labeled with more than one distinguishable fluorescent or pigment color. These color differences provide a means to identify the hybridization positions of specific probes. Moreover, probes that are not separated spatially can be identified by a different color light or pigment resulting from mixing two other colors (e.g., light red+green=yellow) pigment (e.g., blue+yellow=green) or by using a filter set that passes only one color at a time.

[0126] Probes can be labeled directly or indirectly with the fluorophor, utilizing conventional methodology known to one with skill in the art.

VII. Detection Kits and Compositions

[0127] Also provided by the invention are kits for use in the practice of the present invention as disclosed herein. Such kits may comprise containers, each with one or more of the various reagents (typically in concentrated form) utilized in the methods, including, for example, one or more binding agents (antibodies), already attached to a marker or optionally with reagents for coupling a binding agent to an antibody or nucleic acid molecule (as well as the marker itself); buffers, the appropriate nucleotide triphosphates (e.g., dATP, dCTP, dGTP, dTTP, dUTP, ATP, CTP, GTP and UTP), reverse transcriptase, DNA polymerase, RNA polymerase, and one or more sequence-specific or degenerate primers for use in detection of nucleic acid molecules by amplification; and/or reagents and instrumentation for the isolation (optionally by microdissection) to support the practice of the invention. A label or indicator describing, or a set of instructions for use of, kit components in a ligand detection method of the present invention, will also be typically included, where the instructions may be associated with a package insert and/or the packaging of the kit or the components thereof.

[0128] In still further embodiments, the present invention concerns immunodetection kits for use with the immunodetection methods described above. As the antibodies are generally used to detect CD37, the antibodies will preferably be included in the kit. The immunodetection kits will thus comprise, in suitable container means, a first antibody that binds to CD37, and/or optionally, an immunodetection reagent and/or further optionally, a CD37 protein or cell or sample containing a CD37 protein.

[0129] The immunodetection reagents of the kit may take any one of a variety of forms, including those detectable labels that are associated with and/or linked to the given antibody. Detectable labels that are associated with and/or attached to a secondary binding ligand are also contemplated. Exemplary secondary ligands are those secondary antibodies that have binding affinity for the first antibody.

[0130] Further suitable immunodetection reagents for use in the present kits include the two-component reagent that comprises a secondary antibody that has binding affinity for the first antibody, along with a third antibody that has binding affinity for the second antibody, the third antibody being linked to a detectable label. As noted above, a number of exemplary labels are known in the art and/or all such labels may be suitably employed in connection with the present invention.

[0131] The kits may further comprise one or more therapeutic agents for the treatment of cancer, such as an anti-CD37 immunoconjugate and/or a chemotherapeutic agent.

[0132] The kit may further comprise an a CD37 detection reagent used to measure CD37 expression in a subject comprising a CD37 detection reagent, and instructions for use. In one embodiment, the CD37 detection reagent comprises a CD37 binding peptide, protein or a molecular probe (i.e., nucleic acid). In another embodiment, the CD37 detection reagent is an anti- CD37 antibody. In another embodiment, the kit further comprises a secondary antibody which binds the anti- CD37 antibody. In one embodiment the CD37 -specific antibody is included at a concentration of 2.1, 4.2, and 8.4 $\mu\text{g/mL}$. In another embodiment, the antibody is included in concentrated solution with instructions for dilutions to achieve a final concentration of 2.1, 4.2, and 8.4 $\mu\text{g/mL}$. In another embodiment, the kit further comprises a detection reagent selected from the group consisting of: an enzyme, a fluorophore, a radioactive label, and a luminophore. In another embodiment, the detection reagent is selected from the group consisting of: biotin, digoxigenin, fluorescein, tritium, and rhodamine.

[0133] The kit can also include instructions for detection and scoring of CD37 expression. The kit can also include control or reference samples. Non-limiting examples of control or reference samples include cell pellets or tissue culture cell lines derived from negative normal tissue (negative control) or tumor (positive control) samples. Exemplary positive control cell lines include Daudi, Ramos, Namalwa and a negative control includes Colo205 and cell lines stably or transiently transfected with an expression vector that expresses CD37.

VIII. CD37-binding agents

[0134] Any antibodies that bind CD37 can be used in the detection methods of the present invention. Examples of therapeutically effective anti-CD37 antibodies, which can be used in the present methods can be found in US Published Appl. No. 2011/0256153, which is herein incorporated by reference. For example, the anti-CD37 antibody can be mouse, chimiere, or humanized CD37-3, CD37-12, CD37-38, CD37-50, CD37-51, CD37-56 or CD37-57. The full-length amino acid sequence for CD37 is known in the art and also provided herein as represented by SEQ ID NO: 1. A specifically useful antibody for detection of CD37 is the mouse monoclonal anti-huCD37 clone CT1 (Leica # NCL-CD37). An example of a therapeutically effective anti-CD37 antibody is huCD37-3-SMCC-DM1. The polypeptide of SEQ ID NO: 57 corresponds to the variable domain heavy chain version 1.0 of huCD37-3. The polypeptide of SEQ ID NO: 58 corresponds to the variable domain heavy chain version 1.1 of huCD37-3, and the polypeptide of SEQ ID NO: 74 corresponds to the variable domain light chain of huCD37-3, respectively. In certain embodiments, the CD37 antibody can comprise a light chain encoded by the recombinant plasmid DNA phuCD37-3LC (ATCC Deposit

Designation PTA-10722, deposited with the ATCC (10801 University Boulevard, Manassas, Virginia 20110) on March 18, 2010). In certain embodiments, the CD37 antibody can comprise a heavy chain encoded by the recombinant plasmid DNA phuCD37-3HCv.1.0 (ATCC Deposit Designation PTA-10723, deposited with the ATCC on March 18, 2010). In certain embodiments, the CD37 antibody can comprise a light chain encoded by the recombinant plasmid DNA phuCD37-3LC (PTA-10722) and a heavy chain encoded by the recombinant plasmid DNA phuCD37-3HCv.1.0 (PTA-10723). In certain embodiments, the CD37 antibody can comprise the VL-CDRs encoded by the recombinant plasmid DNA phuCD37-3LC (PTA-10722) and the VH-CDRs encoded by the recombinant plasmid DNA phuCD37-3HCv.1.0 (PTA-10723).

[0135] Examples of CD37 immunoconjugates useful in the therapeutic methods of the invention are provided below.

IX. CD37 Immunoconjugates

[0136] The present invention is also increasing the efficacy of conjugates (also referred to herein as immunoconjugates), comprising the anti-CD37 antibodies, antibody fragments, functional equivalents, improved antibodies and their aspects as disclosed herein, linked or conjugated to a cytotoxin (drug) or prodrug. Exemplary CD37 antibodies and immunoconjugates can be found in U.S. Published Application No. 2011/0256153, which is herein incorporated by reference. A particularly effective therapeutic immunoconjugate of the invention comprises the huCD37-3 antibody described above.

[0137] Suitable drugs or prodrugs are known in the art. In certain embodiments, drugs or prodrugs are cytotoxic agents. The cytotoxic agent used in the cytotoxic conjugate of the present invention can be any compound that results in the death of a cell, or induces cell death, or in some manner decreases cell viability, and includes, for example, maytansinoids and maytansinoid analogs, benzodiazepines, taxoids, CC-1065 and CC-1065 analogs, duocarmycins and duocarmycin analogs, enediynes, such as calicheamicins, dolastatin and dolastatin analogs including auristatins, tomaymycin derivatives, leptomycin derivatives, methotrexate, cisplatin, carboplatin, daunorubicin, doxorubicin, vincristine, vinblastine, melphalan, mitomycin C, chlorambucil and morpholino doxorubicin. In certain embodiments, the cytotoxic agents are maytansinoids and maytansinoids analogs.

[0138] The drug or prodrug can, for example, be linked to the anti-CD37 antibody, such as huCD37-3, or fragment thereof through a disulfide bond. The linker molecule or crosslinking agent comprises a reactive chemical group that can react with the anti-CD37 antibody or

fragment thereof. In certain embodiments, reactive chemical groups for reaction with the cell-binding agent are *N*-succinimidyl esters and *N*-sulfosuccinimidyl esters. Additionally the linker molecule comprises a reactive chemical group, in certain embodiments a dithiopyridyl group that can react with the drug to form a disulfide bond. In certain embodiments, linker molecules include, for example, *N*-succinimidyl 3-(2-pyridyldithio) propionate (SPDP) (see, e.g., Carlsson et al., *Biochem. J.*, 173: 723-737 (1978)), *N*-succinimidyl 4-(2-pyridyldithio)butanoate (SPDB) (see, e.g., U.S. Patent No. 4,563,304), *N*-succinimidyl 4-(2-pyridyldithio)2-sulfobutanoate (sulfo-SPDB) (see US Publication No. 20090274713), *N*-succinimidyl 4-(2-pyridyldithio) pentanoate (SPP) (see, e.g., CAS Registry number 341498-08-6), 2-iminothiolane, or acetylsuccinic anhydride.

[0139] Antibody-maytansinoid conjugates with non-cleavable links can also be prepared. Such crosslinkers are described in the art (see ThermoScientific Pierce Crosslinking Technical Handbook and US Patent Application Publication No. 2005/0169933) and include but are not limited to, *N*-succinimidyl 4-(maleimidomethyl) cyclohexanecarboxylate (SMCC), *N*-succinimidyl-4-(*N*-maleimidomethyl)-cyclohexane-1-carboxy-(6-amidocaproate), which is a "long chain" analog of SMCC (LC-SMCC), κ -maleimidoundecanoic acid *N*-succinimidyl ester (KMUA), β -maleimidopropanoic acid *N*-succinimidyl ester (BMPS), γ -maleimidobutyric acid *N*-succinimidyl ester (GMBS), ϵ -maleimidocaproic acid *N*-hydroxysuccinimide ester (EMCS), *m*-maleimidobenzoyl-*N*-hydroxysuccinimide ester (MBS), *N*-(α -maleimidoacetoxy)-succinimide ester (AMAS), succinimidyl-6-(β -maleimidopropionamido)hexanoate (SMPH), *N*-succinimidyl 4-(*p*-maleimidophenyl)-butyrate (SMPB), and *N*-(*p*-maleimidophenyl)isocyanate (PMPI), *N*-succinimidyl-4-(iodoacetyl)-aminobenzoate (SIAB), *N*-succinimidyl iodoacetate (SIA), *N*-succinimidyl bromoacetate (SBA), and *N*-succinimidyl 3-(bromoacetamido)propionate (SBAP). In certain embodiments, the antibody is modified with crosslinking reagents such as succinimidyl 4-(*N*-maleimidomethyl)-cyclohexane-1-carboxylate (SMCC), sulfo-SMCC, maleimidobenzoyl-*N*-hydroxysuccinimide ester (MBS), sulfo-MBS or succinimidyl-iodoacetate, as described in the literature, to introduce 1-10 reactive groups (Yoshitake et al, *Eur. J. Biochem.*, 101:395-399 (1979); Hashida et al, *J. Applied Biochem.*, 56-63 (1984); and Liu et al, *Biochem.*, 18:690-697 (1979)).

[0140] The present invention includes aspects wherein the average molar ratio of the cytotoxic agent (e.g., maytansinoid) to the cell-binding agent in the cell-binding agent cytotoxic agent conjugate is about 1 to about 10. The terms "MAR," "Maytansinoid-Ab Ratio," "drug load," "DAR," and "Drug-Ab Ratio" can be used herein to characterize the ratio of cytotoxic

agent to cell-binding agent in a conjugate comprising a maytansinoid compound as the cytotoxic agent and an antibody or fragment thereof as the cell binding agent. Thus, in some embodiments, the MAR is about 1 to about 10, about 2 to about 7, about 3 to about 5, about 2.5 to about 4.5 (e.g., about 2.5, about 2.6, about 2.7, about 2.8, about 2.9, about 3.0, about 3.1, about 3.3, about 3.4, about 3.5, about 3.6, about 3.7, about 3.8, about 3.9, about 4.0, about 4.1, about 4.2, about 4.3, about 4.4, about 4.5), about 3.0 to about 4.0, about 3.2 to about 4.2, about 4.5 to 5.5 (e.g., about 4.5, about 4.6, about 4.7, about 4.8, about 4.9, about 5.0, about 5.1, about 5.2, about 5.3, about 5.4, about 5.5). In one aspect, the number of drug molecules that can be attached to a cell binding agent can average from about 2 to about 8 (e.g., 1.9, 2.0, 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, 2.9, 3.0, 3.1, 3.2, 3.3, 3.4, 3.5, 3.6, 3.7, 3.8, 3.9, 4.0, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, 5.0, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6.0, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, 7.0, 7.1, 7.2, 7.3, 7.4, 7.5, 7.6, 7.7, 7.8, 7.9, 8.0, 8.1). In certain embodiments, the drug is *N*^{2'}-deacetyl-*N*^{2'}-(3-mercapto-1-oxopropyl)-maytansine (DM1) or *N*^{2'}-deacetyl-*N*^{2'}-(4-mercapto-4-methyl-1-oxopentyl) maytansine (DM4). Thus, in a certain embodiment, the antibody huCD37-3 is conjugated to DM1 or DM4.

X. Correlation of CD37 expression and therapeutic efficacy

[0141] In certain embodiments, the invention provides a method for identifying subjects with an increased likelihood for responding to CD37-targeting anti-cancer therapies. The invention is based, in part, on the discovery that elevated CD37 expression levels correlates with efficacy of CD37-targeting anti-cancer therapeutics and the discovery of methods of detecting a dynamic range of CD37 expression in B-cell samples.

[0142] Evaluation of patient samples and correlation to *in vivo* efficacy using xenograft models demonstrates the power of the expression analysis for selecting subjects more likely to respond to treatment. IHC provides a score for CD37 expression on tumor cells: 0 (no expression) to 3+ (very high levels of expression). Samples scoring 1, 2, 3, or 3+ for CD37 expression (or 2, 3, or 3+) have an increased likelihood to respond to CD37-targeted anti-cancer therapies at clinically-relevant doses of CD37 immunoconjugates (e.g., 0.1 to 10 or more mg/kg xenograft dose of a CD37 immunoconjugate can approximate a 3.0 to 400 mg/m² in patients). Thus, identification of individuals having an elevated CD37 score would help identify those individuals who might respond to a clinically relevant dosage. As described in more detail below, sensitivity to CD37 therapeutics may correlate with CD37 scoring of 2 or higher, especially with level 3 scoring. Moreover, expression of more uniform levels of CD37 can also be used as an indicator of correlation of CD37 expression with therapeutic benefit. Thus, a

homogenous staining uniformity or a combination of increased intensity with heterogenous staining uniformity could indicate increased CD37 expression. For example, scores of greater than 2 hetero may be used as a patient selection criterion for treatment with a CD37 therapeutic agent.

[0143] CD37 expression analysis also identifies patients in whom decreased levels of a CD37-targeting anti-cancer therapy ("low dose therapy") can be effective to cause anti-tumor responses. As is appreciated in the art, compounds are generally administered at the smallest dosage that achieves the desired therapeutic response. This is specifically important for therapeutics that cause clinical, and often undesired, side effects. The ability to recognize those subjects with elevated CD37 expression levels allows for minimization of the dosage of the CD37-targeting therapeutic, thus decreasing possible side effects, while maintaining therapeutic efficacy.

XI. Pharmaceutical compositions and therapeutic methods

[0144] CD37-binding agents (including antibodies, immunoconjugates, and polypeptides) are useful in a variety of applications including, but not limited to, therapeutic treatment methods, such as the treatment of cancer. In certain embodiments, the agents are useful for inhibiting tumor growth, inducing differentiation, reducing tumor volume, and/or reducing the tumorigenicity of a tumor. The methods of use may be *in vitro*, *ex vivo*, or *in vivo* methods. In certain embodiments, the CD37-binding agent or antibody or immunoconjugate, or polypeptide is an antagonist of the human CD37 to which it binds.

[0145] In certain embodiments, the disease treated with the CD37-binding agent or antagonist (e.g., a huCD37-3 antibody or immunoconjugate) is a cancer. In certain embodiments, the cancer is characterized by tumors expressing CD37 to which the CD37-binding agent (e.g., antibody) binds.

[0146] The present invention provides for methods of treating cancer comprising administering a therapeutically effective amount of a CD37-binding agent to a subject (e.g., a subject in need of treatment). In certain embodiments, the cancer is selected from the group consisting of B cell lymphomas, NHL, precursor B cell lymphoblastic leukemia/lymphoma and mature B cell neoplasms, B cell chronic lymphocytic leukemia (CLL)/small lymphocytic lymphoma (SLL), B cell prolymphocytic leukemia, lymphoplasmacytic lymphoma, mantle cell lymphoma (MCL), follicular lymphoma (FL), low grade, intermediate-grade and high-grade (FL), cutaneous follicle center lymphoma, marginal zone B cell lymphoma, MALT type marginal zone B cell lymphoma, nodal marginal zone B cell lymphoma, splenic type marginal

zone B cell lymphoma, hairy cell leukemia, diffuse large B cell lymphoma (DLBCL), Burkitt's lymphoma (BL), plasmacytoma, plasma cell myeloma, post-transplant lymphoproliferative disorder, Waldenstrom's macroglobulinemia, and anaplastic large-cell lymphoma (ALCL). In certain embodiments, the subject is a human.

[0147] The present invention further provides methods for inhibiting tumor growth using the antibodies or other agents described herein. In certain embodiments, the method of inhibiting the tumor growth comprises contacting the cell with a CD37-binding agent (e.g., antibody) *in vitro*. For example, an immortalized cell line or a cancer cell line that expresses CD37 is cultured in medium to which is added the antibody or other agent to inhibit tumor growth. In some embodiments, tumor cells are isolated from a patient sample such as, for example, a tissue biopsy, pleural effusion, or blood sample and cultured in medium to which is added an CD37-binding agent to inhibit tumor growth.

[0148] In some embodiments, the method of inhibiting tumor growth comprises contacting the tumor or tumor cells with the CD37-binding agent (e.g., antibody) *in vivo*. In certain embodiments, contacting a tumor or tumor cell with a CD37-binding agent is undertaken in an animal model. For example, CD37-binding agents can be administered to xenografts expressing one or more CD37s that have been grown in immunocompromised mice (e.g., NOD/SCID mice) to inhibit tumor growth. In some embodiments, the CD37-binding agent is administered at the same time or shortly after introduction of tumorigenic cells into the animal to prevent tumor growth. In some embodiments, the CD37-binding agent is administered as a therapeutic after the tumorigenic cells have grown to a specified size.

[0149] In certain embodiments, the method of inhibiting tumor growth comprises administering to a subject a therapeutically effective amount of a CD37-binding agent. In certain embodiments, the subject is a human. In certain embodiments, the subject has a tumor or has had a tumor removed.

[0150] Thus, in certain embodiments the inventions provides methods of treating cancer using a CD37-3 antibody (e.g., chimeric, humanized, or fully human) or immunoconjugate thereof, wherein the cancer is identified, using the methods described herein, as having increased CD37 expression. In a certain embodiment, the CD37-3 immunoconjugate is huCD37-3-SMCC-DM1.

[0151] In certain embodiments, formulations are prepared for storage and use by combining a purified antibody or agent of the present invention with a pharmaceutically acceptable vehicle (e.g., carrier, excipient) (Remington, The Science and Practice of Pharmacy 20th Edition Mack Publishing, 2000). Suitable pharmaceutically acceptable vehicles include,

but are not limited to, nontoxic buffers such as phosphate, citrate, and other organic acids; salts such as sodium chloride; antioxidants including ascorbic acid and methionine; preservatives (e.g., octadecyldimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium chloride; benzethonium chloride; phenol, butyl or benzyl alcohol; alkyl parabens, such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol; 3-pentanol; and *m*-cresol); low molecular weight polypeptides (e.g., less than about 10 amino acid residues); proteins such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, histidine, arginine, or lysine; carbohydrates such as monosaccharides, disaccharides, glucose, mannose, or dextrans; chelating agents such as EDTA; sugars such as sucrose, mannitol, trehalose or sorbitol; salt-forming counter-ions such as sodium; metal complexes (e.g., Zn-protein complexes); and non-ionic surfactants such as TWEEN or polyethylene glycol (PEG).

[0152] The pharmaceutical compositions of the present invention can be administered in any number of ways for either local or systemic treatment. Administration can be topical (such as to mucous membranes including vaginal and rectal delivery) such as transdermal patches, ointments, lotions, creams, gels, drops, suppositories, sprays, liquids and powders; pulmonary (e.g., by inhalation or insufflation of powders or aerosols, including by nebulizer; intratracheal, intranasal, epidermal and transdermal); oral; or parenteral including intravenous, intraarterial, subcutaneous, intraperitoneal or intramuscular injection or infusion; or intracranial (e.g., intrathecal or intraventricular) administration.

[0153] An antibody or immunoconjugate of the invention can be combined in a pharmaceutical combination formulation, or dosing regimen as combination therapy, with a second compound having anti-cancer properties. The second compound of the pharmaceutical combination formulation or dosing regimen preferably has complementary activities to the ADC of the combination such that they do not adversely affect each other. Pharmaceutical compositions comprising the CD37-binding agent and the second anti-cancer agent are also provided.

[0154] For the treatment of the disease, the appropriate dosage of an antibody or agent of the present invention depends on the type of disease to be treated, the severity and course of the disease, the responsiveness of the disease, whether the antibody or agent is administered for therapeutic or preventative purposes, previous therapy, patient's clinical history, and so on all at the discretion of the treating physician. The antibody or agent can be administered one time or over a series of treatments lasting from several days to several months, or until a cure is effected or a diminution of the disease state is achieved (e.g., reduction in tumor size). Optimal dosing

schedules can be calculated from measurements of drug accumulation in the body of the patient and will vary depending on the relative potency of an individual antibody or agent. The administering physician can easily determine optimum dosages, dosing methodologies and repetition rates. In certain embodiments, dosage is from 0.01 μ g to 100 mg per kg of body weight, and can be given once or more daily, weekly, monthly or yearly. In certain embodiments, the antibody or other CD37-binding agent is given weekly, once every two weeks or once every three weeks. In certain embodiments, the dosage of the antibody or other CD37-binding agent is from about 0.1 mg to about 20 mg per kg of body weight. The treating physician can estimate repetition rates for dosing based on measured residence times and concentrations of the drug in bodily fluids or tissues.

[0155] The combination therapy can provide "synergy" and prove "synergistic," i.e., the effect achieved when the active ingredients used together is greater than the sum of the effects that results from using the compounds separately. A synergistic effect can be attained when the active ingredients are: (1) co-formulated and administered or delivered simultaneously in a combined, unit dosage formulation; (2) delivered by alternation or in parallel as separate formulations; or (3) by some other regimen. When delivered in alternation therapy, a synergistic effect can be attained when the compounds are administered or delivered sequentially, e.g., by different injections in separate syringes. In general, during alternation therapy, an effective dosage of each active ingredient is administered sequentially, i.e., serially, whereas in combination therapy, effective dosages of two or more active ingredients are administered together.

[0156] Embodiments of the present disclosure can be further defined by reference to the following non-limiting examples, which describe in detail preparation of certain antibodies of the present disclosure and methods for using antibodies of the present disclosure. It will be apparent to those skilled in the art that many modifications, both to materials and methods, can be practiced without departing from the scope of the present disclosure.

EXAMPLES

[0157] It is understood that the examples and embodiments described herein are for illustrative purposes only and that various modifications or changes in light thereof will be suggested to persons skilled in the art and are to be included within the spirit and purview of this application.

Example 1

Immunohistochemical staining of CD37 in cell samples- manual methods

[0158] Formalin fixed paraffin embedded cell pellets and tissues were used as test samples with the following staining reagents and conditions.

[0159] Formalin-fixed paraffin-embedded (FFPE) patient lymphoma biopsies were stained with the murine anti-CD37 antibody clone CT1, (muIgG1, Leica, Cat# NCL-CD37), murine anti-CD20 antibody clone L26 (muIgG2a, Dako Cytomation, Cat# M 07 55), and the respective isotype control muIgG1 and muIgG2a antibodies from Coulter as follows. Slides containing samples were baked at 60° C for 30 min in a drying oven and were deparaffinized and rehydrated by sequential immersion in the following solvents: xylenes, absolute ETOH, 95% ETOH and water. Following antigen retrieval in pH 9.5 Borg buffer (Biocare Medical) in a decloaker, slides were washed with PBS (Gibco), and sections were blocked in PBS containing 2% normal horse serum (Vector Labs) and avidin-biotin block (4 drops/mL, Vector Labs) for 30 min. To prepare working solutions of primary antibodies, the CD37-test and -isotype control articles were each diluted to 4.0 µg/mL in diluent [PBS containing 2% normal horse serum and biotin (4 drops/mL)]. The CD20 -test and -isotype control articles were each diluted to 0.5 µg/mL in diluent. Slides were washed in PBS, and incubated at room temperature for 60 minutes with the test articles (anti-CD37 or anti-CD20), or control articles (muIgG1 or muIgG2a), followed by a 30 minute incubation with 10 µg/mL of a biotinylated horse anti-mouse IgG (H+L) secondary antibody (Vector Labs). Slides were washed again in PBS and incubated for 40 minutes with avidin-biotin-peroxidase complex (Vector Labs) to detect bound secondary antibody. Incubation for 5 minutes with DAB (3,3-diaminobenzidine tetrahydrochloride, Dako Cytomation) resulted in the color signal. Slides containing developed tissue sections were counterstained by immersion in a container filled with Hematoxylin (Biocare Medical) for 4 min. Slides were cleared of excess stain followed by a quick immersion in Lithium Carbonate solution (0.135 M Li₂CO₃ aqueous solution, Sigma Aldrich) which enhances the blue nuclear staining. Slides were dehydrated through two rinses each of 95% and 100% ETOH, followed by four washes of Xylene for 1 min each. Coverslips were mounted onto the slides using Mounting medium (Richard Allan Scientific).

[0160] FFPE samples were derived from tumor micro arrays, as well as human tissue blocks from three different CLL tumors, as outlined in **Table 1**.

Table 1: FFPE Test Samples

FFPE Human Tissue Samples	Description	Source
Tissue Micro array	39 Cases	Biomax Cat# LYM401
	48 Cases	Biomax Cat# LM482
CLL	3 FFPE blocks	Analytical Biological Services

[0161] The CD37 test article, murine anti-CD37 antibody clone CT1, was tested to determine binding specificity to the huCD37 antigen. Using the reported IHC staining methods, FFPE sections of 300-19 and 300-19 transfected with huCD37 (300-19/huCD37) cell pellets were stained and evaluated for CD37. The CD37 test article specifically stained 300-19/huCD37 cells and returned no staining in 300-19 cells (3 homo and negative, respectively; see Figure 1). These results demonstrate that clone CT1 specifically targets the huCD37 antigen. (Figure 1). FFPE sections of human normal spleen were also stained and evaluated for CD37. As shown in Figure 2, the white pulp of the spleen (containing lymphoid follicles rich in B lymphocytes) showed strong CD37 staining, while the red pulp of the spleen (containing monocytes and red blood cells) showed little to no CD37 staining.

[0162] The immunoreactivity of each test and control article with tissues and cell pellets was determined by the consulting pathologist, Dr. David Dorfman. Samples were first categorized as either large cell, consisting of diffuse large B-cell lymphoma (DLBCL), or small cell, consisting of mantle cell lymphoma (MCL), mucosa associated lymphoid tissue (MALT), follicular lymphoma (FL), Chronic lymphocytic leukemia (CLL), small lymphocytic leukemia (SLL). The small cell group was further categorized into the respective small cell subtypes.

[0163] For each tissue evaluated, a description of the staining intensity and staining uniformity was reported. The staining intensity score and uniformity scales are described in Table 2. The final reported score for each tissue sample evaluated is the score of the test article minus the score of the respective control article. The ABC (antibodies bound per cell) level for each sample was estimated by comparing the staining score to the calibrated cell pellet controls.

Table 2. Intensity score and uniformity scales used to assess the immunoreactivity of the CD37 antibody clone CT1 with FFPE tissue samples.

Intensity (amount of stain)		Uniformity (number of stained cells)
0	Negative	

1	Weak	0	Negative
2	Moderate	Focal	<25%
3	Strong	Heterogeneous (hetero)	25-75%
3+	Very Strong	Homogeneous (homo)	>75%

[0164] The levels of CD37-expression in tumor cell lines were determined using an anti-CD37 antibody-PE conjugate and the QuantiBRITE system (BD Biosciences). Several B-cell malignancy cell lines were included in the study. In order to obtain reliable ABC values, the binding experiments with an antibody-PE conjugate should be performed at a saturating concentration (concentration, at which all available binding sites are occupied by the conjugate). To determine such concentration for the anti-CD37 antibody-PE conjugate, binding experiments were performed on a panel of CD37-positive cell lines with various CD37 expression levels. The cells were incubated with a wide concentration range of PE conjugate for two hours on ice, washed with FACS buffer (PBS with 1% BSA), fixed with 1% formaldehyde in PBS and analyzed on a FACSCalibur flow cytometer (BD Biosciences). The concentration at which the conjugate saturates cell surface binding sites on all tested cell lines is determined. In subsequent binding ABC-experiments the PE conjugate was used at that concentration. Each sample was analyzed in duplicate or triplicate; several independent experiments were performed on each cell line.

[0165] Antibodies bound per cell (ABC) values were determined for CD37 for each of the positive control cell lines, Daudi, Ramos and RL, using flow cytometry methods by staining cells with a saturating concentration of phycoerythrin (PE)-labeled anti-CD37 antibody (huCD37-PE). Immunohistochemical staining conditions were then optimized for CD37 so that Daudi, Ramos, and RL positive control cells, which each express a uniform level of CD37 and a different ABC value by flow cytometry, also showed varying levels of staining intensity by IHC (see Figure 3 and Figure 4). Daudi and Ramos exhibited homogeneous staining with high intensity, while staining of RL was of a lower intensity with a heterogeneous pattern. The CD37 staining intensity trends observed from the cell pellets correspond to the reported ABC values, where higher ABC values of 360,000 and 120,000 ABC resulted in more intense staining than an ABC value of 55,000. The staining results and respective ABC values are listed in Table 3. CD20 staining was optimized so that staining scores for CD20 and CD37 were similar in cell pellets expressing similar levels of CD20 and CD37, respectively (see Figure 5).

Table 3: ABC values and respective staining results for CD37 on cell lines.

Cell Line	CD37	
	ABC	Score
Daudi	360,000	3 homo
Ramos	120,000	3 homo
RL	55,000	3 hetero

[0166] Among the neoplastic cell types evaluated, CD37 was predominantly expressed in B-NHL (Table 4). Varying levels of uniform CD37 expression were demonstrated in B-cell NHL including subtypes such as FL, MALT lymphoma, DLBCL, BL, and MCL by immunohistochemistry (see Figure 6). As demonstrated in Figure 6, most NHL samples show CD37 expression with an IHC score of ≥ 2 . This corresponds to the level of staining of control cell line pellets such as Daudi, Ramos and RL with ABC values of $\geq 55,000$. Representative photographs showing lymphoma samples stained for CD37 are shown in Figure 7. T-cell lymphomas and Multiple Myeloma (MM) samples did not show staining for either CD37 or CD20.

Table 4. Summary of Staining Results of CD37 and CD20 in Neoplastic Cell Types.

Neoplastic Cell Type	# of samples stained	# samples ≥ 1 hetero (%)	
		CD37	CD20
Non-Hodgkin Lymphoma	56	49 (88%)	53 (95%)
Hodgkin Lymphoma	12	1 (8%)	1 (8%)
T cell Lymphoma	3	0	0
Multiple Myeloma	10	0	0

Example 2

Anti-tumor activity of huCD37-3 antibody, and huCD37-3-SMCC-DM1 in female CB.17 SCID mice bearing SU-DHL-4 (human DLBCL) xenografts

[0167] In this study, the anti-tumor activity (median tumor volume, mm³) of CD37-3 antibody and huCD37-3-SMCC-DM1 were evaluated in female SCID mice bearing subcutaneous SU-DHL-4 tumors, a diffuse large B-cell lymphoma model. Mice were

randomized into groups ($n = 10$ per group) by body weight. Treatment was the day after randomization, and groups included a control group dosed with PBS (200 μ L/injection), huCD37-3 antibody, and non-cleavable huCD37-3-SMCC-DM1 conjugate. Treatments were administered as single intravenous bolus of 10 mg of protein/kg/injection for antibody and huCD37-3-SMCC-DM1. All treatments were well tolerated with no body weight loss as with PBS control animals. Ten out of ten PBS control animals developed tumors (100% tumor take rate), reaching a median tumor volume of 1000 mm^3 on 37 days post cell inoculation. The mean and median tumor volumes were calculated for each treatment group. In addition, for each treatment a %T/C value was calculated which corresponds to the median tumor volume of each treated group divided by the median tumor volume of the vehicle treated group. A treatment with a % T/C value at or below 42% is considered active, while a treatment with a % T/C value at or below 12% is considered highly active.

[0168] Single intravenous treatment of huCD37-3 antibody (10 mg/kg/injection) was active in this study with a 32% T/C; however there were no tumor-free survivors (TFS). huCD37-3-SMCC-DM1 (10 mg/kg/injection) was highly active with %T/C of 1 %. Anti-tumor activity (median tumor volume, mm^3) of huCD37-3-SMCC-DM1 only as a single intravenous treatment (10 mg/kg/injection) is shown in Figure 8.

[0169] An additional study was conducted to evaluate CD37-3 antibody and huCD37-3-SMCC-DM1 in female SCID mice bearing subcutaneous SU-DHL-4 tumors as outlined in Example 17 of (U.S. Published Application No. 2011/0256153, herein incorporated by reference). Animals were randomized by body weight into treatment groups and treated once on day 15 post cell inoculation with either 10 mg/kg of huCD37-3 Ab or huCD37-3-SMCC-DM1. The %T/C value on day 38 post cell inoculation corresponded to 34% or 4% for huCD37-3 or huCD37-3-SMCC-DM1, respectively. On day 74 post cell inoculation, huCD37-3-SMCC-DM1 treatment resulted in 8 of 10 tumor-free survivors. No TFS were observed in the huCD37-3 antibody or PBS vehicle control groups. The huCD37-3-SMCC-DM1 conjugate also showed strong efficacy at single doses of 2.5 or 5 mg/kg in this model with %T/C values on day 37 post cell innoculation of 18% and 6%, respectively. Therefore, huCD37-3-SMCC-DM1 was highly active in the SU-DHL-4 model at a single dose of 10 mg/kg and was active at a single dose of 2.5 mg/kg.

Example 3

Anti-tumor efficacy of huCD37 antibody huCD37-3, huCD37-3-SMCC-DM1 and standard-of-care chemotherapeutics in SCID mice bearing DoHH2 xenografts, a human follicular lymphoma model

[0170] In this study, the antitumor activity of huCD37-3 antibody, huCD37-3-SMCC-DM1, Rituximab® antibody, and CVP (cyclophosphamide, vincristine and prednisone) were investigated in female SCID mice bearing subcutaneous DoHH2 tumors, a human follicular lymphoma model. Eleven days after tumor cell inoculation eighty-one mice were randomized into 9 groups (n = 9 per group) by tumor volume. Treatment was initiated the day after randomization (Day 12), and groups included a control group dosed with PBS (200 μ L/injection), six groups administered single intravenous doses of either huCD37-3 antibody or huCD37-3-SMCC-DM1 conjugate at 10, 5, or 2.5 mg/kg, one group administered six intravenous Rituximab antibody doses at 2 mg/kg, twice per week times three, and one group administered a single intravenous dose of cyclophosphamide at 40 mg/kg and vincristine at 0.5 mg/kg, along with five daily oral doses of prednisone at 0.2 mg/kg.

[0171] Single treatments at 10, 5, and 2.5 mg/kg of huCD37-3 antibody and huCD37-3-SMCC-DM1 conjugate as well as rituximab antibody at 2 mg/kg/injection, 2qw x 3, were well tolerated with no body weight loss as with PBS control animals. Treatment with CVP was toxic with one animal related drug death and 12% mean body weight loss (day 18 nadir). This animal was excluded from data analysis.

[0172] Nine out of nine PBS control animals developed tumors (100% tumor take rate), reaching a median tumor volume of 800 mm³ on 19 days post cell inoculation. The median and mean tumor volume was calculated for each treatment group. Single intravenous treatments with 2.5 and 5 mg/kg of huCD37-3 antibody and huCD37-3-SMCC-DM1 conjugate, as well as, Rituximab® antibody (2 mg/kg, twice weekly time three) were inactive in this study with > 42% T/Cs. Single intravenous treatment with 10 mg/kg of huCD37-3 antibody and huCD37-3-SMCC-DM1 conjugate were active with 37% and 16% T/C, respectively. Treatment with the doses and schedule of CVP administered, although highly active with 2% T/C, was above the tolerated dose for this regimen. Anti-tumor activity (median tumor volume, mm³) of huCD37-3 antibody, huCD37-3-SMCC-DM1, and standard chemotherapeutics in SCID mice bearing DoHH2 human tumor xenografts are shown in Figure 9. Anti-tumor activity (median tumor volume, mm³) of huCD37-3-SMCC-DM1 only as a single intravenous treatment (10 mg/kg/injection) in this model is shown in Figure 10.

Example 4

Anti-Tumor Efficacy of Antibody huCD37-3, huCD37-3-SMCC-DM1, and Standard of Care Agents in SCID Mice Bearing JVM-3 Xenografts, a Human B Cell Chronic Lymphocytic Leukemia (CLL) Model

[0173] In this study, the anti-tumor activity of huCD37-3 antibody, the non-cleavable conjugate huCD37-3-SMCC-DM1, and two standard-of-care agents: Ofatumumab, an antibody targeting CD20, and Bendamustine, a chemotherapeutic agent, was evaluated in a human B cell chronic lymphocytic leukemia model using JVM-3 (CD37+/CD20+) cells implanted subcutaneously in female SCID mice. Six days after tumor cell inoculation ninety mice were randomized into nine groups (n = 10 per group) by tumor volume. Treatment was initiated the day after randomization, and groups included a control group dosed with PBS (200 μ L/injection), huCD37-3 antibody, non-cleavable huCD37-3-SMCC-DM1 conjugate, Ofatumumab antibody and Bendamustine. Treatments were administered as a single intravenous dose of 10, 5, and 2.5 mg/kg for huCD37-3 antibody and huCD37-3-SMCC-DM1, at 5 mg/kg, twice weekly times three for Ofatumumab and as a single dose of 50 mg/kg for Bendamustine.

[0174] Single treatments at 10, 5, and 2.5 mg/kg of huCD37-3 antibody and huCD37-3-SMCC-DM1 conjugate as well as Ofatumumab antibody at 5 mg/kg/injection, 2qw x 3, were well tolerated with no body weight loss as with PBS control animals. Treatment with Bendamustine was tolerated with 8 % mean body weight loss (day 9 nadir). Ten out of ten PBS control animals developed tumors (100% tumor take rate), reaching a median tumor volume of 500 mm³ on 16 days post cell inoculation. The median and mean tumor volume was calculated for each treatment group. The results were plotted against days post inoculation for mean tumor volume and for median tumor volume. Treatment with standard of care agents Ofatumumab (5 mg/kg, twice weekly time three) and Bendamustine (single intravenous dose of 50 mg/kg) were active in this study with 39% and 31% T/C, respectively. Single intravenous treatments with 2.5 mg/kg of huCD37-3 antibody and huCD37-3-SMCC-DM1 conjugate were inactive in this study with > 42% T/Cs. Single intravenous treatment with 10 mg/kg of huCD37-3 antibody and huCD37-3-SMCC-DM1 conjugate were active with 29% and 26% T/C, respectively, and treatment with an intermediate dose (5 mg/kg single injection) of huCD37-3 antibody and huCD37-3-SMCC-DM1 conjugate were active with 31% and 16% T/C, respectively. Anti-tumor activity (median tumor volume, mm³) of huCD37-3 antibody, huCD37-3-SMCC-DM1, Ofatumumab, and Bendamustine in SCID mice bearing JVM-3 human tumor xenografts is shown in Figure 11. Anti-tumor activity (median tumor volume, mm³) of huCD37-3-SMCC-

DM1 only as a single intravenous treatment (10 mg/kg/injection) in this model is shown in Figure 12.

Example 5

Correlation of anti-tumor activity (median tumor volume, mm³) of huCD37-3-SMCC-DM1 as a single intravenous treatment (10 mg/kg/injection) in xenograft models with IHC staining scores

[0175] The antitumor effect of huCD37-3-SMCC-DM1 was evaluated in three lymphoma xenograft models as described in Examples 2, 3, and 4 and correlated with respective CD37 expression, determined by IHC as described in Example 1. FFPE samples prepared from mouse xenograft tumor models were evaluated for CD37 positivity using the manual assay method described in Example 1. FFPE mouse xenograft tissues derived from the following cell lines showed the following staining patterns: SU-DHL-4 showed homogeneous staining patterns with level 3 intensity; DOHH-2 showed homogeneous staining patterns with levels 2 and 3 intensity; JVM-3 showed heterogenous patterns with level 2 and 3 intensity. Representative photographs of tumor xenografts and respective *in vivo* activity from a single intravenous treatment of huCD37-3-SMCC-DM1 (10 mg/kg/injection) are shown in Figures 8, 10 and 12. A summary of the *in vivo* activity and respective CD37 staining scores for each xenograft are listed in Table 5. Among the three xenografts evaluated, the tumor with highest expression (3 homo) also showed the highest activity when treated with huCD37-3-SMCC-DM1. The other 2 models showed lower expression and lower activity.

Table 5. *In vivo* activity of huCD37-3-SMCC-DM1 and respective CD37 staining scores in xenograft models.

Xenograft Model	Activity from a single intravenous treatment (10 mg/kg/injection)	CD37 IHC staining score
SU-DHL-4 (derived from human DLBCL)	Highly Active	3 homo
DOHH-2 (derived from human FL)	Active	2-3 homo
JVM-3 (derived from human CLL)	Active	2-3 hetero

Example 6

Immunohistochemical staining of CD37 in formalin fixed paraffin embedded (FFPE) samples-automated methods.

[0176] The IHC staining assay used the murine anti-CD37 antibody clone CT1 (Leica Cat# NCL-CD37) as the test article and murine IgG1 isotype control (Leica, Cat# MOPC21 AB) and was performed on the Leica Bond RX automated stainer. Paraffin wax was removed when slides containing samples were baked at 60° C. Then the excess paraffin wax was removed with Dewax solution (Leica). Following antigen retrieval in pH 6.0 Bond Epitope Retrieval Solution 1 (ER1, Leica), sections were blocked in 3-4% peroxide. To prepare working solutions of primary antibodies, the CD37-test and isotype control articles were each diluted to 4.2 µg/mL in antibody diluent. Slides were incubated with the test article (anti-CD37), or control article (mulgG1), followed by incubation with the post primary reagent (rabbit anti-mouse IgG, Leica), then by incubation with a polymer (goat anti-rabbit-HRP-IgG, Leica). Slides were developed by incubation with DAB (3,3-diaminobenzidine tetrahydrochloride, Leica) resulting in the color signal. Slides containing developed tissue sections were counterstained with Hematoxylin (Leica) then cleared of excess stain and dehydrated through a series of 95% and 100% ETOH immersion, followed by immersion in Xylene. Coverslips were mounted onto the slides using mounting medium (Richard Allan Scientific).

[0177] All stained samples were evaluated and scored. Control samples were first evaluated followed by test samples (whole sections and individual cores from the tissue micro arrays). For each tumor tissue or cell pellet evaluated, a description of the staining intensity and respective proportion of tumor cells stained was reported. Membrane associated staining was recorded for every sample. When duplicate scores were evaluated from one patient, only the higher score was included in the analysis. If the score describes only cytoplasmic staining, then the final score was reported as zero (0). Intensity and uniformity scores were given to each sample as described in Table 6. Staining intensity and distribution patterns were scored relative to control IgG staining (non-specific). Intensity was scored on a scale of 0 to 3 (0 = no staining, 1 = weak, 2 = moderate and 3 = strong), and distribution was scored as focal (<25% of cells stained), heterogeneous (25-75% of cells stained), and homogeneous (>75% of cells stained). In normal tissue, only the defined substructures were evaluated when calculating intensity and proportion.

Table 6. IHC Scoring System Consisting of Intensity and Uniformity Scales

Intensity (amount of stain)		Uniformity (number of stained cells)	
0	Negative	0	Negative
1	Weak	Focal	<25%
2	Moderate	Heterogeneous (hetero)	25-75%
3	Strong	Homogeneous (homo)	>75%

[0178] FFPE tumor samples were derived from tumor micro arrays, as well as human tissue blocks.

[0179] Cells (tumor cells or transfected cells) were formalin fixed and paraffin embedded (FFPE). FFPE cell pellet samples shown to exhibit varying ranges of CD37 expression by flow cytometry (Daudi, Ramos, Namalwa, and Colo205), normal human tissues (spleen and tonsil), and Non-Hodgkin's lymphoma tissue samples were used to characterize positive and negative controls and for analysis of specificity.

[0180] To determine assay conditions, a range of dilutions of test and control article was tested to select conditions that exhibit an appropriate level of sensitivity. Experiments were performed on a panel of FFPE samples including CD37-positive cell pellets, normal human tissue, and tissue micro arrays consisting of CD37 positive Non-Hodgkin's lymphoma samples. Each sample was stained with a serial dilution of test article concentrations (2.1, 4.2, and 8.4 $\mu\text{g/mL}$) or control article. All samples were evaluated and scored by a board certified pathologist and categorized as either small cell (follicular lymphoma [FL], Mantle cell lymphoma [MCL], MALT type marginal zone B cell lymphoma, marginal zone B cell lymphoma, unclassified small cell lymphoma, unclassified non-hodgkin's lymphoma [NHL]) or large cell (DLBCL). The relative staining intensities for each dilution were compared for each sample to identify the optimal dilution. The criteria for optimal dilution was a dilution which 1) caused no background staining in samples stained with isotype control 2) caused no staining in negative tissue controls stained with test article and 3) differentiated between varying levels of membrane-associated CD37 expression among test samples representing the indication of interest (e.g., DLBCL, FL, CLL). The test article concentration of 4.2 $\mu\text{g/mL}$ was experimentally identified as an optimal dilution and is therefore a particularly useful concentration. A summary of staining results for large cell lymphoma samples is shown in Table 7, and a graph of the scoring distribution for each concentration is shown in Figure 13. A

summary of staining results for small cell lymphoma samples is listed in Table 8, and a graph of the scoring distribution for each concentration is depicted in Figure 14.

Table 7. Staining distribution in large cell lymphoma samples

Scores	No. of Samples in Each Staining Category		
	8.4 $\mu\text{g/mL}$	4.2 $\mu\text{g/mL}$	2.1 $\mu\text{g/mL}$
3 homo	82	51	4
2-3 homo	9	18	8
2 homo	24	29	53
2 hetero	0	2	0
1-2 homo	9	13	22
1-2 hetero	0	1	4
1 homo	5	11	12
1 hetero	0	2	4
0-1 homo	0	0	7
0-1 hetero	0	0	4
1 focal	0	0	1
0	3	4	12
Total	135	135	135

Table 8. Staining distribution in small cell lymphoma samples at 3 concentrations

	FL			MALT			MCL			Small Cell unclassified			Unclassified NHL		
	Concentration (µg/mL)														
Scores	8.4	4.2	2.1	8.4	4.2	2.1	8.4	4.2	2.1	8.4	4.2	2.1	8.4	4.2	2.1
3 homo	8	6	2	3	-	-	2	2	-	12	6	-	2	2	1
2-3 homo	2	1	1	-	2	-	-	-	-	1	5	1	-	-	-
1-3 homo	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-
2 homo	1	3	1	2	3	1	-	-	-	1	3	9	1	1	1
2 hetero	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
1-2 homo	-	-	3	-	-	1	-	-	-	-	-	3	-	-	-
1-2 hetero	-	-	-	1	1	2	-	-	2	-	-	1	-	-	-
1 homo	-	1	1	-	-	-	-	-	-	-	-	-	-	-	-
1 hetero	-	-	-	-	-	1	-	-	-	-	-	1	-	-	-
0-1 homo	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-
1 focal	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-
0	-	-	-	-	-	1	-	-	-	3	3	3	1	1	1
Total	11			6			2			17/17/18			4		

Example 7

Identification and characterization of controls that characterize the dynamic range of the assay-automated staining methods

[0181] **Quality controls:** The mantle zone and the marginal zone of normal human spleen and germinal zone and mantle zone of the tonsil were used as positive controls in each assay to verify that the staining procedure performed as expected. The interfollicular areas of normal human tonsil and the red pulp of human normal spleen were used as negative controls. These controls were used as assay verification controls during the optimization and validation phases. These results were reviewed to confirm that the selected controls give consistent results and to confirm they spanned the dynamic range of the assay. Exemplary staining scores for the quality controls are listed in Table 9 at four staining concentrations (2.1, 4.2, 8.4, and 16.7 $\mu\text{g/mL}$) and indicate that the concentration of primary antibody did affect staining results of tested samples.

Table 9.

Control Sample	Isotype control	CD37 Antibody			
	(16.7 $\mu\text{g/mL}$) D7	(1:20, 16.7 $\mu\text{g/mL}$) D1	(1:40, 8.4 $\mu\text{g/mL}$) D2	(1:80, 4.2 $\mu\text{g/mL}$) D4	(1:160, 2.1 $\mu\text{g/mL}$) D6
Daudi cell pellet	0	3 homo	3 homo	3 homo	2 homo
Ramos cell pellet	0	3 homo	2 homo	2 homo	2 hetero
RL cell pellet	0	2 hetero	2 hetero	1-2 hetero	1 focal
Namalwa cell pellet	0	2 hetero	2 hetero	2 hetero	1 focal
Colo205 cell pellet	0	0	0	0	0
Normal human spleen	MG = 0	MG = 3 homo	MG = 3 homo	MG = 2 homo	MG = 1-2 homo
	MT/F = 0	MT/F = 3 homo	MT/F = 3 homo	MT/F = 3 homo	MT/F = 2 homo
	RP = 0	RP = 0	RP = 0	RP = 0	RP = 0
Normal human tonsil	GC = 0	GC = 3 homo	GC = 3 homo	GC = 3 homo	GC = 3 homo
	MT = 0	MT = 3 homo	MT = 3 homo	MT = 3 homo	MT = 2 homo
	IF = 0	IF = 0	IF = 0	IF = 0	IF = 0
MG = marginal zone; MT = mantle zone; IF = interfollicular; F = follicle; GC = germinal center; RP = red pulp					

Example 8

Performance analysis of the automated staining method

[0182] The intended use of this assay is to specifically detect CD37 reproducibly and with the appropriate sensitivity to differentiate varying levels and uniformity of membrane-associated CD37 expression (optimal dynamic range) in B-cell malignancies. Therefore, specificity, reproducibility, and sensitivity are considered as performance criteria.

[0183] The specificity and sensitivity of the study assay was characterized by staining and evaluating a panel of tissue micro arrays. Staining was observed to confirm that positive staining is consistently localized to the tumor tissue with normal adjacent tissue components including stroma, blood vessels, and normal organ tissue staining negative or positive as expected. For each subtype of B-cell malignancy, the distribution of staining scores among tissue micro arrays was observed. A similar distribution of scores suggests the method performed well and was not overly sensitive to minor variations in various fixation and processing conditions. The precision of the study assay was also investigated by evaluating intra-run and inter-run reproducibility of the assay using FFPE samples consisting of cell pellets that express varying levels of CD37: Daudi (high CD37 expression), Ramos (intermediate CD37 expression), Namalwa (low CD37 expression), and Colo205 (negative). Additionally, normal human spleen (two samples), normal human tonsil, and a marginal zone lymphoma sample were included. For intra-run reproducibility, nine slides each containing a section of each control were placed at random locations on the Leica Bond RX. For inter-run reproducibility, three slides containing sections from the same samples were stained on three different days. All slides from both intra-run and inter-run reproducibility experiments were evaluated and found to be reproducible.

Example 9

A CD37 staining score by IHC correlates with activity of huCD37-3-SMCC-DM1

[0184] Potency and specificity of huCD37-3-SMCC-DM1 is analyzed against CD37-positive cell lines with a wide range of CD37 expression. The level of CD37 expression is determined by flow cytometry as described in Example 1. Alternatively, the level of CD37 expression is determined by IHC using a manual staining method as described in Example 1 or by IHC using an automated staining method as described in Examples 6-8. Potency is evaluated

using suitable in vivo xenograft models as described in Examples 2-4. Dosing of huCD37-3-SMCC-DM1 is done intravenously at doses such as 10 mg/kg, 5 mg/kg and/or 2.5 mg/kg. In addition, suitable CD37-positive cells with low CD37 expression levels can be used such as, for example, Namalwa. To verify specificity of activity, CD37-negative cell lines, such as Colo205, can be included in the experiments.

[0185] All publications, patents, patent applications, internet sites, and accession numbers/database sequences (including both polynucleotide and polypeptide sequences) cited herein are hereby incorporated by reference in their entirety for all purposes to the same extent as if each individual publication, patent, patent application, internet site, or accession number/database sequence were specifically and individually indicated to be so incorporated by reference.

SEQUENCES

SEQ ID NO:1 - human CD37

MSAQESCLSLIKYFLFVFNLFVFLGSLIFCFGIWILIDKTSFVSFVGLAFVPLQIWSKVLAI
 SGIFTMGIALLGCVGALKELRCLLGLYFGMLLLLFATQITLGILISTQRAQLERSLRDVVE
 KTIQKYGTNPEETAEEESWDYVQFQLRCCGWHYPQDWFQVLILRGNGSEAHRVPCSC
 YNLSATNDSTILDKVILPQLSRLGHLARSRHADICAVPAESHIYREGCAQGLQKWLHN
 NLISIVGICLGVGLLELGFMTLSIFLCRNLDHVYNRLAYR

Variable heavy chain CDR amino acid sequences:

Antibody	VH-CDR1	VH-CDR2	VH-CDR3
CD37-3	TSGVS (SEQ ID NO:4)	VIWGDGSTN (SEQ ID NO:5)	GGYSLAH (SEQ ID NO:6)
CD37-12	KYGMN (SEQ ID NO:7)	WINTNTGESR (SEQ ID NO:8)	GTVVAD (SEQ ID NO:9)
CD37-38	SGFGWH (SEQ ID NO:10)	YILYSGGTD (SEQ ID NO:11)	GYGYGAWFVY (SEQ ID NO:12)
CD37-50	SGFAWH (SEQ ID NO:13)	YILYSGSTV (SEQ ID NO:14)	GYGYGAWFAY (SEQ ID NO:15)
CD37-51	SGFAWH (SEQ ID NO:16)	YIHYSGSTN (SEQ ID NO:17)	GYYGFGAWFVY (SEQ ID NO:18)
CD37-56	SGFAWH (SEQ ID NO:19)	YIHYSGGTN (SEQ ID NO:20)	GYYGFGAWFAY (SEQ ID NO:21)
CD37-57	SGFAWH (SEQ ID NO:22)	YILYSGSTV (SEQ ID NO:23)	GYGYGAWFAY (SEQ ID NO:24)
CONSENSUS	SGF[A or G]WH (SEQ ID NO:25)	YI[L or H]YSG[G or S]T[D,V, or N] (SEQ ID NO:26)	GYYG[Y or F]GAWF[V or A]Y (SEQ ID NO:27)

Variable light chain CDR amino acid sequences

Antibody	VL-CDR1	VL-CDR2	VL-CDR3
CD37-3	RASENIRSNLA (SEQ ID NO:28)	VATNLAD (SEQ ID NO:29)	QHYWGTTWT (SEQ ID NO:30)
CD37-12	RASQSVSTSSYSYLY (SEQ ID NO:31)	YASNLAS (SEQ ID NO:32)	QHSWEIPYT (SEQ ID NO:33)
CD37-38	SASSSVTYMH (SEQ ID NO:34)	DTSKLAS (SEQ ID NO:35)	QQWISNPPT (SEQ ID NO:36)
CD37-50	SATSSVTYMH (SEQ ID NO:37)	DTSKLPY (SEQ ID NO:38)	QQWSDNPPT (SEQ ID NO:39)
		Humanized DTSNLPY (SEQ ID NO:40)	
CD37-51	SATSSVTYMH (SEQ ID NO:41)	DTSKLAS (SEQ ID NO:42)	QQWSSNPPT (SEQ ID NO:43)
CD37-56	SASSSVTYMH (SEQ ID NO:44)	DTSKLAS (SEQ ID NO:45)	QQWISDPPT (SEQ ID NO:46)
		Humanized DTSNLAS (SEQ ID NO:47)	
CD37-57	SATSSVTYMH (SEQ ID NO:48)	DTSKLAS (SEQ ID NO:49)	QQWSDNPPT (SEQ ID NO:50)
		Humanized DTSNLAS (SEQ ID NO:51)	
CONSENSUS	SA[T or S]SSVTYMH (SEQ ID NO:52)	DTS[K or N]L[A or P][S or Y] (SEQ ID NO:53)	QQW[I or S][S or D][N or D]PPT (SEQ ID NO:54)

Variable heavy chain amino acid sequences

Antibody	VH Amino Acid Sequence (SEQ ID NO)
muCD37-3	QVQVKESGPGLVAPSQSL SITCTVSGFSLTTSVSWVRQPPGKGLEWLGVIW GDGSTNYHSALKSRLSIKKDHKSQVFLKLNSLQTDDTATYYCAKGGYSLA HWGQGTTLTVSA (SEQ ID NO:55)
chCD37-3	QVQVKESGPGLVAPSQSL SITCTVSGFSLTTSVSWVRQPPGKGLEWLGVIW GDGSTNYHSALKSRLSIKKDHKSQVFLKLNSLQTDDTATYYCAKGGYSLA HWGQGTTLTVSA (SEQ ID NO:56)
huCD37-3v1.0	QVQVQESGPGLVAPSQTL SITCTVSGFSLTTSVSWVRQPPGKGLEWLGVIW GDGSTNYHPSLKSRLSIKKDHKSQVFLKLNSLTAADTATYYCAKGGYSLA HWGQGTTLTVSS (SEQ ID NO:57)
huCD37-3v1.1	QVQVQESGPGLVAPSQTL SITCTVSGFSLTTSVSWVRQPPGKGLEWLGVIW GDGSTNYHSSLKSRLSIKKDHKSQVFLKLNSLTAADTATYYCAKGGYSLA HWGQGTTLTVSS (SEQ ID NO:58)
muCD37-12	QIQLVQSGPELKKPGETVKISKASGYTFTKYGMNWVKQAQKGLKWMG WINTNTGESRNAEEFKGRFAFSLETSASTAYLQINNLYEDTATYFCGRGT VADWGQGTTLTVSS (SEQ ID NO:59)
chCD37-12	QIQLVQSGPELKKPGETVKISKASGYTFTKYGMNWVKQAQKGLKWMG WINTNTGESRNAEEFKGRFAFSLETSASTAYLQINNLYEDTATYFCGRGT VADWGQGTTLTVSS (SEQ ID NO:60)
muCD37-38	DVQLQESGPDLVKPSQSLSLTCTVTGYSITSGFGWHWIRQFPGNKLEWMAY

	ILYSGGTDYNPSLKSRSITRDTSKNQFFLRLLSSVTTEDTATYYCARGYYGYG AWFVYWGQGLTVTVSA (SEQ ID NO:61)
chCD37-38	QVQLQESGPDLVKPSQSLSLTCTVTGYSITSGFGWHWIRQFPGNKLEWMAYI ILYSGGTDYNPSLKSRSITRDTSKNQFFLRLLSSVTTEDTATYYCARGYYGYG AWFVYWGQGLTVTVSA (SEQ ID NO:62)
huCD37-38	QVQLQESGPGLVKPSQSLSLTCTVSGYSITSGFGWHWIRQFPGKGLEWMAYI LYSGGTDYNPSLKSRSITRDTSKNQFFLRLLSSVTAADTATYYCARGYYGYG AWFVYWGQGLTVTVSS (SEQ ID NO:63)
muCD37-50	DVQLQESGPDLLKPSQSLSLTCTVTGYSITSGFAWHWIRQFPGNKLEWMGYI LYSGSTVYSPSLKSRISITRDTSKNHFFLQLNSVTTEDTATYYCARGYYGYG AWFAYWGQGLTVTVSA (SEQ ID NO:64)
huCD37-50	QVQLQESGPGLLKPSQSLSLTCTVSGYSITSGFAWHWIRQHPGNKLEWMGYI ILYSGSTVYSPSLKSRISITRDTSKNHFFLQLNSVTAADTATYYCARGYYGYG AWFAYWGQGLTVTVSA (SEQ ID NO:65)
muCD37-51	DVQLQESGPDLLKPSQSLSLTCTVTGYSISSGFAWHWIRQFPGNKLEWMGYI HYSGSTNYSPSLKSRISITRDSSKNQFFLQLNSVTTEDTATYYCARGYYGFGA WVYWGQGLTVTVSA (SEQ ID NO:66)
huCD37-51	EVQLVESGPEVLKPGESLSLTCTVSGYSISSGFAWHWIRQFPGKGLEWMGYI HYSGSTNYSPSLQGRISITRDSSINQFFLQLNSVTASDTATYYCARGYYGFGA WVYWGQGLTVTVSA (SEQ ID NO:67)
muCD37-56	DVQLQESGPDLVKPSQSLSLTCTVTGYSITSGFAWHWIRQFPGNKLEWMGYI IHYSGGTNYNPSLKSRSVITRDTSKNQFFLQLNSVTTEDTATYYCARGYYGF GAWFAYWGQGLTVPVSA (SEQ ID NO:68)
huCD37-56	QVQLQESGPGLVKPSQSLSLTCTVSGYSITSGFAWHWIRQFPGKGLEWMGYI HYSGGTNYNPSLKSRSVITRDTSKNQFFLQLNSVTAADTATYYCARGYYGF GAWFAYWGQGLTVPVSA (SEQ ID NO:69)
muCD37-57	DVQLQESGPDLLKPSQSLSLTCTVTGYSITSGFAWHWIRQFPGNKLEWMGYI LYSGSTVYSPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYCARGYYGYG AWFAYWGQGLTVTVSA (SEQ ID NO:70)
huCD37-57	QVQLQESGPGLLKPSQSLSLTCTVSGYSITSGFAWHWIRQFPGKGLEWMGYI LYSGSTVYSPSLKSRISITRDTSKNQFFLQLNSVTAADTATYYCARGYYGYG AWFAYWGQGLTVTVSA (SEQ ID NO:71)

Variable light chain amino acid sequences

Antibody	VL Amino Acid Sequence (SEQ ID NO)
muCD37-3	DIQMTQSPASLSVSVGETVTITCRASENIRSNLAWYQQKQKGKSPQLLVNVAT NLADGVPSRFSGSGSGTQYSLKINSLQSEDFGTYYCQHYWGTTWTFGGGK LEIKR (SEQ ID NO:72)
chCD37-3	DIQMTQSPASLSVSVGETVTITCRASENIRSNLAWYQQKQKGKSPQLLVNVAT NLADGVPSRFSGSGSGTQYSLKINSLQSEDFGTYYCQHYWGTTWTFGGGK LEIKR (SEQ ID NO:73)
huCD37-3 (1.0 and 1.1)	DIQMTQSPSSLSVSVGERVTITCRASENIRSNLAWYQQKPGKSPKLLNVAT NLADGVPSRFSGSGSGTDYSLKINSLQPEDFGTYYCQHYWGTTWTFGQGTK LEIKR (SEQ ID NO:74)
muCD37-12	DIVLTQSPASLAVSLGQRATISCRASQSVSTSSYSYLYWFQQKPGQPPKLLIK YASNLAGVPARFSGSGSGTDFTLNHPVEEEDTATYYCQHSWEIPYTFGGG TKLEIKR (SEQ ID NO:75)
chCD37-12	DIVLTQSPASLAVSLGQRATISCRASQSVSTSSYSYLYWFQQKPGQPPKLLIK YASNLAGVPARFSGSGSGTDFTLNHPVEEEDTATYYCQHSWEIPYTFGGG TKLEIKR (SEQ ID NO:76)
muCD37-38	QIVLTQSPAIMASAPGEKVTMTCSASSSVTYMHWYQQKSGTSPKRWIYDTS

	KLASGVPARFSGGGSGTSYSLTISSMEAEDAATYYCQQWISNPPTFGGGTKL EIKR (SEQ ID NO:77)
chCD37-38	QIVLTQSPAISASPGKEVTMTCSASSSVTYMHWYQQKSGTSPKRWIYDTS KLASGVPARFSGGGSGTSYSLTISSMEAEDAATYYCQQWISNPPTFGGGTKL EIKR (SEQ ID NO:78)
huCD37-38	DIVLTQSPASMSASPGERVMTMTCSASSSVTYMHWYQQKPGTSPKRWIYDTS KLASGVPARFSGGGSGTSYSLTISSMEAEDAATYYCQQWISNPPTFGGGTKL EIKR (SEQ ID NO:79)
muCD37-50	QIVLTQSPAISASPGKEVTMTCSATSSSVTYMHWYQQKSGTSPKRWIYDTS KLPYGVPGRFSGSGSGTSYSLTISSMEAEDAATYYCQQWSDNPPTFGSGTKL EIKR (SEQ ID NO:80)
huCD37-50	EIVLTQSPATMSASPGERVMTMTCSATSSSVTYMHWYQQKPGQSPKRWIYDTS NLPYGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSDNPPTFGQGTKL EIKR (SEQ ID NO:81)
muCD37-51	QIVLTQSPAISASPGKEVTMTCSATSSSVTYMHWYQQKSGTSPKRWIYDTS KLASGVPARFSGSGSGTSYSLTISNMEAEDAATYYCQQWSSNPPTFGSGTKL EIKR (SEQ ID NO:82)
huCD37-51	EIVLTQSPATMSASPGERVMTMTCSATSSSVTYMHWYQQKPGQSPKRWIYDTS KLASGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPPTFGQGTKL EIKR (SEQ ID NO:83)
muCD37-56	QIVLTQSPAFMSASPGDKVTMTCSASSSVTYMHWYQQKSGTSPKRWIYDTS KLASGVPARFSGGGSGTSYSLTISTMEAEDAATYYCQQWISDPPTFGGGTKL EIKR (SEQ ID NO:84)
huCD37-56	DIVLTQSPAFMSASPGKEVTMTCSASSSVTYMHWYQQKPDQSPKRWIYDTS NLASGVPSRFSGGGSGTDYSLTISSMEAEDAATYYCQQWISDPPTFGQGTKL EIKR (SEQ ID NO:85)
muCD37-57	QIVLTQSPAISASPGKEVTMTCSATSSSVTYMHWYQQKSGTSPKRWIYDTS KLASGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSDNPPTFGSGTKL EIKR (SEQ ID NO:86)
huCD37-57	EIVLTQSPATMSASPGERVMTMTCSATSSSVTYMHWYQQKPGQSPRRWIYDTS NLASGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSDNPPTFGQGTKL EIKR (SEQ ID NO:87)

Full-length heavy chain amino acid sequences

Antibody	Full-Length Heavy Chain Amino Acid Sequence (SEQ ID NO)
muCD37-3	QVQVKESGPGLVAPSQSL SITCTVSGFSLTTSVSWVRQPPGKGLEWLGVIW GDGSTNYHSALKSRLSIKKDHSSQVFLKLNSLQTDDTATYYCAKGGYSLA HWGQGT LVTVSAAKTTAPSVYPLAPVCGD TTGSSVTLGCLVKGYFPEPVT L TWN SGLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTK VDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMSLSPIVTCVVV DVSEDDPDVQISWVFNNEVHTAQTQTHREDYNSTLRVVSALPIQH QDWM SGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPEEEMTKKQVTLT CMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDS DGSYFMYSKLRVEKKN WVERNYSYSCSVVHEGLHNHHTTKSFSRTPGK (SEQ ID NO:88)
chCD37-3	QVQVKESGPGLVAPSQSL SITCTVSGFSLTTSVSWVRQPPGKGLEWLGVIW GDGSTNYHSALKSRLSIKKDHSSQVFLKLNSLQTDDTATYYCAKGGYSLA HWGQGT LVTVSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSSVTVPSSSLGTQTYICNVN HKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ

	DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:89)
huCD37-3v1.0	QVQVQESGPGGLVAPSQTLSITCTVSGFSLTTSQVSWVRQPPGKGLEWLGVIW GDGSTNYHPSLKSRLSIKKDHSSKSQVFLKLNSLTAADTATYYCAKGGYSLA HWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO:90)
huCD37-3v1.1	QVQVQESGPGGLVAPSQTLSITCTVSGFSLTTSQVSWVRQPPGKGLEWLGVIW GDGSTNYHSSLKSRLSIKKDHSSKSQVFLKLNSLTAADTATYYCAKGGYSLA HWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG (SEQ ID NO:91)
muCD37-12	QIQLVQSGPELKKPGETVKISKASGYTFTKYGMNWVKQAQGGKGLKWMG WINTNTGESRNAEEFKGRFAFSLETSASTAYLQINNLYEDTATYFCGRGT VADWGQGTTLTVSSAKTTAPSVYPLAPVCGDITGSSVTLGCLVKGYFPEPV TLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASS TKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMSLSPIVTCV VVDVSEDDPDVQISWVFNVEVHTAQTQTHREDYNSTLRVVSALPIQHQQD WMSGKEFKCKVNNKDLPAPIERTISKPKGVRAPQVYVLPPEEEMTKKQV TLTCMVTDFMPEDIYVEWTNNGKTELNYKNTPEVLDSGYSYFMYSKLRVE KKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK (SEQ ID NO:92)
chCD37-12	QIQLVQSGPELKKPGETVKISKASGYTFTKYGMNWVKQAQGGKGLKWMG WINTNTGESRNAEEFKGRFAFSLETSASTAYLQINNLYEDTATYFCGRGT VADWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:93)
muCD37-38	DVQLQESGPDVLKPSQSLSLTCTVTGYTSITSGFGWHWIRQFPGNKLEWMAY ILYSGGTDYNPSLKSRSITRDTSKNQFFLRLSSVTTEDTATYYCARGYYGYG AWFVYWGQGTTLTVSAAKTPPSVYPLAPGSAAQTNMVTLGCLVKGYFP EPVTVTWNSGSLSSGVHTFPAVLES DLYTLSSSVTVPSSMRPSETVTCNVAH PASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLITLTPKVTCV VDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWL NGKEFKCRVNSAFAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLT CMITDFFPEDITVEWQWNGQPAENYKNTQPMINTNGSYFVYSKLVNQKSN WEAGNTFTCSVLHEGLHNHHTTEKSLSHSPGK (SEQ ID NO:94)
chCD37-38	QVQLQESGPDVLKPSQSLSLTCTVTGYTSITSGFGWHWIRQFPGNKLEWMAY ILYSGGTDYNPSLKSRSITRDTSKNQFFLRLSSVTTEDTATYYCARGYYGYG AWFVYWGQGTTLTVSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT

	VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG (SEQ ID NO:95)
huCD37-38	QVQLQESGPGLVKPSQSLSTCTVSGYSITSGFGWHWIRQFPGKGLEWMAYILYSGGTDYNPSLKSRIISITRDTSKNQFFLRLSSVTAADTATYYCARGYYGYGAWFVYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG (SEQ ID NO:96)
muCD37-50	DVQLQESGPDLLKPSQSLSTCTVTGYSITSGFAWHWIRQFPGNKLEWMGYILYSGSTVYSPSLKSRISITRDTSKNHFFLQLNSVTTEDTATYYCARGYYGYGAWFAYWGQGTLLTVSAAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMSLSPIVTCVVDVSEDDPDVQISWVFNNEVHTAQQTQTHREDYNSTLRVVSALPIQHQQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSGYSFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK (SEQ ID NO:97)
huCD37-50	QVQLQESGPGLLKPSQSLSTCTVSGYSITSGFAWHWIRQHPGNKLEWMGYILYSGSTVYSPSLKSRISITRDTSKNHFFLQLNSVTAADTATYYCARGYYGYGAWFAYWGQGTLLTVSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG (SEQ ID NO:98)
muCD37-51	DVQLQESGPDLLKPSQSLSTCTVTGYSISSGFAWHWIRQFPGNKLEWMGYIHYSGSTNYSPSLKSRISITRDSSKNQFFLQLNSVTTEDTATYYCARGYYGFGAWFVYWGQGTLLTVSAAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMSLSPIVTCVVDVSEDDPDVQISWVFNNEVHTAQQTQTHREDYNSTLRVVSALPIQHQQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSGYSFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK (SEQ ID NO:99)
huCD37-51	EVQLVESGPVLPKPGESLSTCTVSGYSISSGFAWHWIRQFPGKGLEWMGYIHYSGSTNYSPSLQGRISITRDSSINQFFLQLNSVTASDTATYYCARGYYGFGAWFVYWGQGTLLTVSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG (SEQ ID NO:100)
muCD37-56	DVQLQESGPDLVKPSQSLSTCTVTGYSITSGFAWHWIRQFPGNKLEWMGYIHYSGGTNYNPSLKSRSITRDTSKNQFFLQLNSVTTEDTATYYCARGYYGFGAWFAYWGQGTLLVPVSAKTTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLESPLYTLSSSVTVPSSMRPSETVTCNVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLITLTPKVTCTVVDDISKDDPEVQFSWFVDDVEVHTAQQTQPREEQFNSTFRSVSELPIMHQDW

	LNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSL TCMITDFFPEDITVEWQWNGQPAENYKNTQPIMNTNGSYFVYSKLNQKSN WEAGNTFTCSVLHEGLHNHTEKSLSHSPGK (SEQ ID NO:101)
huCD37-56	QVQLQESGPGLVKPSQSLSLTCTVSGYSITSGFAWHWIRQFPGKGLEWMGYI HYSGGTNYNPSLKSRSVITRDTSKNQFFLQLNSVTAADTATYYCARGYYGF GAWFAYWGQGTLPVSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG (SEQ ID NO:102)
muCD37-57	DVQLQESGPDLLKPSQSLSLTCTVTGYSITSGFAWHWIRQFPGNKLEWMGYI LYSGSTVYSPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYCARGYYGYG AWFAYWGQGTLPVSAAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFP EPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHP ASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMSLSPIV TCVVVDVSEDDPDVQISWVFNNEVHTAQTQTHREDYNSTLRVVSALPIQH QDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPEEEMTKK QVTLTCMVTDMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLR VEKKNWVERNYSYSCSVVHEGLHNHHTTKSFSRTPGK (SEQ ID NO:103)
huCD37-57	QVQLQESGPGLLKPSQSLSLTCTVSGYSITSGFAWHWIRQFPGKGLEWMGYI LYSGSTVYSPSLKSRISITRDTSKNQFFLQLNSVTAADTATYYCARGYYGYG AWFAYWGQGTLPVSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRT EVTCTVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG (SEQ ID NO:104)

Full-length light chain amino acid sequences

Antibody	Full-length Light Chain Amino Acid Sequence (SEQ ID NO)
muCD37-3	DIQMTQSPASLSVSVGETVTITCRASENIRSNLAWYQQKQKGKSPQLLVNVAT NLADGVPSRFSGSGSGTQYSLKINSLQSEDFGTYQCQHYWGTTWTFGGGTK LEIKRADAAPTVISIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSE NGVLNSWTDQDSKSTYSMSSTLTTLTKDEYERHNSYTCEATHKTSTSPIVKS FNRNEC (SEQ ID NO:105)
chCD37-3	DIQMTQSPASLSVSVGETVTITCRASENIRSNLAWYQQKQKGKSPQLLVNVAT NLADGVPSRFSGSGSGTQYSLKINSLQSEDFGTYQCQHYWGTTWTFGGGTK LEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ SGNSQESVTEQDSKSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTK SFNRGEC (SEQ ID NO:106)
huCD37-3 (1.0 and 1.1)	DIQMTQSPSSLSVSVGERVTITCRASENIRSNLAWYQQKPGKSPKLLNVNAT NLADGVPSRFSGSGSGTDYSLKINSLQPEDFGTYQCQHYWGTTWTFGQGTK LEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ SGNSQESVTEQDSKSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTK SFNRGEC (SEQ ID NO:107)
muCD37-12	DIVLTQSPASLAVSLGQRATISCRASQSVSTSSYSYLYWFQQKPGQPPKLLIK YASNLASGVPARFSGSGSGTDFTLNHPVEEEDTATYYCQHSWEIPYTFGGG TKLEIKRADAAPTVISIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSE

	RQNGVLNSWTDQDSKDYMSSTLTTLTKDEYERHNSYTCEATHKTSTSPI VKSFNRNEC (SEQ ID NO:108)
chCD37-12	DIVLTQSPASLAVSLGQRATISCRASQSVSTSSYSYLYWFQQKPGQPPLLIK YASNLASGVPARFSGSGSGTDFLTNIHPVEEEDTATYYCQHSWEIPYTFGGG TKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDYMSSTLTTLTKADYEKHKVYACEVTHQGLSSPV TKSFNRNEC (SEQ ID NO:109)
muCD37-38	QIVLTQSPAIMASAPGEKVTMTCSASSSVTYMHYQKSGTSPKRWIYDTS KLASGVPARFSGGGSGTSSYSLTISSMEAEDAATYYCQQWISNPPTFGGGTKL EIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQN GVLNSWTDQDSKDYMSSTLTTLTKDEYERHNSYTCEATHKTSTSPIVKSF NRNEC (SEQ ID NO:110)
chCD37-38	QIVLTQSPAIMASAPGEKVTMTCSASSSVTYMHYQKSGTSPKRWIYDTS KLASGVPARFSGGGSGTSSYSLTISSMEAEDAATYYCQQWISNPPTFGGGTKL EIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS GNSQESVTEQDSKDYMSSTLTTLTKADYEKHKVYACEVTHQGLSSPVTKS FNRGEC (SEQ ID NO:111)
huCD37-38	DIVLTQSPASMSAPGERVTMTCSASSSVTYMHYQKPGTSPKRWIYDTS KLASGVPARFSGSGSGTSSYSLTISSMEAEDAATYYCQQWISNPPTFGGGTKL EIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS GNSQESVTEQDSKDYMSSTLTTLTKADYEKHKVYACEVTHQGLSSPVTKS FNRGEC (SEQ ID NO:112)
muCD37-50	QIVLTQSPAIMASAPGEKVTMTCSATSSSVTYMHYQKSGTSPKRWIYDTS KLPGVPGRFSGSGSGTSSYSLTISSMEAEDAATYYCQQWSDNPPTFGSGTKL EIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQN GVLNSWTDQDSKDYMSSTLTTLTKDEYERHNSYTCEATHKTSTSPIVKSF NRNEC (SEQ ID NO:113)
huCD37-50	EIVLTQSPATMSAPGERVTMTCSATSSSVTYMHYQKPGQSPKRWIYDTS NLPYGVPARFSGSGSGTSSYSLTISSMEAEDAATYYCQQWSDNPPTFGQGTKL EIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS GNSQESVTEQDSKDYMSSTLTTLTKADYEKHKVYACEVTHQGLSSPVTKS FNRGEC (SEQ ID NO:114)
muCD37-51	QIVLTQSPAIMASAPGEKVTMTCSATSSSVTYMHYQKSGTSPKRWIYDTS KLASGVPARFSGSGSGTSSYSLTISNMEAEDAATYYCQQWSSNPPTFGSGTKL EIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQN GVLNSWTDQDSKDYMSSTLTTLTKDEYERHNSYTCEATHKTSTSPIVKSF NRNEC (SEQ ID NO:115)
huCD37-51	EIVLTQSPATMSAPGERVTMTCSATSSSVTYMHYQKPGQSPKRWIYDTS KLASGVPARFSGSGSGTSSYSLTISSMEAEDAATYYCQQWSSNPPTFGQGTKL EIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS GNSQESVTEQDSKDYMSSTLTTLTKADYEKHKVYACEVTHQGLSSPVTKS FNRGEC (SEQ ID NO:116)
muCD37-56	QIVLTQSPAFMSAPGDKVTMTCSASSSVTYMHYQKSGTSPKRWIYDTS KLASGVPARFSGGGSGTSSYSLTISTMEAEDAATYYCQQWISDPPTFGGGTKL EIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQN GVLNSWTDQDSKDYMSSTLTTLTKDEYERHNSYTCEATHKTSTSPIVKSF NRNEC (SEQ ID NO:117)
huCD37-56	DIVLTQSPAFMSAPGEKVTMTCSASSSVTYMHYQKPDQSPKRWIYDTS NLASGVPSRFSGGGSGTDYSLTISSMEAEDAATYYCQQWISDPPTFGQGTKL EIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS GNSQESVTEQDSKDYMSSTLTTLTKADYEKHKVYACEVTHQGLSSPVTKS FNRGEC (SEQ ID NO:118)
muCD37-57	QIVLTQSPAIMASAPGEKVTMTCSATSSSVTYMHYQKSGTSPKRWIYDTS KLASGVPARFSGSGSGTSSYSLTISSMEAEDAATYYCQQWSDNPPTFGSGTKL

	EIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSEKQNGVLNSWTDQDSKSTYSMSSTLTTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC (SEQ ID NO:119)
huCD37-57	EIVLTQSPATMSASPGERVMTCSATSSVTYMHWYQQKPGQSPRRWIYDTSNLSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSDNPPTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:120)

Variable heavy chain polynucleotide sequences

Antibody	VH Polynucleotide Sequence (SEQ ID NO)
muCD37-3	cagggtgcagggtgaaggagtcaggacctggcctggcgcgcctcacagagcctgtccattacatgcactgtctcagggttctcattaaccacctctggtgtaagctgggttcgccagcctccaggaaagggtctggagtgctgggagtaatatggggtgacgggagcacaactatcattcagctctcaaatccagactgagcatcaagaagatcactccaagagccaagttttcttaaaactgaacagctctgcaaaactgatgacacagccacgtactactgtgccaaggagggtactcgttggtcactggggccaaggactctggtcacagtctctgca (SEQ ID NO:121)
chCD37-3	aagcttgccaccatggctgtcctggcactgtcctctgctggtgacatacccaagctgtgtcctatcacaggtgcagggtgaaggagtcaggacctggcctggcgcgcctcacagagcctgtccattacatgcactgtctcagggttctcattaaccacctctgtgtgaagctgggttcgccagcctccaggaaagggtctggagtggtgggagtaatatggggtgacgggagcacaactatcattcagctctcaaatccagactgagcatcaagaagatcactccaagagccaagttttcttaaaactgaacagctgcaaaactgatgacacagccacgtactactgtgccaaggagggtactcgttggtcactggggccaagggtactgtgtcactgtcagcctctcagaaggcccc (SEQ ID NO:122)
huCD37-3v1.0	aagcttgccaccatgggttgagctgcattattctgtttctggcgcaccgcaccgggtgtgactcacaagtccaagtcagaatctgtccagggtctgggtggccttcccaaacctctgagcatcactgtaccgtttctggtttagccttaccacctctggtgtgagttgggtacgccaaaccaccggtaagggtctcgaatggctgggtgtaatctggggtgatgttccacaattaccatccttccctcaagtcctgccttagcatcaaaaaggatcacagcaaaagtcagtttctgaaactgaatagctgacagcagccgatacagccacactactattgcgccaagggtggttatagcttgcacactggggtcaagggtaccctcgttaccgtctctcagctagtagcaaaaggcccc (SEQ ID NO:123)
huCD37-3v1.1	aagcttgccaccatgggttgagctgtatcattctgtttctggcgcacagctactgggttccactccaagtgcagggtacaagagtcgggcctggattggtgcaccaagccagaccctctctatcactgtaccgttagcgggttctctgacaaccagtgagtgagttgggtgagcagccaccaggaaagggtgagtggtgggtgatttggggcgacggcgagcaaaactatcattcagctcttaaatctcggtgtccattaaaaaagaccatagtaaatctcaagtttctgaaactcaatagctgacagccgcagacactgtactgtattactgcgcaaaaggaggtacagctgtggtcactggggacaggggacacctggtgacctgtcagctcagcatcaaaaaggcccc (SEQ ID NO:124)
muCD37-12	cagatccagttggtgcagctgtgacctgagctgaagaagcctggagagacagtcagatctctgcaaggctctgtgggtatccttcacaaagtatggaatgaactgggtgaagcaggctcaaggaaagggttaagtggatgggtggataaacacacactggagagtcagaagaatgctgaagaattcaagggtgaggtttgccttcctttggaaacctctgccagcactgcctatttgcagatcaacaacctcaaatataggacacgggtacatatttctgtggaaggggcacggtagtagcggactggggccaaggcaccactctcacagtctctca (SEQ ID NO:125)
chCD37-12	aagcttgccaccatgggttgatgcataatccttttctggcgtactgtaccgtgtgactcacagattcagctggttcaaaagtggccagagctgaaaaagccaggggaaacagtgaataaagtgaaggcatccggttacatttcacaaagtacggcatgaactgggtcaagcagggccaggggcaagggtcacaatggatgggttgatcaatacaacactggcgagcttaggaatgctgaggagtttaaggggcgggttgccttcagcctggagacaagtccagcacagcttacctgcaaatcaacaatctgaagtataggatagcagaacctatttctgcggccgaggcactgtcgttcagactggggacaagggtacaccttgcactgtacagtgccagcactaaggcccc (SEQ ID NO:126)
muCD37-38	gatgtgcagcttcaggagtcaggacctgacctgggtgaaaccttctcagtcactttcactcacctgcactgtcactggctactccatcaccagtgggtttggtggcactggatccggcagtttcaggaaacaagctggaatggatggcctacatactctacagtggtggcactgactacaacctctctcaaaagtcgaatctctatc

	actcgagacacttccaagaaccagttcttctcggttgagttctgtgactactgaggacacagccacat attactgtgcaagaggctactatgtgtacgggacctggttggttactggggccaagggactctgtgcac tctcttca (SEQ ID NO:127)
chCD37-38	aagcttgccaccatgggctggagtgatcattctgttttgggtggccaccgacctggagtcattccaagtgaactcc aggaatctggccctgacctggtaagccatctcagagcctctccctgacctgcactgttacagatactcaatcacatcag gctttggctggcactggatcagacaatttccgggaacaagtggatggatggcttacattctgtatagcgggggtaccg attacaatccttccctcaagagccgaatctctatcaccaggatacaagaagaaccaatttttccgcctcagctctgtg actaccgaagataccgctacttactattgtgccaggggctactatggalatggtgcatggttcgtctattggggccaggga accctgtgactgtgagcctcctctaccaaggggccc (SEQ ID NO:128)
huCD37-38	aagcttgccaccatgggttgagctgcattcttttctggtcgtactgcaactggagtcactcacaggtccagctgc aagagtccggctctggcgttgtaaacccagccagtcctcagctcacctgtactgtctggtactctattaccagtg gttcggctggcattggattaggcagtttcccggaaggggctggagtgatggcatatctgtacagcggagggaacc gattacaaccaagtctgaagagcaggatcagcattaccgggacacaagcaaaaaccagttttcttcggtctgtagt gttacagctgcagacaccgctacttacttgtctcggggttactatggctatgggctgtgttgggttattggggacaag gactctgtgacctgaacagcctcaacaaggggccc (SEQ ID NO:129)
muCD37-50	gatgtgcagcttcaggagtcaggacctgacctgtgaaaccttctcagtcactttcactcacctgcactg tcactggtactccatcaccagtgggttgcctggcactggatccggcagttccaggaaacaaactgga atggatgggctacatactctacagtggtagcactgtctacagccatctctcaaaagtcgaatctctatc actcgagacacatccaagaaccacttctctcagttgaattctgtgactactgaggacacagccacat attactgtgcaagagggtactatggttacggcgctggttgctactggggccaagggactctggtcac tctcttca (SEQ ID NO:130)
huCD37-50	aagcttgccaccatgggttggtcctgcataatcttttctggttgctactgtaccggagtcattcacaggtgcagctgc aggagtccggccccggcctgtcaagccttctcagagtctgagtctgactgtactgttctggctacagcataaccagcg gtttcgttggtcactggatcagacagatcccggaacaaactggagtgatgggatacactgtactcaggtcaact gtctattccccctccctgaaatcccgatcagttaccggtgacacttcaagaaccatttttctgcagctgaacagcgtt accgcagctgacactgcaacctactactgtgccggggatattatggatacggagcttggttcgttactggggccaagg cacctctgaactgtgagtgctgttccaccaaggggccc (SEQ ID NO:2)
muCD37-51	gatgtgcagcttcaggagtcaggacctgacctgtgaaaccttctcagtcactttcactcacctgcactg tcactggtactccatcaccagtgggttgcctggcactggatccggcagttccaggaaacaaactgga atggatgggctacatactacagtggtagcactaactacagccatctctcaaaagtcgaatctctatc actcgagactcatccaagaaccagttctctcagttgaattctgtgactactgaggacacagccacat attactgtgcaagaggatactatggttcggcgctggttggttactggggccaagggactctggtcac tctcttca (SEQ ID NO:131)
huCD37-51	Aagcttgccaccatgggttggtcctgcataatcttttctggttgccactgcccgtgcattcagaagttcagttgg tggagtccggcccagaagtgtgaaacccggcgaatcactgtccctgactgtaccgtgtcaggttatagcatcagcagc ggctttgcttggtcactggattcggcagttccaggcaagggactggaatggatgggctacatcattacagttggtcaac caattacagccctagcctgcagggccgaatctctattaccagggatagttctattaaccagttttctgcagcttaattccgt gactgctctgacacagcaacttactattgcgccgtggctactacgggttcggagcctggttgatactgggggtcaggg cacctgtgacttctcagccgctctaccaaggggccc (SEQ ID NO:3)
muCD37-56	gatgtgcagcttcaggagtcaggacctgacctgtgaaaccttctcagtcactttcactcacctgcactg tcactggtactccatcaccagtgggttgcctggcactggatccggcagttccaggaaacaaactgga atggatgggctacatactacagtgggtggcactaactacaacccatctctcaaaagtcgagtctctatc actcgagacacatccaagaaccagttctctcagttgaattctgtgactactgaggacacagccacatattactgtgcaa gaggctactatggttcggggcctggttgcttactggggccaagggactctggtccc tctcttca (SEQ ID NO:132)
huCD37-56	aagcttgccaccatgggttggtcctgcattatcctgttctcgtcgcaccgcaaccggcgtccactccaggtgcagct gcaagaaagcgggcccaggattggtaaaaccttccagctctctgagtttactgtaccgtatctggatacagtatcacatct ggcttgcctggcattggattgccagtttccggcaaggggcttgagtgatggggtatattcatttctggaggtacca actacaaccttccctgaagagtcgagttcaattaccagggacacttccaagaaccaattcttttgcagcttaattcagtg accgctgccgacaccgctacttactactgcgccggggctactatgggttgggtgctggttcgctactggggccaggg gacctgtgcccgtgtctctcctcacaaggggccc (SEQ ID NO:133)
muCD37-57	gatgtgcagcttcaggagtcaggacctgacctgtgaaaccttctcagtcactttcactcacctgcactg tcactggtactccatcaccagtgggttgcctggcactggatccggcagttccaggaaacaaactgga atggatgggctacatactctacagtggtagcacttctacagccatctctcaaaagtcgaatctctatc

	actcgagacacatccaagaaccagttcttctgcagttgaattctgtgactactgaggacacagccacatattactgtgcaa gagggtactatggttacggcgctggttgcttactggggccaaggagctctggtcactgtctctgca (SEQ ID NO:134)
huCD37-57	aagcttgccaccatgggctggagctgcatcattctgttctggggccacagcaactggcggtcacagtcaagtccaactg caggagagcggccccggactcctgaaaccatctcagtcactcagctgacatgtactgtgagcggctacagcattacctc aggcttcgcttgccattggatcaggcagttccccggaaaaggctcggagtggtgggtacattctgtacagcggcagta cagtgtattcaccctccttgaatctaggatatcaatcacacgtgatacaagcaaaaaicagttcttctccagctgaactcc gtcaccggcgagacacagcaacctatttgtgtcgcggatactacggatatggcgcatggttcgctattggggcca ggggacactctgacgtttccaccctccacaaagggccc (SEQ ID NO:135)

Variable light chain polynucleotide sequences

Antibody	VL Polynucleotide Sequence (SEQ ID NO)
muCD37-3	gacatccagatgactcagtcctccagcctcccttctgtatctgiggagaaactgtcaccatcacatgtc gagcaagtgaataattcgcagtaatttagcatggtatcagcagaaacagggaaaaatctcctcagctcct ggtaaatgttgcaaaaacttagcagatggtgtgccatcaagggtcagtggcagtggtacaggcacacag tattccctcaagatcaacagcctgcagtcgaagatttgggacttattactgtcaacattattggggtgta ctacgtggacgttcggtggaggcaccagctggaaatcaaacgt (SEQ ID NO:136)
chCD37-3	gaattcgccaccatgagtggtgccactcaggtcctggggtgctgctgtggttacagatgccagatgtgacatccag atgactcagtcctccagcctcccttctgtatctgtgggagaaactgtcaccatcacatgtcgagcaagtgaataatcgca gtaatttagcatggtatcagcagaaacagggaaaaatctcctcagctcctggtcaatgttgcaaaaacttagcagatggtg gccatcaagggtcagtggcagtggtacaggcacacagattccctcaagatcaacagcctgcagtcgaagatttggga cttattactgtcaacattattgggtactacgtggacgttcggtggaggcaccagctggaaatcaaacgtacg (SEQ ID NO:137)
huCD37-3 (1.0 and 1.1)	gaattcgccaccatgggttggtcctgcacatcttgttctcgtggccacagccaccggtgtcactctgatatacaaatgac tcaaaagccttcagtttgagcgttaagtgtgggtgaacgcgtacaatcacctgtagagctagtgaataatccgcagta atctcgcagtggtaccaaaaaagccaggttaagtcacctaagctcctcgtgaatgtgtctaccaacctcgtgatggtgtgc cttcacgattctctggttcaggttcgggtaccgattattacttaagatcaactcactccaaccagaagatttcggtacatatta ctgtcaaacactactgggttacgacctggacattcgggtcaagggtactaagctggaaatcaaacgtacg (SEQ ID NO:138)
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Full-length heavy chain polynucleotide sequences

Antibody	Full-Length Heavy Chain Polynucleotide Sequence (SEQ ID NO)
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Full-length light chain polynucleotide sequences

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WHAT IS CLAIMED IS:

1. A method for increasing the efficacy of cancer therapy with an anti-CD37 antibody, or anti-CD37 immunoconjugate, said method comprising administering to a subject having cancer an anti-CD37 antibody, or anti-CD37 immunoconjugate, wherein increased expression of CD37 gene or protein in a cancerous sample from said subject has been detected using a detection method that distinguishes between staining intensity or staining uniformity in a CD37 expressing cancerous sample as compared to staining intensity or staining uniformity in one or more reference samples.
2. A method of identifying a cancer as sensitive to treatment with an anti-CD37 antibody, or anti-CD37 immunoconjugate, said method comprising:
 - (a) measuring the level of CD37 expression in a cancerous sample obtained from said cancer, wherein said measuring comprises the use of a detection method that distinguishes between staining intensity or staining uniformity in a CD37 expressing cancerous sample as compared to staining intensity or staining uniformity in one or more reference samples;
 - (b) determining a CD37 staining intensity or staining uniformity score for said cancerous sample; and
 - (c) comparing the CD37 staining intensity or staining uniformity score determined in step (b) to a relative value determined by measuring CD37 protein expression in at least one reference sample, wherein said at least one reference sample is a tissue, cell, or cell pellet sample which is not sensitive to treatment with an anti-CD37 antibody, or anti-CD37 immunoconjugate, and wherein a CD37 staining intensity score for said sample determined in step (b) that is higher than said relative value identifies said cancer as being sensitive to treatment with an anti-CD37 antibody, or anti-CD37 immunoconjugate.
3. A method for identifying a cancer likely to respond to an anti-CD37 antibody, or anti-CD37 immunoconjugate, said method comprising:
 - (a) contacting a biological sample comprising cells from said cancer with an agent that binds CD37 protein on the cell surface;
 - (b) detecting binding of said agent that binds CD37 protein on the cell surface of said biological sample of (a);

- (c) assigning a score to said binding of step (b), wherein said score is assigned based on comparison to one or more reference samples; and
 - (d) comparing said score in step (c) to the score of a reference tissue or cell, wherein a score for said cancer CD37 level that is greater than the score for a negative or low CD37 expressing reference sample or a score for said cancer CD37 level that is equal to or greater than the score for a high CD37 expressing reference sample identifies said cancer as likely to respond to an anti-CD37 antibody or anti-CD37 immunoconjugate.
4. A method of identifying a subject having a cancer as likely to respond to a low dose anti-CD37 antibody or anti-CD37 immunoconjugate treatment regimen, said method comprising:
- (a) contacting a biological sample comprising cells from said cancer with an agent that binds cell surface CD37 protein;
 - (b) detecting binding of said agent to said biological sample of (a);
 - (c) assigning a score to said binding of step (b), wherein said score is assigned based on comparison to one or more reference samples; and
 - (d) comparing said score in step (c) to the score of a reference tissue or cell, wherein a score for said cancer CD37 level that is greater than the score for a negative or low CD37 expressing reference sample or a score for said cancer CD37 level that is equal to or greater than the score for a high CD37 expressing reference sample identifies said cancer as likely to respond to a low dose anti-CD37 antibody or anti-CD37 immunoconjugate.
5. A method of optimizing a therapeutic regimen with an anti-CD37 antibody or an anti-CD37 immunoconjugate for a subject having cancer, said method comprising:
- (a) detecting the level of CD37 expression in a cancerous sample obtained from said subject;
 - (b) comparing the level of CD37 expression in the cancerous sample to the CD37 expression in a reference sample;
 - (c) determining a CD37 staining intensity score for said cancerous sample; and
 - (d) administering an increased dose of an anti-CD37 antibody or an anti-CD37 immunoconjugate to the subject if the score is low or administering a decreased dose of an anti-CD37 antibody or an anti-CD37 immunoconjugate to the subject if the score is high.

6. A method of detecting the expression of cell surface CD37 on cancer cells in a cancerous sample from a subject, said method comprising:
 - (a) obtaining a cancerous sample, wherein said sample is formalin-fixed paraffin embedded;
 - (b) contacting said sample with an antibody that specifically binds cell surface CD37;
 - (c) measuring the binding of said antibody in (b) to said cell surface CD37 in said cancerous sample using a detection method that can distinguish between staining intensity or staining uniformity in a CD37 expressing sample as compared to staining intensity or staining uniformity in one or more reference samples; and
 - (d) assigning a CD37 expression score to said CD37 after comparing the level of cell surface CD37 staining intensity or staining uniformity in said tumor cancerous sample to one or more reference samples.
7. The method of any one of claims 1-6, wherein the detection is by immunohistochemistry (IHC).
8. The method of claim 7, wherein said IHC is calibrated IHC that can distinguish different levels of CD37 expression.
9. The method of any one of claims 1-8, wherein said detection method produces a range of staining intensity for samples having low cell surface CD37 expression, intermediate CD37 cell surface expression, or high CD37 cell surface expression.
10. The method of any one of 1-9, wherein said detection method distinguishes between staining intensity and staining uniformity in a CD37 expressing cancerous sample as compared to a reference sample.
11. The method of any one of claims 1-10, wherein the cancerous sample or biological sample has a staining intensity score of 2, 3, or 3+ for CD37 expression by immunohistochemistry.
12. The method of claim 11, wherein the cancerous sample or biological sample has a staining intensity score of 2, 3, or 3+ for CD37 expression by immunohistochemistry on a formalin fixed paraffin embedded sample.

13. The method of any of claims 10-12, wherein the cancerous sample or biological sample has a staining uniformity for CD37 expression that is homogenous.
14. The method of any one of claims 7-12, wherein the cancerous sample or biological sample has a staining intensity score of 2, 3, or 3+ for CD37 and a staining uniformity that is heterogeneous or homogenous.
15. The method of any one of claims 7-14, wherein the immunohistochemistry is performed manually.
16. The method of any one of claims 7-14, wherein the immunohistochemistry is performed using an automated system.
17. The method of any one of claims 1-16, wherein said reference sample is a positive reference sample or a negative reference sample.
18. The method of any one of claims 1-17, wherein the reference sample comprises cells, cell pellets, or tissue.
19. The method of any one of claims 1-18, wherein the detection comprises detecting CD37 expression with an antibody that specifically binds cell surface CD37.
20. The method of claim 19, wherein said antibody is CT1.
21. The method of claim 19 or 20, wherein said antibody further comprises a detection reagent selected from the group consisting of: an enzyme, a fluorophore, a radioactive label, and a luminophore.
22. The method of claim 21, wherein said detection reagent is selected from the group consisting of: biotin, digoxigenin, fluorescein, tritium, rhodamine, and horseradish peroxidase.
23. The method of any one of claims 19-22, wherein the concentration of said antibody is about 1- 10 $\mu\text{g/mL}$.

24. The method of claim 23, wherein the concentration of said antibody is about 4-5 $\mu\text{g/mL}$.
25. The method of claim 24, wherein the concentration of said antibody is about 4.2 $\mu\text{g/mL}$.
26. The method of any one of claims 1-25, wherein said cancer is selected from the group consisting of B cell lymphomas, NHL, precursor B cell lymphoblastic leukemia/lymphoma and mature B cell neoplasms, B cell chronic lymphocytic leukemia (CLL)/small lymphocytic lymphoma (SLL), B cell prolymphocytic leukemia, lymphoplasmacytic lymphoma, mantle cell lymphoma (MCL), follicular lymphoma (FL), low grade, intermediate-grade and high-grade (FL), cutaneous follicle center lymphoma, marginal zone B cell lymphoma, MALT type marginal zone B cell lymphoma, nodal marginal zone B cell lymphoma, splenic type marginal zone B cell lymphoma, hairy cell leukemia, diffuse large B cell lymphoma (DLBCL), Burkitt's lymphoma (BL), plasmacytoma, plasma cell myeloma, post-transplant lymphoproliferative disorder, Waldenstrom's macroglobulinemia, and anaplastic large-cell lymphoma (ALCL).
27. The method of any one of claims 1-26, wherein said cancerous sample or said biological sample is tissue, blood, plasma, bone marrow or lymph.
28. An article of manufacture comprising an anti-CD37 antibody or an anti-CD37 immunoconjugate, a container, and a package insert or label indicating that the antibody or immunoconjugate can be used to treat a cancer characterized by the expression of CD37 at a level of 2, 3, or 3+ measured by IHC.
29. A combination diagnostic and pharmaceutical kit comprising a murine anti-CD37 antibody for use in diagnosis and an anti-CD37 antibody or an anti-CD37 immunoconjugate for use in therapy.
30. The combination diagnostic and pharmaceutical kit of claim 29, wherein the diagnostic antibody is a detection antibody that is able to detect CD37 expression by IHC.
31. A diagnostic kit comprising a detection antibody that specifically binds to cell surface CD37, a reagent for immunohistochemistry (IHC), and one or more standardized reference samples,

wherein said standardized reference samples comprise cells, cell pellets, or formalin fixed paraffin embedded tissue samples, and wherein said one or more standardized referenced samples are from non-CD37 expressing, low-CD37 expressing, or high CD37 expressing cells, cell pellets, or tissues.

32. The article of manufacture of claim 28 or the kit of claim 30 or 31, wherein said IHC is calibrated IHC that can distinguish different levels of CD37 expression.
33. The article of manufacture or kit of claim 32, wherein said calibrated IHC produces a range of staining intensity for samples having low cell surface CD37 expression, intermediate cell surface CD37 expression, or high cell surface CD37 expression.
34. The article of manufacture or the kit of any one of claims 28 or 30-33, wherein said IHC distinguishes between staining intensity and staining uniformity in a CD37 expressing sample as compared to a reference sample.
35. The article of manufacture or kit of any one of claims 28 or 30-33, wherein said IHC is performed on a formalin fixed paraffin embedded sample.
36. The article of manufacture or kit of any one of claims 28 or 30-33, wherein said IHC is performed manually.
37. The article of manufacture or kit of any one of claims 28 or 30-33, wherein said IHC is performed using an automated system.
38. The article of manufacture or kit of any one of claims 28-30 or 32-37, wherein the CD37 immunoconjugate comprises an anti-CD37 antibody, a linker, and a cytotoxin.
39. The article of manufacture or kit of claim 38, wherein the anti-CD37 antibody is chimeric, or humanized CD37-3, CD37-38, or CD37-50.
40. The article of manufacture or kit of claim 38 or 39, wherein said linker is selected from the group consisting of a cleavable linker, a non-cleavable linker, a hydrophilic linker, and a dicarboxylic acid based linker.

41. The article of manufacture or kit of claim 40, wherein said linker is selected from the group consisting: N-succinimidyl 4-(2-pyridyldithio)pentanoate (SPP) or N-succinimidyl 4-(2-pyridyldithio)-2-sulfopentanoate (sulfo-SPP); N-succinimidyl 4-(2-pyridyldithio)butanoate (SPDB) or N-succinimidyl 4-(2-pyridyldithio)-2-sulfobutanoate (sulfo-SPDB); N-succinimidyl 4-(maleimidomethyl) cyclohexanecarboxylate (SMCC); N-sulfosuccinimidyl 4-(maleimidomethyl) cyclohexanecarboxylate (sulfoSMCC); N-succinimidyl-4-(iodoacetyl)-aminobenzoate (SIAB); and N-succinimidyl-[(N-maleimidopropionamido)-tetraethyleneglycol] ester (NHS-PEG4-maleimide).
42. The article of manufacture or kit of claim 41, wherein said linker is N-succinimidyl 4-(maleimidomethyl) cyclohexanecarboxylate (SMCC).
43. The article of manufacture or kit of any one of claims 38-42, wherein said cytotoxin is selected from the group consisting of a maytansinoid, maytansinoid analog, benzodiazepine, taxoid, CC-1065, CC-1065 analog, duocarmycin, duocarmycin analog, calicheamicin, dolastatin, dolastatin analog, auristatin, tomaymycin derivative, and leptomyacin derivative or a prodrug of the cytotoxin.
44. The article of manufacture or kit of claim 43, wherein said cytotoxin is a maytansinoid.
45. The article of manufacture or kit of claim 44, wherein said maytansinoid is N(2')-deacetyl-N(2')-(3-mercapto-1-oxopropyl)-maytansine or N(2')-deacetyl-N2-(4-mercapto-4-methyl-1-oxopentyl)-maytansine.
46. The article of manufacture or kit of claim 45, wherein said maytansinoid is N(2')-deacetyl-N(2')-(3-mercapto-1-oxopropyl)-maytansine (DM1).
47. The article of manufacture or kit of any one of claims 38-46, wherein said immunoconjugate comprises the antibody huCD37-3, the linker SMCC, and the maytansinoid DM1.
48. The combination diagnostic and pharmaceutical kit of any one of claims 29-30 and 32-47, further comprising one or more reference samples.

49. The combination diagnostic and pharmaceutical kit of claim 48, wherein said reference sample is a positive reference sample or a negative reference sample.
50. The combination diagnostic and pharmaceutical kit of claim 48 or 49, wherein the reference sample comprises cells, cell pellets, or tissue.
51. The kit of any one of claims 30-37, wherein said detection antibody further comprises a detection reagent selected from the group consisting of: an enzyme, a fluorophore, a radioactive label, and a luminophore.
52. The kit of claim 51, wherein said detection reagent is selected from the group consisting of: biotin, digoxigenin, fluorescein, tritium, rhodamine, and horseradish peroxidase.
53. The kit of claim any one of claims 30-37 or 51-52, wherein the concentration of the detection antibody is about 1-10 $\mu\text{g/mL}$.
54. The kit of claim 53, wherein the concentration of the detection antibody is about 4-5 $\mu\text{g/mL}$.
55. The kit of claim 54, wherein the concentration of the detection antibody is about 4.2 $\mu\text{g/mL}$.
56. The kit of claim 31, wherein the low-CD37 expressing control is Namalwa or RL tumor cells.
57. The kit of claim 31, wherein the high-CD37 expressing control is selected from the group consisting of: Daudi and Ramos cell lines, and a cell line stably or transiently transfected with CD37.
58. The kit of claim 57, wherein said cell line stably or transiently transfected with CD37 is 300-19/CD37.

Figure 1.

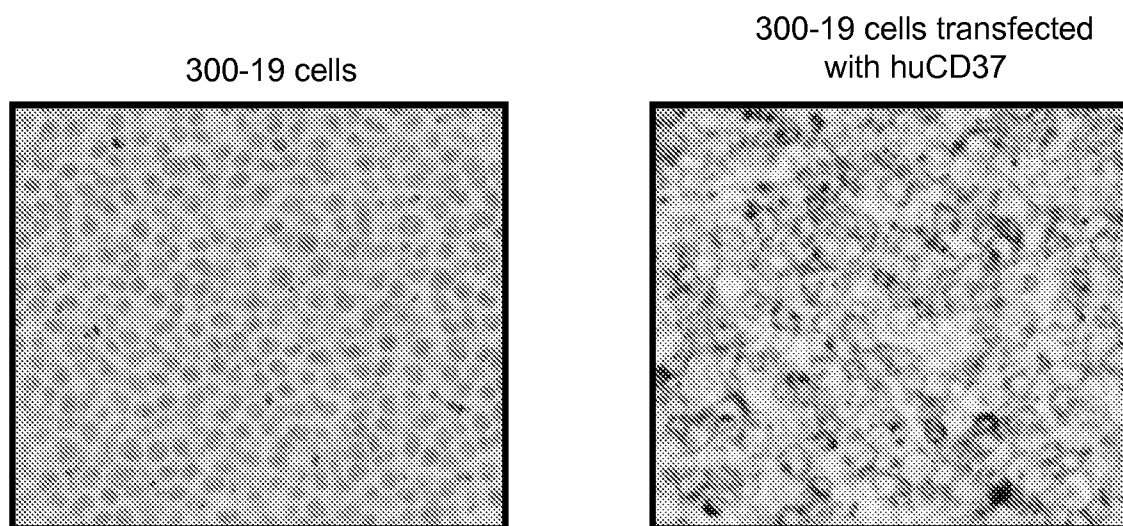


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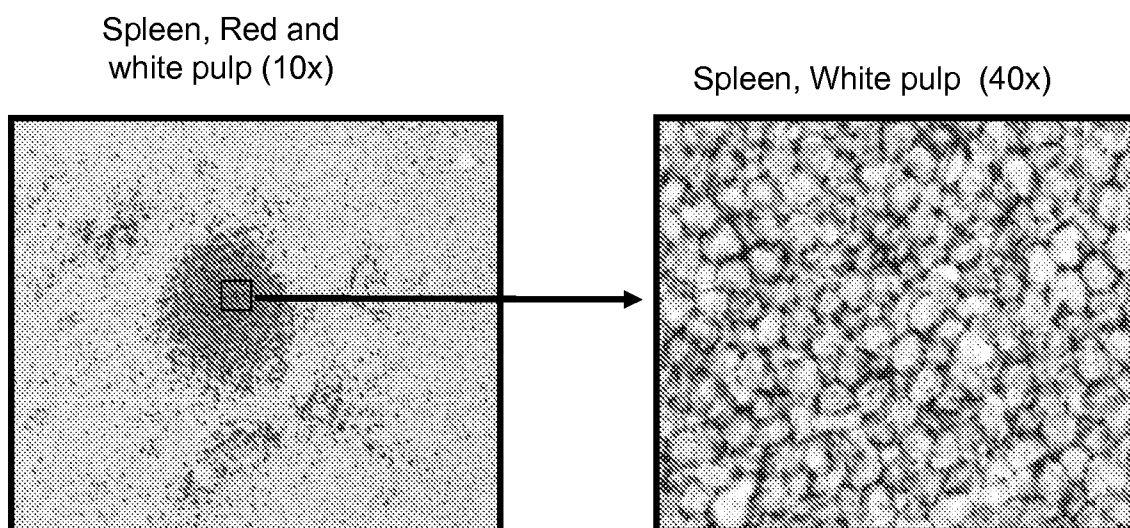


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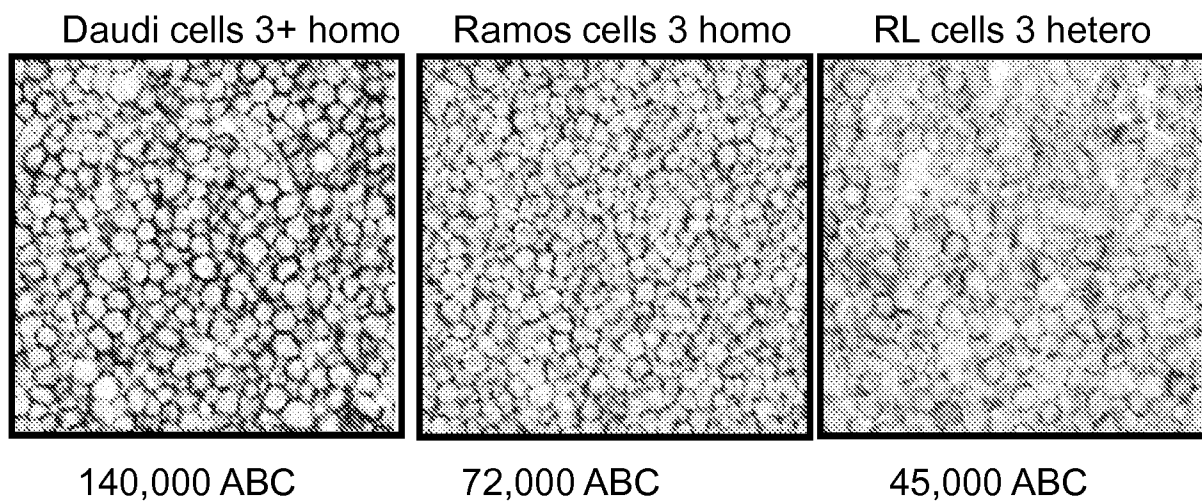


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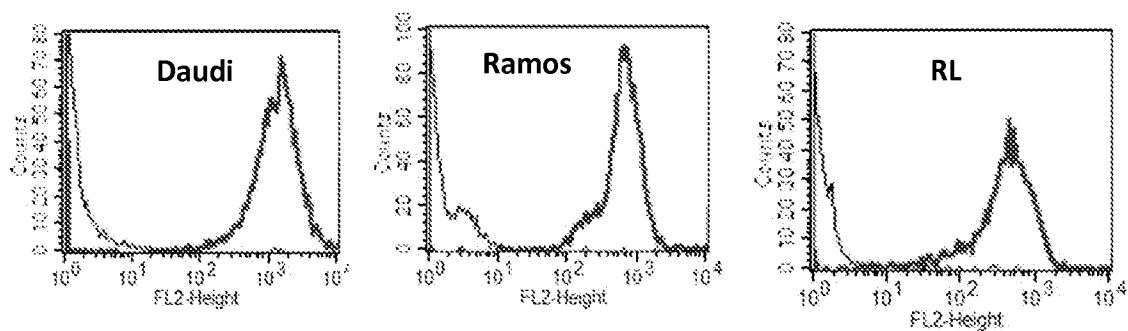


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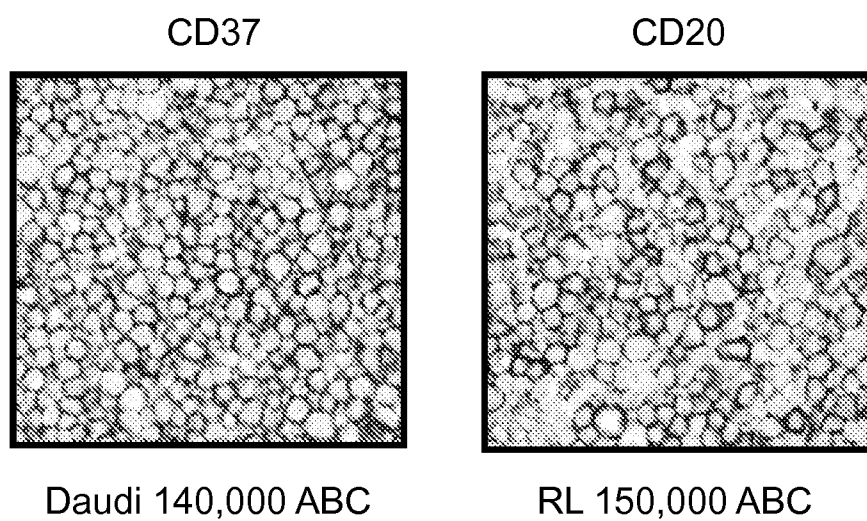


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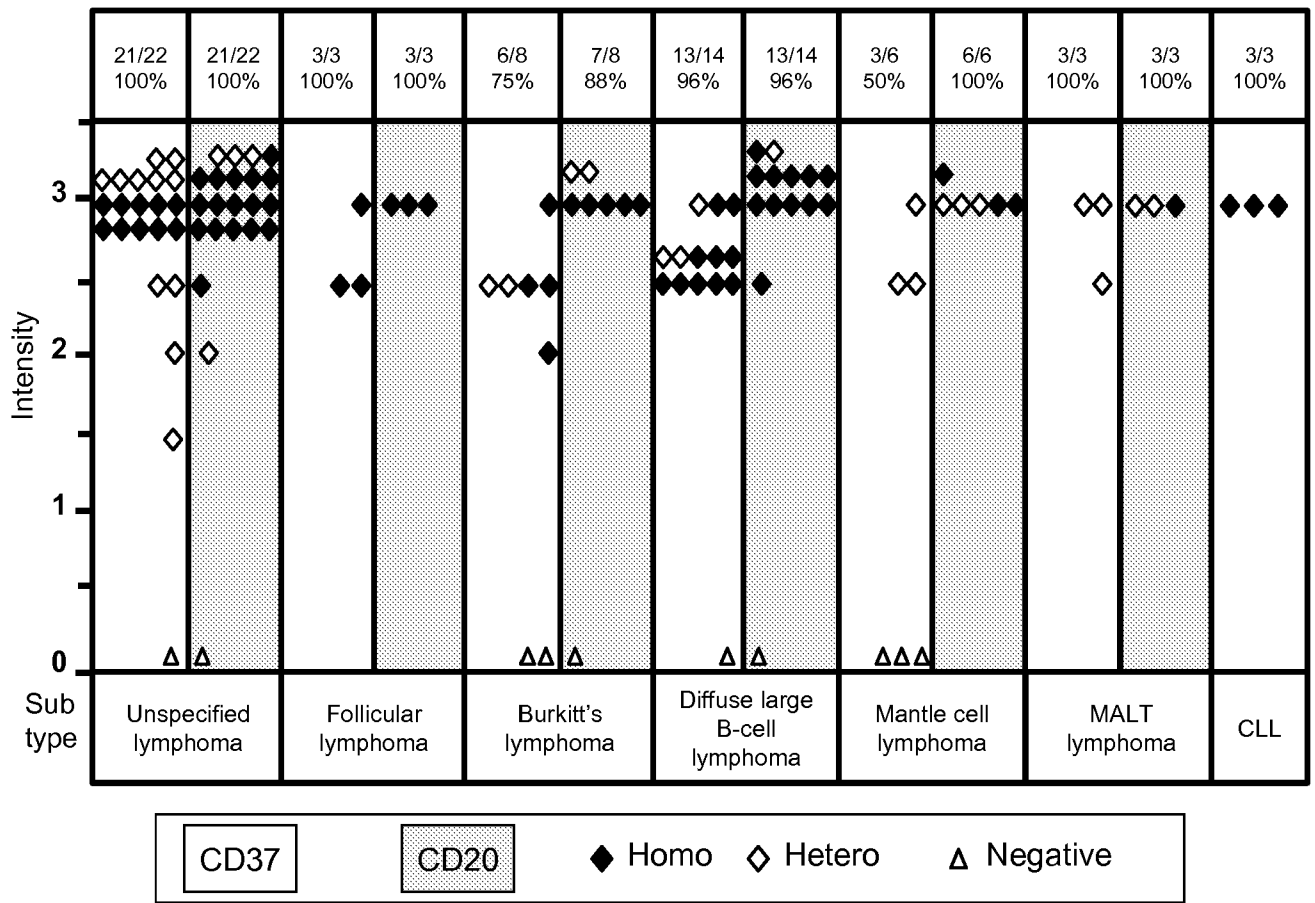


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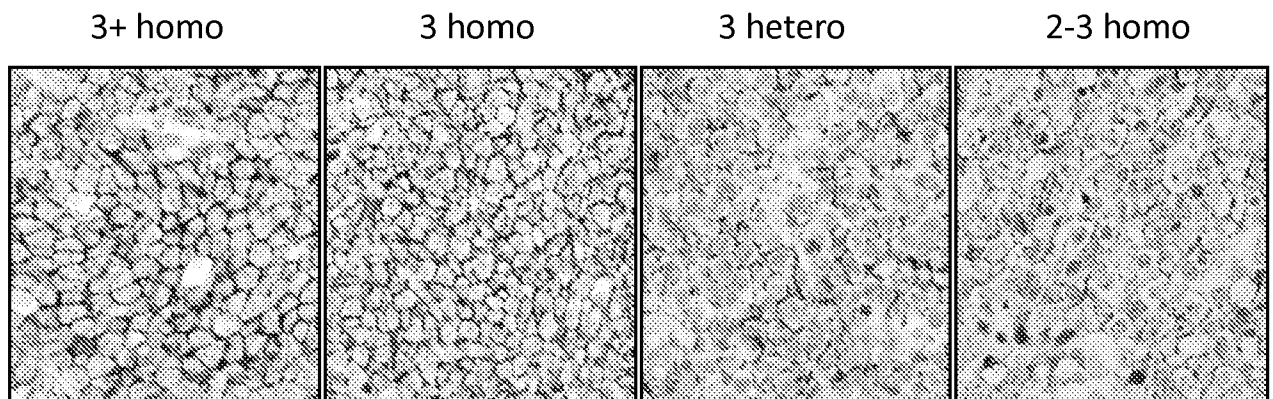
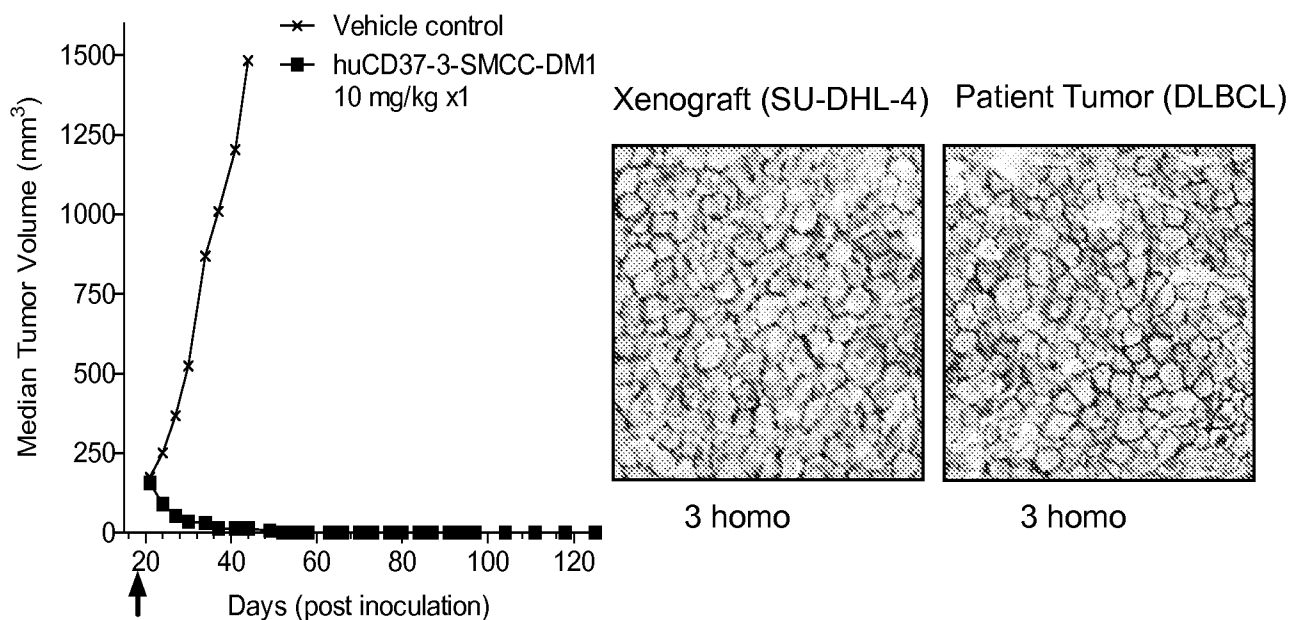


Figure 8.



	Dose	% T/C d37	T-C in days	PR	CR	TFS d125	Comments
Control	-	-	-	0/10	0/10	0/10	
huCD37-3-SMCC-DM1	10 mg/kg	1	31	10/10	8/10	6/10	Highly active

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Figure 9.

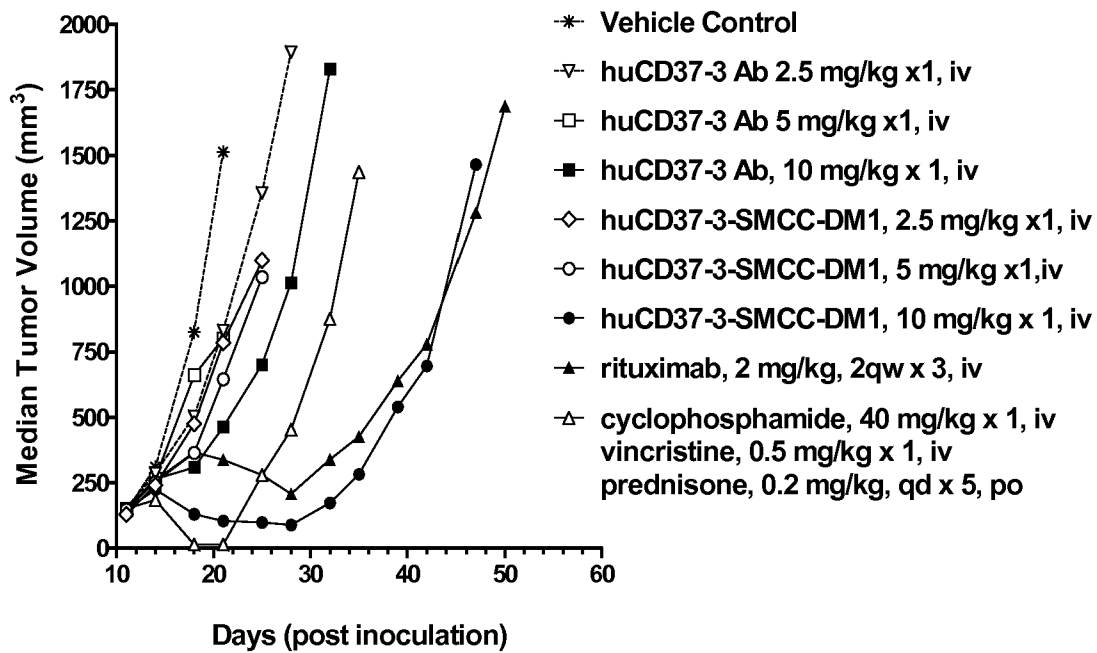
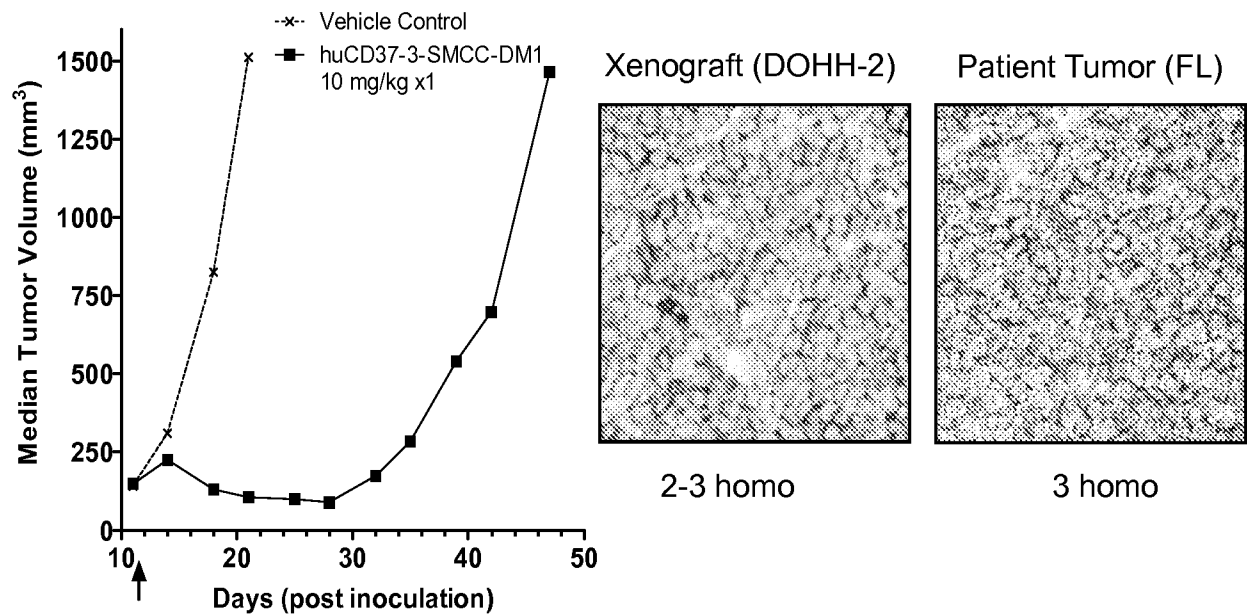


Figure 10.



	Dose	% T/C d19	T-C in days	PR	CR	TFS d130	Comments
Control	-	-	-	0/9	0/9	0/9	
huCD37-3-SMCC-DM1	10 mg/kg	16	21	4/9	2/9	1/9	Active

Figure 11.

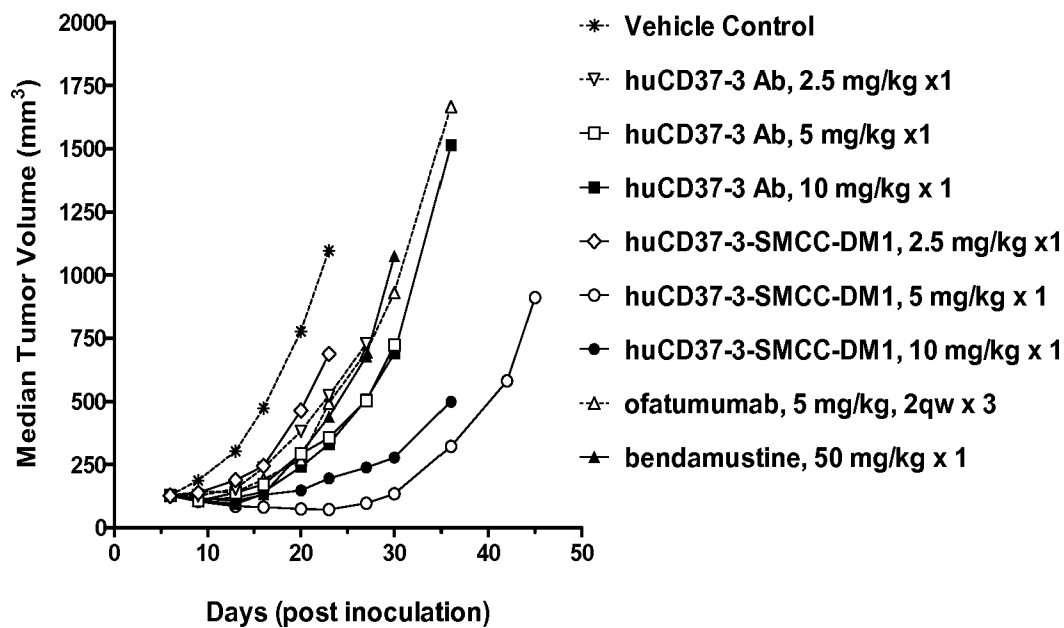
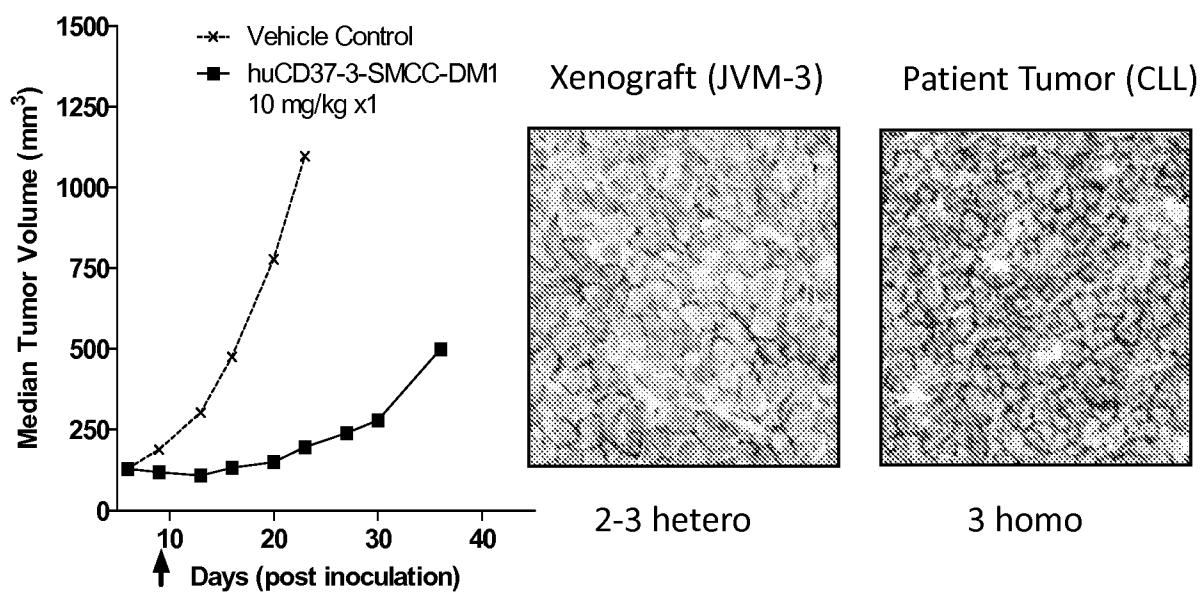
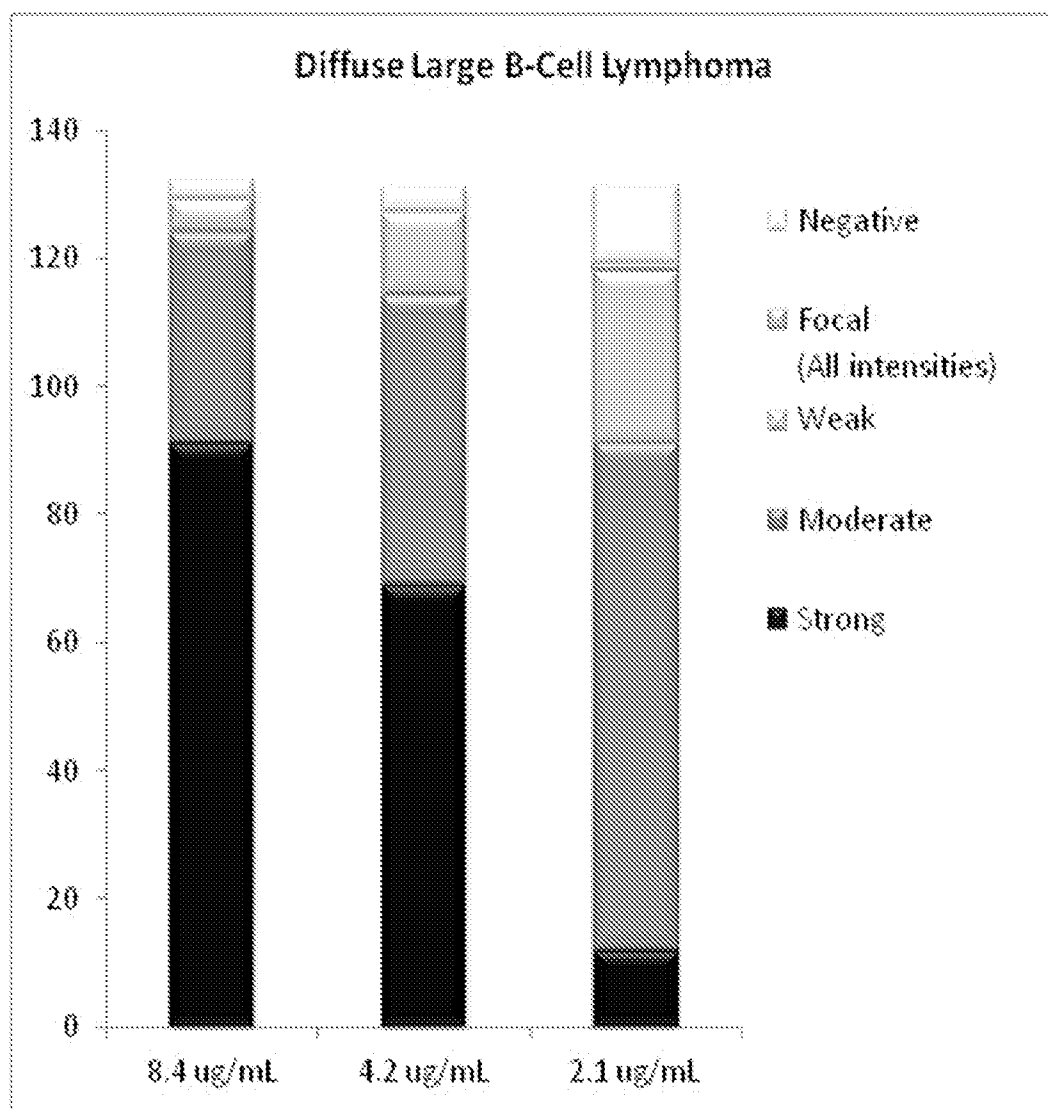


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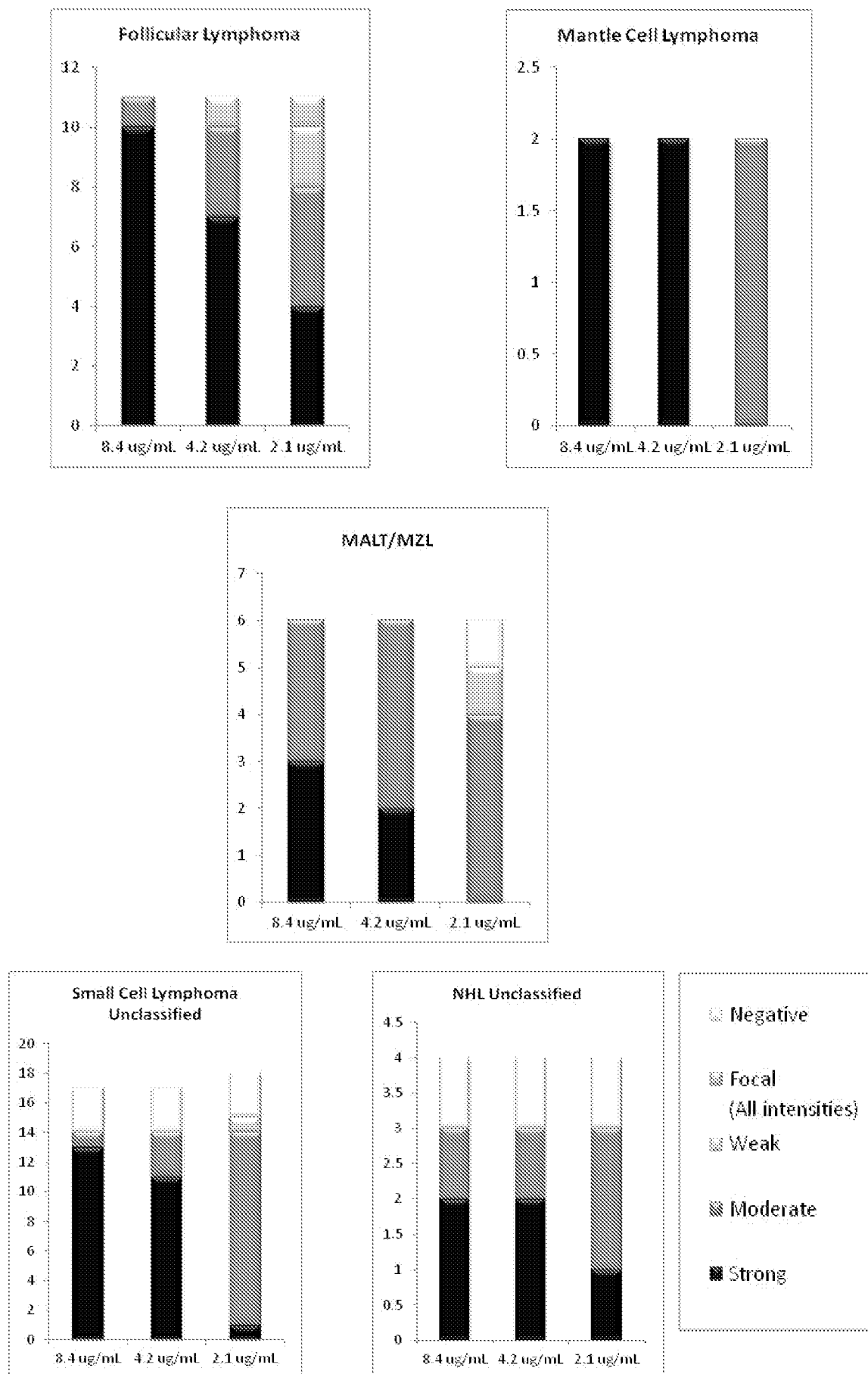
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Control	-	-	-	0/10	0/10	0/10	
huCD37-3-SMCC-DM1	10 mg/kg	26	16.5	4/10	2/10	1/10	Active

Figure 13.



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Figure 14.



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Carrigan, Christina

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<223> CD37-57 VL-CDR1

<400> 48

Ser	Ala	Thr	Ser	Ser	Val	Thr	Tyr	Met	His
1				5					10

<210> 49

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> CD37-57 VL-CDR2

<400> 49

Asp	Thr	Ser	Lys	Leu	Ala	Ser
1				5		

<210> 50

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> CD37-57 VL-CDR3

<400> 50

Gln	Gln	Trp	Ser	Asp	Asn	Pro	Pro	Thr
1				5				

<210> 51

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized VL-CDR2

<400> 51

Asp	Thr	Ser	Asn	Leu	Ala	Ser
1				5		

<210> 52

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> CONSENSUS VL-CDR1

<220>

<221> MSC_FEATURE

<222> (3)..(3)

<223> X is T or S

<400> 52

Ser	Ala	Xaa	Ser	Ser	Val	Thr	Tyr	Met	His
1				5					10

<210> 53
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CONSENSUS VL- CDR2

<220>
 <221> M SC_FEATURE
 <222> (4)..(4)
 <223> X i s K or N

<220>
 <221> M SC_FEATURE
 <222> (6)..(6)
 <223> X i s A or P

<220>
 <221> M SC_FEATURE
 <222> (7)..(7)
 <223> X i s S or Y

<400> 53

Asp Thr Ser Xaa Leu Xaa Xaa
 1 5

<210> 54
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CONSENSUS VL- CDR3

<220>
 <221> M SC_FEATURE
 <222> (4)..(4)
 <223> X i s I or S

<220>
 <221> M SC_FEATURE
 <222> (5)..(5)
 <223> X i s S or D

<220>
 <221> M SC_FEATURE
 <222> (6)..(6)
 <223> X i s N or D

<400> 54

G n G n Trp Xaa Xaa Xaa Pro Pro Thr
 1 5

<210> 55
 <211> 115
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> muCD37- 3

2921032PC01SequenceLi st i ng. t xt

<400> 55

G n Val G n Val Lys G u Ser G y Pro G y Leu Val Al a Pro Ser G n
1 5 10 15

Ser Leu Ser Ile Thr Oys Thr Val Ser G y Phe Ser Leu Thr Thr Ser
20 25 30

G y Val Ser Trp Val Arg G n Pro Pro G y Lys G y Leu G u Trp Leu
35 40 45

G y Val Ile Trp G y Asp G y Ser Thr Asn Tyr Hi s Ser Al a Leu Lys
50 55 60

Ser Arg Leu Ser Ile Lys Lys Asp Hi s Ser Lys Ser G n Val Phe Leu
65 70 75 80

Lys Leu Asn Ser Leu G n Thr Asp Asp Thr Al a Thr Tyr Tyr Oys Al a
85 90 95

Lys G y G y Tyr Ser Leu Al a Hi s Trp G y G n G y Thr Leu Val Thr
100 105 110

Val Ser Al a
115

<210> 56

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> chCD37-3

<400> 56

G n Val G n Val Lys G u Ser G y Pro G y Leu Val Al a Pro Ser G n
1 5 10 15

Ser Leu Ser Ile Thr Oys Thr Val Ser G y Phe Ser Leu Thr Thr Ser
20 25 30

G y Val Ser Trp Val Arg G n Pro Pro G y Lys G y Leu G u Trp Leu
35 40 45

G y Val Ile Trp G y Asp G y Ser Thr Asn Tyr Hi s Ser Al a Leu Lys
50 55 60

Ser Arg Leu Ser Ile Lys Lys Asp Hi s Ser Lys Ser G n Val Phe Leu
65 70 75 80

Lys Leu Asn Ser Leu G n Thr Asp Asp Thr Al a Thr Tyr Tyr Oys Al a
85 90 95

2921032PC01SequenceLi st i ng. t xt

Lys G y G y Tyr Ser Leu Al a Hi s Trp G y G n G y Thr Leu Val Thr
100 105 110

Val Ser Al a
115

<210> 57
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD37-3v1.0

<400> 57

G n Val G n Val G n G u Ser G y Pro G y Leu Val Al a Pro Ser G n
1 5 10 15

Thr Leu Ser Ile Thr Oys Thr Val Ser G y Phe Ser Leu Thr Thr Ser
20 25 30

G y Val Ser Trp Val Arg G n Pro Pro G y Lys G y Leu G u Trp Leu
35 40 45

G y Val Ile Trp G y Asp G y Ser Thr Asn Tyr Hi s Pro Ser Leu Lys
50 55 60

Ser Arg Leu Ser Ile Lys Lys Asp Hi s Ser Lys Ser G n Val Phe Leu
65 70 75 80

Lys Leu Asn Ser Leu Thr Al a Al a Asp Thr Al a Thr Tyr Tyr Oys Al a
85 90 95

Lys G y G y Tyr Ser Leu Al a Hi s Trp G y G n G y Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 58
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD37-3v1.1

<400> 58

G n Val G n Val G n G u Ser G y Pro G y Leu Val Al a Pro Ser G n
1 5 10 15

Thr Leu Ser Ile Thr Oys Thr Val Ser G y Phe Ser Leu Thr Thr Ser
20 25 30

2921032PC01SequenceLi st i ng. t xt

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

Gly Val Ile Trp Gly Asp Gly Ser Thr Asn Tyr His Ser Ser Leu Lys
50 55 60

Ser Arg Leu Ser Ile Lys Lys Asp His Ser Lys Ser Gln Val Phe Leu
65 70 75 80

Lys Leu Asn Ser Leu Thr Ala Ala Asp Thr Ala Thr Tyr Tyr Cys Ala
85 90 95

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

Val Ser Ser
115

<210> 59
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD37-12

<400> 59

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

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

Gly Met Asn Trp Val Lys Gln Ala Gln Gly Lys Gly Leu Lys Trp Met
35 40 45

Gly Trp Ile Asn Thr Asn Thr Gly Glu Ser Arg Asn Ala Glu Glu Phe
50 55 60

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

Leu Gln Ile Asn Asn Leu Lys Tyr Glu Asp Thr Ala Thr Tyr Phe Cys
85 90 95

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

Val Ser Ser
115

<210> 60

2921032PC01SequenceLi st i ng. t xt

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

<220>
<223> chCD37-12

<400> 60

G n I l e G n L e u V a l G n S e r G y P r o G u L e u L y s L y s P r o G y G u
1 5 10 15
T h r V a l L y s I l e S e r O y s L y s A l a S e r G y T y r T h r P h e T h r L y s T y r
20 25 30
G y M e t A s n T r p V a l L y s G n A l a G n G y L y s G y L e u L y s T r p M e t
35 40 45
G y T r p I l e A s n T h r A s n T h r G y G u S e r A r g A s n A l a G u G u P h e
50 55 60
L y s G y A r g P h e A l a P h e S e r L e u G u T h r S e r A l a S e r T h r A l a T y r
65 70 75 80
L e u G n I l e A s n A s n L e u L y s T y r G u A s p T h r A l a T h r T y r P h e C y s
85 90 95
G y A r g G y T h r V a l V a l A l a A s p T r p G y G n G y T h r T h r L e u T h r
100 105 110
V a l S e r S e r
115

<210> 61
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD37-38

<400> 61

A s p V a l G n L e u G n G u S e r G y P r o A s p L e u V a l L y s P r o S e r G n
1 5 10 15
S e r L e u S e r L e u T h r O y s T h r V a l T h r G y T y r S e r I l e T h r S e r G y
20 25 30
P h e G y T r p H i s T r p I l e A r g G n P h e P r o G y A s n L y s L e u G u T r p
35 40 45
M e t A l a T y r I l e L e u T y r S e r G y G y T h r A s p T y r A s n P r o S e r L e u
50 55 60
L y s S e r A r g I l e S e r I l e T h r A r g A s p T h r S e r L y s A s n G n P h e P h e
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65

70

75

80

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

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

Gly Thr Leu Val Thr Val Ser Ala
115 120

<210> 62

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> chCD37-38

<400> 62

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

Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Gly
20 25 30

Phe Gly Trp His Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
35 40 45

Met Ala Tyr Ile Leu Tyr Ser Gly Gly Thr Asp Tyr Asn Pro Ser Leu
50 55 60

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

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

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

Gly Thr Leu Val Thr Val Ser Ala
115 120

<210> 63

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> huCD37-38

<400> 63

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

1 5 10 15

Ser Leu Ser Leu Thr Oys Thr Val Ser Gly Tyr Ser Ile Thr Ser Gly
20 25 30

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

Met Ala Tyr Ile Leu Tyr Ser Gly Gly Thr Asp Tyr Asn Pro Ser Leu
50 55 60

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 64
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> muCD37-50

<400> 64

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

Ser Leu Ser Leu Thr Oys Thr Val Thr Gly Tyr Ser Ile Thr Ser Gly
20 25 30

Phe Ala Trp His Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
35 40 45

Met Gly Tyr Ile Leu Tyr Ser Gly Ser Thr Val Tyr Ser Pro Ser Leu
50 55 60

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

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

Ala Arg Gly Tyr Tyr Gly Tyr Gly Ala Trp Phe Ala Tyr Trp Gly Gln
100 105 110

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G y Thr Leu Val Thr Val Ser Al a
115 120

<210> 65
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD37-50

<400> 65

G n Val G n Leu G n G u Ser G y Pro G y Leu Leu Lys Pro Ser G n
1 5 10 15

Ser Leu Ser Leu Thr Cys Thr Val Ser G y Tyr Ser Ile Thr Ser G y
20 25 30

Phe Al a Trp His Trp Ile Arg G n His Pro G y Asn Lys Leu G u Trp
35 40 45

Met G y Tyr Ile Leu Tyr Ser G y Ser Thr Val Tyr Ser Pro Ser Leu
50 55 60

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

Leu G n Leu Asn Ser Val Thr Al a Al a Asp Thr Al a Thr Tyr Tyr Cys
85 90 95

Al a Arg G y Tyr Tyr G y Tyr G y Al a Trp Phe Al a Tyr Trp G y G n
100 105 110

G y Thr Leu Val Thr Val Ser Al a
115 120

<210> 66
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD37-51

<400> 66

Asp Val G n Leu G n G u Ser G y Pro Asp Leu Leu Lys Pro Ser G n
1 5 10 15

Ser Leu Ser Leu Thr Cys Thr Val Thr G y Tyr Ser Ile Ser Ser G y
20 25 30

Phe Al a Trp His Trp Ile Arg G n Phe Pro G y Asn Lys Leu G u Trp
35 40 45

2921032PC01SequenceLi st i ng. t xt

Met Gly Tyr Ile His Tyr Ser Gly Ser Thr Asn Tyr Ser Pro Ser Leu
50 55 60

Lys Ser Arg Ile Ser Ile Thr Arg Asp Ser Ser Lys Asn Gl n Phe Phe
65 70 75 80

Leu Gl n Leu Asn Ser Val Thr Thr Gl u Asp Thr Al a Thr Tyr Tyr Cys
85 90 95

Al a Arg Gly Tyr Tyr Gly Phe Gly Al a Trp Phe Val Tyr Trp Gly Gl n
100 105 110

Gly Thr Leu Val Thr Val Ser Al a
115 120

<210> 67
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD37-51

<400> 67

Gl u Val Gl n Leu Val Gl u Ser Gly Pro Gl u Val Leu Lys Pro Gly Gl u
1 5 10 15

Ser Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Ser Ser Gly
20 25 30

Phe Al a Trp His Trp Ile Arg Gl n Phe Pro Gly Lys Gly Leu Gl u Trp
35 40 45

Met Gly Tyr Ile His Tyr Ser Gly Ser Thr Asn Tyr Ser Pro Ser Leu
50 55 60

Gl n Gly Arg Ile Ser Ile Thr Arg Asp Ser Ser Ile Asn Gl n Phe Phe
65 70 75 80

Leu Gl n Leu Asn Ser Val Thr Al a Ser Asp Thr Al a Thr Tyr Tyr Cys
85 90 95

Al a Arg Gly Tyr Tyr Gly Phe Gly Al a Trp Phe Val Tyr Trp Gly Gl n
100 105 110

Gly Thr Leu Val Thr Val Ser Al a
115 120

<210> 68
<211> 120
<212> PRT
<213> Artificial Sequence

2921032PC01SequenceLi st i ng. t xt

<220>

<223> muCD37-56

<400> 68

Asp Val G n Leu G n G u Ser G y Pro Asp Leu Val Lys Pro Ser G n
1 5 10 15

Ser Leu Ser Leu Thr Cys Thr Val Thr G y Tyr Ser Ile Thr Ser G y
20 25 30

Phe Ala Trp His Trp Ile Arg G n Phe Pro G y Asn Lys Leu G u Trp
35 40 45

Met G y Tyr Ile His Tyr Ser G y G y Thr Asn Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Val Ser Ile Thr Arg Asp Thr Ser Lys Asn G n Phe Phe
65 70 75 80

Leu G n Leu Asn Ser Val Thr Thr G u Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg G y Tyr Tyr G y Phe G y Ala Trp Phe Ala Tyr Trp G y G n
100 105 110

G y Thr Leu Val Pro Val Ser Ala
115 120

<210> 69

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> huCD37-56

<400> 69

G n Val G n Leu G n G u Ser G y Pro G y Leu Val Lys Pro Ser G n
1 5 10 15

Ser Leu Ser Leu Thr Cys Thr Val Ser G y Tyr Ser Ile Thr Ser G y
20 25 30

Phe Ala Trp His Trp Ile Arg G n Phe Pro G y Lys G y Leu G u Trp
35 40 45

Met G y Tyr Ile His Tyr Ser G y G y Thr Asn Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Val Ser Ile Thr Arg Asp Thr Ser Lys Asn G n Phe Phe
65 70 75 80

Leu G n Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Thr Tyr Tyr Cys

Phe Ala Trp His Trp Ile Arg Gln Phe Pro Gly Lys Gly Leu Glu Trp
 35 40 45
 Met Gly Tyr Ile Leu Tyr Ser Gly Ser Thr Val Tyr Ser Pro Ser Leu
 50 55 60
 Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
 65 70 75 80
 Leu Gln Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Thr Tyr Tyr Cys
 85 90 95
 Ala Arg Gly Tyr Tyr Gly Tyr Gly Ala Trp Phe Ala Tyr Trp Gly Gln
 100 105 110
 Gly Thr Leu Val Thr Val Ser Ala
 115 120

<210> 72
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> muCD37-3

<400> 72

Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Val Ser Val Gly
 1 5 10 15
 Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Arg Ser Asn
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
 35 40 45
 Asn Val Ala Thr Asn Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Ser
 65 70 75 80
 Glu Asp Phe Gly Thr Tyr Tyr Cys Gln His Tyr Trp Gly Thr Thr Trp
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
 100 105

<210> 73
 <211> 108
 <212> PRT

<213> Artificial Sequence

<220>

<223> chCD37-3

<400> 73

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

Glu Thr Val Thr Ile Thr Oys Arg Ala Ser Glu Asn Ile Arg Ser Asn
20 25 30

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

Asn Val Ala Thr Asn Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Gly Thr Tyr Tyr Oys Gln His Tyr Trp Gly Thr Thr Trp
85 90 95

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

<210> 74

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> huCD37-3 (1.0 and 1.1)

<400> 74

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

Glu Arg Val Thr Ile Thr Oys Arg Ala Ser Glu Asn Ile Arg Ser Asn
20 25 30

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

Asn Val Ala Thr Asn Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Lys Ile Asn Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Gly Thr Tyr Tyr Oys Gln His Tyr Trp Gly Thr Thr Trp
85 90 95

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Thr Phe Gly G n Gly Thr Lys Leu Gu Ile Lys Arg
100 105

<210> 75
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD37-12

<400> 75

Asp Ile Val Leu Thr G n Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

G n Arg Ala Thr Ile Ser Cys Arg Ala Ser G n Ser Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Leu Tyr Trp Phe G n G n Lys Pro Gly G n Pro Pro
35 40 45

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

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

Pro Val Gu Gu Gu Asp Thr Ala Thr Tyr Tyr Cys G n His Ser Trp
85 90 95

Gu Ile Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Gu Ile Lys Arg
100 105 110

<210> 76
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> chCD37-12

<400> 76

Asp Ile Val Leu Thr G n Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

G n Arg Ala Thr Ile Ser Cys Arg Ala Ser G n Ser Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Leu Tyr Trp Phe G n G n Lys Pro Gly G n Pro Pro
35 40 45

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

2921032PC01SequenceLi st i ng. t xt

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

Pro Val Gu Gu Gu Asp Thr Ala Thr Tyr Tyr Cys G n His Ser Trp
85 90 95

Gu Ile Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Gu Ile Lys Arg
100 105 110

<210> 77
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD37-38

<400> 77

G n Ile Val Leu Thr G n Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
1 5 10 15

Gu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met
20 25 30

His Trp Tyr G n G n Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
35 40 45

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Gu Ala Gu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys G n G n Trp Ile Ser Asn Pro Pro Thr
85 90 95

Phe Gly Gly Gly Thr Lys Leu Gu Ile Lys Arg
100 105

<210> 78
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> chCD37-38

<400> 78

G n Ile Val Leu Thr G n Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
1 5 10 15

Gu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met
20 25 30

2921032PC01SequenceLi st i ng. t xt

Hi s Trp Tyr G n G n Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
35 40 45

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys G n G n Trp Ile Ser Asn Pro Pro Thr
85 90 95

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

<210> 79
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD37-38

<400> 79

Asp Ile Val Leu Thr G n Ser Pro Ala Ser Met Ser Ala Ser Pro Gly
1 5 10 15

Glu Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met
20 25 30

Hi s Trp Tyr G n G n Lys Pro Gly Thr Ser Pro Lys Arg Trp Ile Tyr
35 40 45

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys G n G n Trp Ile Ser Asn Pro Pro Thr
85 90 95

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

<210> 80
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD37-50

<400> 80

2921032PC01SequenceLi st i ng. t xt

G n I l e Val Leu Thr G n Ser Pro Al a I l e Met Ser Al a Ser Pro Gly
1 5 10 15

G u Lys Val Thr Met Thr Cys Ser Al a Thr Ser Ser Val Thr Tyr Met
20 25 30

Hi s Trp Tyr G n G n Lys Ser Gly Thr Ser Pro Lys Arg Trp I l e Tyr
35 40 45

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr I l e Ser Ser Met Gl u Al a Gl u
65 70 75 80

Asp Al a Al a Thr Tyr Tyr Cys G n G n Trp Ser Asp Asn Pro Pro Thr
85 90 95

Phe Gly Ser Gly Thr Lys Leu Gl u I l e Lys
100 105

<210> 81
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD37-50

<400> 81

G u I l e Val Leu Thr G n Ser Pro Al a Thr Met Ser Al a Ser Pro Gly
1 5 10 15

G u Arg Val Thr Met Thr Cys Ser Al a Thr Ser Ser Val Thr Tyr Met
20 25 30

Hi s Trp Tyr G n G n Lys Pro Gly G n Ser Pro Lys Arg Trp I l e Tyr
35 40 45

Asp Thr Ser Asn Leu Pro Tyr Gly Val Pro Al a Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr I l e Ser Ser Met Gl u Al a Gl u
65 70 75 80

Asp Al a Al a Thr Tyr Tyr Cys G n G n Trp Ser Asp Asn Pro Pro Thr
85 90 95

Phe Gly G n Gly Thr Lys Leu Gl u I l e Lys Arg
100 105

<210> 82

2921032PC01SequenceLi st i ng. t xt

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

<220>
<223> muCD37-51

<400> 82

G n I l e Val Leu Thr G n Ser Pro Al a I l e Met Ser Al a Ser Pro G y
1 5 10 15

G u Lys Val Thr Met Thr Cys Ser Al a Thr Ser Ser Val Thr Tyr Met
20 25 30

Hi s Trp Tyr G n G n Lys Ser G y Thr Ser Pro Lys Arg Trp I l e Tyr
35 40 45

Asp Thr Ser Lys Leu Al a Ser G y Val Pro Al a Arg Phe Ser G y Ser
50 55 60

G y Ser G y Thr Ser Tyr Ser Leu Thr I l e Ser Asn Met G u Al a G u
65 70 75 80

Asp Al a Al a Thr Tyr Tyr Cys G n G n Trp Ser Ser Asn Pro Pro Thr
85 90 95

Phe G y Ser G y Thr Lys Leu G u I l e Lys Arg
100 105

<210> 83
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD37-51

<400> 83

G u I l e Val Leu Thr G n Ser Pro Al a Thr Met Ser Al a Ser Pro G y
1 5 10 15

G u Arg Val Thr Met Thr Cys Ser Al a Thr Ser Ser Val Thr Tyr Met
20 25 30

Hi s Trp Tyr G n G n Lys Pro G y G n Ser Pro Lys Arg Trp I l e Tyr
35 40 45

Asp Thr Ser Lys Leu Al a Ser G y Val Pro Al a Arg Phe Ser G y Ser
50 55 60

G y Ser G y Thr Ser Tyr Ser Leu Thr I l e Ser Ser Met G u Al a G u
65 70 75 80

Asp Al a Al a Thr Tyr Tyr Cys G n G n Trp Ser Ser Asn Pro Pro Thr

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

<210> 84
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> muCD37-56

<400> 84

Gln Ile Val Leu Thr Gln Ser Pro Ala Phe Met Ser Ala Ser Pro Gly
 1 5 10 15

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

His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
 35 40 45

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Thr Met Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ile Ser Asp Pro Pro Thr
 85 90 95

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

<210> 85
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> huCD37-56

<400> 85

Asp Ile Val Leu Thr Gln Ser Pro Ala Phe Met Ser Ala Ser Pro Gly
 1 5 10 15

Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met
 20 25 30

His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Arg Trp Ile Tyr
 35 40 45

Asp Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Gly

50

G y Ser G y Thr Asp Tyr Ser Leu Thr Ile Ser Ser Met Gl u Al a Gl u
65 70 75 80

Asp Al a Al a Thr Tyr Tyr Cys G n G n Trp Ile Ser Asp Pro Pro Thr
85 90 95

Phe G y G n G y Thr Lys Leu Gl u Ile Lys Arg
100 105

<210> 86
<211> 107
<212> PRT
<213> Art if i ci al Sequence

<220>
<223> muCD37-57

<400> 86

G n Ile Val Leu Thr G n Ser Pro Al a Ile Met Ser Al a Ser Pro Gly
1 5 10 15

Gl u Lys Val Thr Met Thr Cys Ser Al a Thr Ser Ser Val Thr Tyr Met
20 25 30

Hi s Trp Tyr G n G n Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Leu Al a Ser Gly Val Pro Al a Arg Phe Ser Gly Ser
50 55 60

G y Ser G y Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Gl u Al a Gl u
65 70 75 80

Asp Al a Al a Thr Tyr Tyr Cys G n G n Trp Ser Asp Asn Pro Pro Thr
85 90 95

Phe G y Ser G y Thr Lys Leu Gl u Ile Lys Arg
100 105

<210> 87
<211> 107
<212> PRT
<213> Art if i ci al Sequence

<220>
<223> huCD37-57

<400> 87

Gl u Ile Val Leu Thr G n Ser Pro Al a Thr Met Ser Al a Ser Pro Gly
1 5 10 15

Gl u Arg Val Thr Met Thr Cys Ser Al a Thr Ser Ser Val Thr Tyr Met
Page 33

20

25

30

H i s Trp Tyr 35 G n G n Lys Pro Gly 40 G n Ser Pro Arg Arg 45 Trp I l e Tyr
 Asp Thr 50 Ser Asn Leu Al a Ser 55 Gly Val Pro Al a Arg 60 Phe Ser Gly Ser
 Gly 65 Ser Gly Thr Ser Tyr 70 Ser Leu Thr I l e Ser 75 Ser Met Gl u Al a Gl u 80
 Asp Al a Al a Thr Tyr 85 Tyr Cys G n G n Trp 90 Ser Asp Asn Pro Pro 95 Thr
 Phe Gly G n Gly 100 Thr Lys Leu Gl u I l e Lys Arg 105

<210> 88
 <211> 445
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> muCD37-3

<400> 88

G n Val G n Val Lys 5 Gl u Ser Gly Pro Gly 10 Leu Val Al a Pro Ser G n 15
 Ser Leu Ser I l e Thr 20 Cys Thr Val Ser 25 Gly Phe Ser Leu Thr 30 Thr Ser
 Gly Val Ser 35 Trp Val Arg G n Pro 40 Pro Gly Lys Gly 45 Leu Gl u Trp Leu
 Gly Val 50 I l e Trp Gly Asp 55 Gly Ser Thr Asn Tyr Hi s 60 Ser Al a Leu Lys
 Ser 65 Arg Leu Ser I l e Lys 70 Lys Asp Hi s Ser Lys 75 Ser G n Val Phe Leu 80
 Lys Leu Asn Ser 85 Leu G n Thr Asp Asp 90 Thr Al a Thr Tyr Tyr 95 Cys Al a
 Lys Gly Gly Tyr 100 Ser Leu Al a Hi s Trp 105 Gly G n Gly Thr Leu 110 Val Thr
 Val Ser Al a 115 Al a Lys Thr Thr Al a 120 Pro Ser Val Tyr Pro 125 Leu Al a Pro
 Val Cys 130 Gly Asp Thr Thr Gly 135 Ser Ser Val Thr Leu 140 Gly Cys Leu Val

2921032PC01SequenceLi st i ng. t xt

Lys 145 Gly Tyr Phe Pro Gu 150 Pro Val Thr Leu Thr 155 Trp Asn Ser Gly 160 Ser
 Leu Ser Ser Gly Val 165 His Thr Phe Pro Ala 170 Val Leu Gl n Ser Asp 175 Leu
 Tyr Thr Leu Ser 180 Ser Ser Val Thr Val 185 Thr Ser Ser Thr Trp 190 Pro Ser
 Gl n Ser Ile 195 Thr Cys Asn Val Ala 200 His Pro Ala Ser Ser 205 Thr Lys Val
 Asp Lys 210 Lys Ile Gu Pro Arg 215 Gly Pro Thr Ile Lys 220 Pro Cys Pro Pro
 Cys 225 Lys Cys Pro Ala Pro 230 Asn Leu Leu Gly Gly 235 Pro Ser Val Phe Ile 240
 Phe Pro Pro Lys Ile 245 Lys Asp Val Leu Met 250 Ile Ser Leu Ser Pro Ile 255
 Val Thr Cys Val 260 Val Val Asp Val Ser 265 Gu Asp Asp Pro Asp 270 Val Gl n
 Ile Ser Trp 275 Phe Val Asn Asn Val 280 Gu Val His Thr Ala 285 Gl n Thr Gl n
 Thr His 290 Arg Gu Asp Tyr Asn 295 Ser Thr Leu Arg Val 300 Val Ser Ala Leu
 Pro 305 Ile Gl n His Gl n Asp 310 Trp Met Ser Gly Lys 315 Gu Phe Lys Cys Lys 320
 Val Asn Asn Lys Asp 325 Leu Pro Ala Pro Ile Gu Arg Thr Ile Ser 335 Lys
 Pro Lys Gly Ser 340 Val Arg Ala Pro Gl n 345 Val Tyr Val Leu Pro 350 Pro Pro
 Gu Gu Gu 355 Met Thr Lys Lys Gl n 360 Val Thr Leu Thr Cys 365 Met Val Thr
 Asp Phe Met Pro Gu Asp Ile 375 Tyr Val Gu Trp Thr 380 Asn Asn Gly Lys
 Thr 385 Gu Leu Asn Tyr Lys 390 Asn Thr Gu Pro Val 395 Leu Asp Ser Asp Gly 400
 Ser Tyr Phe Met Tyr 405 Ser Lys Leu Arg Val 410 Gu Lys Lys Asn Trp 415 Val

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G u A r g A s n S e r T y r S e r O y s S e r V a l V a l H i s G u G y L e u H i s A s n
420 425 430

H i s H i s T h r T h r L y s S e r P h e S e r A r g T h r P r o G y L y s
435 440 445

<210> 89
<211> 445
<212> PRT
<213> A r t i f i c i a l S e q u e n c e

<220>
<223> c h C D 3 7 - 3

<400> 89

G n V a l G n V a l L y s G u S e r G y P r o G y L e u V a l A l a P r o S e r G n
1 5 10 15

S e r L e u S e r I l e T h r O y s T h r V a l S e r G y P h e S e r L e u T h r T h r S e r
20 25 30

G y V a l S e r T r p V a l A r g G n P r o P r o G y L y s G y L e u G u T r p L e u
35 40 45

G y V a l I l e T r p G y A s p G y S e r T h r A s n T y r H i s S e r A l a L e u L y s
50 55 60

S e r A r g L e u S e r I l e L y s L y s A s p H i s S e r L y s S e r G n V a l P h e L e u
65 70 75 80

L y s L e u A s n S e r L e u G n T h r A s p A s p T h r A l a T h r T y r T y r O y s A l a
85 90 95

L y s G y G y T y r S e r L e u A l a H i s T r p G y G n G y T h r L e u V a l T h r
100 105 110

V a l S e r A l a A l a S e r T h r L y s G y P r o S e r V a l P h e P r o L e u A l a P r o
115 120 125

S e r S e r L y s S e r T h r S e r G y G y T h r A l a A l a L e u G y O y s L e u V a l
130 135 140

L y s A s p T y r P h e P r o G u P r o V a l T h r V a l S e r T r p A s n S e r G y A l a
145 150 155 160

L e u T h r S e r G y V a l H i s T h r P h e P r o A l a V a l L e u G n S e r S e r G y
165 170 175

L e u T y r S e r L e u S e r S e r V a l V a l T h r V a l P r o S e r S e r S e r L e u G y
180 185 190

T h r G n T h r T y r I l e O y s A s n V a l A s n H i s L y s P r o S e r A s n T h r L y s

2921032PC01SequenceLi st i ng. t xt

195

200

205

Val Asp Lys Lys Val Gu Pro Lys Ser Oys Asp Lys Thr Hi s Thr Oys
 210 215 220
 Pro Pro Oys Pro Al a Pro Gu Leu Leu Gy Gy Pro Ser Val Phe Leu
 225 230 235 240
 Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Gu
 245 250 255
 Val Thr Oys Val Val Val Asp Val Ser Hi s Gu Asp Pro Gu Val Lys
 260 265 270
 Phe Asn Trp Tyr Val Asp Gy Val Gu Val Hi s Asn Al a Lys Thr Lys
 275 280 285
 Pro Arg Gu Gu Gn Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 290 295 300
 Thr Val Leu Hi s Gn Asp Trp Leu Asn Gy Lys Gu Tyr Lys Oys Lys
 305 310 315 320
 Val Ser Asn Lys Al a Leu Pro Al a Pro Ile Gu Lys Thr Ile Ser Lys
 325 330 335
 Al a Lys Gy Gn Pro Arg Gu Pro Gn Val Tyr Thr Leu Pro Pro Ser
 340 345 350
 Arg Asp Gu Leu Thr Lys Asn Gn Val Ser Leu Thr Oys Leu Val Lys
 355 360 365
 Gy Phe Tyr Pro Ser Asp Ile Al a Val Gu Trp Gu Ser Asn Gy Gn
 370 375 380
 Pro Gu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gy
 385 390 395 400
 Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gn
 405 410 415
 Gn Gy Asn Val Phe Ser Oys Ser Val Met Hi s Gu Al a Leu Hi s Asn
 420 425 430
 Hi s Tyr Thr Gn Lys Ser Leu Ser Leu Ser Pro Gy Lys
 435 440 445

<210> 90
 <211> 444
 <212> PRT
 <213> Artificial Sequence

2921032PC01SequenceLi st i ng. t xt

<220>

<223> huCD37-3v1.0

<400> 90

G n Val G n Val G n G u Ser G y Pro G y Leu Val Al a Pro Ser G n
1 5 10 15

Thr Leu Ser Ile Thr Cys Thr Val Ser G y Phe Ser Leu Thr Thr Ser
20 25 30

G y Val Ser Trp Val Arg G n Pro Pro G y Lys G y Leu G u Trp Leu
35 40 45

G y Val Ile Trp G y Asp G y Ser Thr Asn Tyr Hi s Pro Ser Leu Lys
50 55 60

Ser Arg Leu Ser Ile Lys Lys Asp Hi s Ser Lys Ser G n Val Phe Leu
65 70 75 80

Lys Leu Asn Ser Leu Thr Al a Al a Asp Thr Al a Thr Tyr Tyr Cys Al a
85 90 95

Lys G y G y Tyr Ser Leu Al a Hi s Trp G y G n G y Thr Leu Val Thr
100 105 110

Val Ser Ser Al a Ser Thr Lys G y Pro Ser Val Phe Pro Leu Al a Pro
115 120 125

Ser Ser Lys Ser Thr Ser G y G y Thr Al a Al a Leu G y Cys Leu Val
130 135 140

Lys Asp Tyr Phe Pro G u Pro Val Thr Val Ser Trp Asn Ser G y Al a
145 150 155 160

Leu Thr Ser G y Val Hi s Thr Phe Pro Al a Val Leu G n Ser Ser G y
165 170 175

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu G y
180 185 190

Thr G n Thr Tyr Ile Cys Asn Val Asn Hi s Lys Pro Ser Asn Thr Lys
195 200 205

Val Asp Lys Lys Val G u Pro Lys Ser Cys Asp Lys Thr Hi s Thr Cys
210 215 220

Pro Pro Cys Pro Al a Pro G u Leu Leu G y G y Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro G u
245 250 255

2921032PC01SequenceLi st i ng. t xt

Val Thr Oys Val Val Val Asp Val Ser His Gu Asp Pro Gu Val Lys
260 265 270

Phe Asn Trp Tyr Val Asp Gy Val Gu Val His Asn Ala Lys Thr Lys
275 280 285

Pro Arg Gu Gu Gn Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gn Asp Trp Leu Asn Gy Lys Gu Tyr Lys Oys Lys
305 310 315 320

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Gu Lys Thr Ile Ser Lys
325 330 335

Ala Lys Gy Gn Pro Arg Gu Pro Gn Val Tyr Thr Leu Pro Pro Ser
340 345 350

Arg Asp Gu Leu Thr Lys Asn Gn Val Ser Leu Thr Oys Leu Val Lys
355 360 365

Gy Phe Tyr Pro Ser Asp Ile Ala Val Gu Trp Gu Ser Asn Gy Gn
370 375 380

Pro Gu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gy
385 390 395 400

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gn
405 410 415

Gn Gy Asn Val Phe Ser Oys Ser Val Met His Gu Ala Leu His Asn
420 425 430

His Tyr Thr Gn Lys Ser Leu Ser Leu Ser Pro Gy
435 440

<210> 91
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD37-3v1.1

<400> 91

Gn Val Gn Val Gn Gu Ser Gy Pro Gy Leu Val Ala Pro Ser Gn
1 5 10 15

Thr Leu Ser Ile Thr Oys Thr Val Ser Gy Phe Ser Leu Thr Thr Ser
20 25 30

Gy Val Ser Trp Val Arg Gn Pro Pro Gy Lys Gy Leu Gu Trp Leu

G y Val Ile Trp G y Asp G y Ser Thr Asn Tyr Hi s Ser Ser Leu Lys
 50 55 60
 Ser Arg Leu Ser Ile Lys Lys Asp Hi s Ser Lys Ser G n Val Phe Leu
 65 70 75 80
 Lys Leu Asn Ser Leu Thr Al a Al a Asp Thr Al a Thr Tyr Tyr Cys Al a
 85 90 95
 Lys G y G y Tyr Ser Leu Al a Hi s Trp G y G n G y Thr Leu Val Thr
 100 105 110
 Val Ser Ser Al a Ser Thr Lys G y Pro Ser Val Phe Pro Leu Al a Pro
 115 120 125
 Ser Ser Lys Ser Thr Ser G y G y Thr Al a Al a Leu G y Cys Leu Val
 130 135 140
 Lys Asp Tyr Phe Pro G u Pro Val Thr Val Ser Trp Asn Ser G y Al a
 145 150 155 160
 Leu Thr Ser G y Val Hi s Thr Phe Pro Al a Val Leu G n Ser Ser G y
 165 170 175
 Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu G y
 180 185 190
 Thr G n Thr Tyr Ile Cys Asn Val Asn Hi s Lys Pro Ser Asn Thr Lys
 195 200 205
 Val Asp Lys Lys Val G u Pro Lys Ser Cys Asp Lys Thr Hi s Thr Cys
 210 215 220
 Pro Pro Cys Pro Al a Pro G u Leu Leu G y G y Pro Ser Val Phe Leu
 225 230 235 240
 Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro G u
 245 250 255
 Val Thr Cys Val Val Val Asp Val Ser Hi s G u Asp Pro G u Val Lys
 260 265 270
 Phe Asn Trp Tyr Val Asp G y Val G u Val Hi s Asn Al a Lys Thr Lys
 275 280 285
 Pro Arg G u G u G n Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 290 295 300
 Thr Val Leu Hi s G n Asp Trp Leu Asn G y Lys G u Tyr Lys Cys Lys

305 310 315 320

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Gu Lys Thr Ile Ser Lys
325 330 335

Ala Lys Gly Gn Pro Arg Gu Pro Gn Val Tyr Thr Leu Pro Pro Ser
340 345 350

Arg Asp Gu Leu Thr Lys Asn Gn Val Ser Leu Thr Cys Leu Val Lys
355 360 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Gu Trp Gu Ser Asn Gly Gn
370 375 380

Pro Gu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385 390 395 400

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gn
405 410 415

Gn Gly Asn Val Phe Ser Cys Ser Val Met His Gu Ala Leu His Asn
420 425 430

His Tyr Thr Gn Lys Ser Leu Ser Leu Ser Pro Gly
435 440

<210> 92
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD37-12

<400> 92

Gn Ile Gn Leu Val Gn Ser Gly Pro Gu Leu Lys Lys Pro Gly Gu
1 5 10 15

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

Gly Met Asn Trp Val Lys Gn Ala Gn Gly Lys Gly Leu Lys Trp Met
35 40 45

Gly Trp Ile Asn Thr Asn Thr Gly Gu Ser Arg Asn Ala Gu Gu Phe
50 55 60

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

Leu Gn Ile Asn Asn Leu Lys Tyr Gu Asp Thr Ala Thr Tyr Phe Cys
85 90 95

2921032PC01SequenceLi st i ng. t xt

G y Arg G y Thr Val Val Ala Asp Trp G y G n G y Thr Thr Leu Thr
 100 105 110
 Val Ser Ser Ala Lys Thr Thr Ala Pro Ser Val Tyr Pro Leu Ala Pro
 115 120 125
 Val Cys G y Asp Thr Thr G y Ser Ser Val Thr Leu G y Cys Leu Val
 130 135 140
 Lys G y Tyr Phe Pro Gu Pro Val Thr Leu Thr Trp Asn Ser G y Ser
 145 150 155 160
 Leu Ser Ser G y Val His Thr Phe Pro Ala Val Leu G n Ser Asp Leu
 165 170 175
 Tyr Thr Leu Ser Ser Ser Val Thr Val Thr Ser Ser Thr Trp Pro Ser
 180 185 190
 G n Ser Ile Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val
 195 200 205
 Asp Lys Lys Ile Gu Pro Arg G y Pro Thr Ile Lys Pro Cys Pro Pro
 210 215 220
 Cys Lys Cys Pro Ala Pro Asn Leu Leu G y G y Pro Ser Val Phe Ile
 225 230 235 240
 Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile
 245 250 255
 Val Thr Cys Val Val Val Asp Val Ser Gu Asp Asp Pro Asp Val G n
 260 265 270
 Ile Ser Trp Phe Val Asn Asn Val Gu Val His Thr Ala G n Thr G n
 275 280 285
 Thr His Arg Gu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu
 290 295 300
 Pro Ile G n His G n Asp Trp Met Ser G y Lys Gu Phe Lys Cys Lys
 305 310 315 320
 Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Gu Arg Thr Ile Ser Lys
 325 330 335
 Pro Lys G y Ser Val Arg Ala Pro G n Val Tyr Val Leu Pro Pro Pro
 340 345 350
 Gu Gu Gu Met Thr Lys Lys G n Val Thr Leu Thr Cys Met Val Thr
 355 360 365

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Asp Phe Met Pro Gu Asp Ile Tyr Val Gu Trp Thr Asn Asn Gly Lys
370 375 380

Thr Gu Leu Asn Tyr Lys Asn Thr Gu Pro Val Leu Asp Ser Asp Gly
385 390 395 400

Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Gu Lys Lys Asn Trp Val
405 410 415

Gu Arg Asn Ser Tyr Ser Cys Ser Val Val His Gu Gly Leu His Asn
420 425 430

His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
435 440 445

<210> 93
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> chCD37-12

<400> 93

Gn Ile Gn Leu Val Gn Ser Gly Pro Gu Leu Lys Lys Pro Gly Gu
1 5 10 15

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

Gly Met Asn Trp Val Lys Gn Ala Gn Gly Lys Gly Leu Lys Trp Met
35 40 45

Gly Trp Ile Asn Thr Asn Thr Gly Gu Ser Arg Asn Ala Gu Gu Phe
50 55 60

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

Leu Gn Ile Asn Asn Leu Lys Tyr Gu Asp Thr Ala Thr Tyr Phe Cys
85 90 95

Gly Arg Gly Thr Val Val Ala Asp Trp Gly Gn Gly Thr Thr Leu Thr
100 105 110

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
115 120 125

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
130 135 140

Lys Asp Tyr Phe Pro Gu Pro Val Thr Val Ser Trp Asn Ser Gly Ala

145 150 155 160
 Leu Thr Ser Gly Val₁₆₅ His Thr Phe Pro Ala₁₇₀ Val Leu Gln Ser Ser₁₇₅ Gly
 Leu Tyr Ser Leu₁₈₀ Ser Ser Val Val Thr₁₈₅ Val Pro Ser Ser₁₉₀ Leu Gly
 Thr Gln Thr₁₉₅ Tyr Ile Cys Asn Val₂₀₀ Asn His Lys Pro Ser₂₀₅ Asn Thr Lys
 Val Asp₂₁₀ Lys Lys Val Glu Pro₂₁₅ Lys Ser Cys Asp Lys₂₂₀ Thr His Thr Cys
 Pro₂₂₅ Pro Cys Pro Ala Pro₂₃₀ Glu Leu Leu Gly Gly₂₃₅ Pro Ser Val Phe Leu₂₄₀
 Phe Pro Pro Lys Pro₂₄₅ Lys Asp Thr Leu Met₂₅₀ Ile Ser Arg Thr Pro₂₅₅ Glu
 Val Thr Cys Val₂₆₀ Val Val Asp Val Ser₂₆₅ His Glu Asp Pro Glu₂₇₀ Val Lys
 Phe Asn Trp₂₇₅ Tyr Val Asp Gly Val₂₈₀ Glu Val His Asn Ala₂₈₅ Lys Thr Lys
 Pro Arg₂₉₀ Glu Glu Gln Tyr Asn₂₉₅ Ser Thr Tyr Arg Val₃₀₀ Val Ser Val Leu
 Thr₃₀₅ Val Leu His Gln Asp Trp Leu Asn Gly Lys₃₁₅ Glu Tyr Lys Cys Lys₃₂₀
 Val Ser Asn Lys Ala₃₂₅ Leu Pro Ala Pro Ile₃₃₀ Glu Lys Thr Ile Ser₃₃₅ Lys
 Ala Lys Gly Gln₃₄₀ Pro Arg Glu Pro Gln₃₄₅ Val Tyr Thr Leu Pro₃₅₀ Pro Ser
 Arg Asp Glu₃₅₅ Leu Thr Lys Asn Gln Val Ser Leu Thr Cys₃₆₅ Leu Val Lys
 Gly Phe Tyr Pro Ser Asp Ile₃₇₅ Ala Val Glu Trp Glu₃₈₀ Ser Asn Gly Gln
 Pro₃₈₅ Glu Asn Asn Tyr Lys₃₉₀ Thr Thr Pro Pro Val₃₉₅ Leu Asp Ser Asp Gly₄₀₀
 Ser Phe Phe Leu Tyr₄₀₅ Ser Lys Leu Thr Val₄₁₀ Asp Lys Ser Arg Trp Gln₄₁₅
 Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn

420

425

430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 94

<211> 444

<212> PRT

<213> Artificial Sequence

<220>

<223> muCD37-38

<400> 94

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

Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Gly
 20 25 30

Phe Gly Trp His Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
 35 40 45

Met Ala Tyr Ile Leu Tyr Ser Gly Gly Thr Asp Tyr Asn Pro Ser Leu
 50 55 60

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

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

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

Gly Thr Leu Val Thr Val Ser Ala Ala Lys Thr Thr Pro Pro Ser Val
 115 120 125

Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr
 130 135 140

Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr
 145 150 155 160

Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175

Leu Glu Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser
 180 185 190

Ser Met Arg Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala
 195 200 205

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Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Oys Gly Oys
210 215 220

Lys Pro Oys Ile Oys Thr Val Pro Gu Val Ser Ser Val Phe Ile Phe
225 230 235 240

Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val
245 250 255

Thr Oys Val Val Val Asp Ile Ser Lys Asp Asp Pro Gu Val Gln Phe
260 265 270

Ser Trp Phe Val Asp Asp Val Gu Val His Thr Ala Gln Thr Gln Pro
275 280 285

Arg Gu Gu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Gu Leu Pro
290 295 300

Ile Met His Gln Asp Trp Leu Asn Gly Lys Gu Phe Lys Oys Arg Val
305 310 315 320

Asn Ser Ala Ala Phe Pro Ala Pro Ile Gu Lys Thr Ile Ser Lys Thr
325 330 335

Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys
340 345 350

Gu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Oys Met Ile Thr Asp
355 360 365

Phe Phe Pro Gu Asp Ile Thr Val Gu Trp Gln Trp Asn Gly Gln Pro
370 375 380

Ala Gu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asn Thr Asn Gly Ser
385 390 395 400

Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Gu Ala
405 410 415

Gly Asn Thr Phe Thr Oys Ser Val Leu His Gu Gly Leu His Asn His
420 425 430

His Thr Gu Lys Ser Leu Ser His Ser Pro Gly Lys
435 440

<210> 95
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> chCD37-38

2921032PC01SequenceLi st i ng. t xt

<400> 95

G n Val G n Leu G n G u Ser G y Pro Asp Leu Val Lys Pro Ser G n
1 5 10 15

Ser Leu Ser Leu Thr Oys Thr Val Thr G y Tyr Ser Ile Thr Ser G y
20 25 30

Phe G y Trp His Trp Ile Arg G n Phe Pro G y Asn Lys Leu G u Trp
35 40 45

Met Ala Tyr Ile Leu Tyr Ser G y G y Thr Asp Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn G n Phe Phe
65 70 75 80

Leu Arg Leu Ser Ser Val Thr Thr G u Asp Thr Ala Thr Tyr Tyr Oys
85 90 95

Ala Arg G y Tyr Tyr G y Tyr G y Ala Trp Phe Val Tyr Trp G y G n
100 105 110

G y Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys G y Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser G y G y Thr Ala Ala
130 135 140

Leu G y Oys Leu Val Lys Asp Tyr Phe Pro G u Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser G y Ala Leu Thr Ser G y Val His Thr Phe Pro Ala Val
165 170 175

Leu G n Ser Ser G y Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu G y Thr G n Thr Tyr Ile Oys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val G u Pro Lys Ser Oys Asp
210 215 220

Lys Thr His Thr Oys Pro Pro Oys Pro Ala Pro G u Leu Leu G y G y
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255

Ser Arg Thr Pro G u Val Thr Oys Val Val Val Asp Val Ser His G u

260

265

270

Asp Pro G u Val Lys Phe Asn Trp Tyr Val Asp G y Val G u Val Hi s
 275 280 285

Asn Al a Lys Thr Lys Pro Arg G u G u G n Tyr Asn Ser Thr Tyr Arg
 290 295 300

Val Val Ser Val Leu Thr Val Leu Hi s G n Asp Trp Leu Asn G y Lys
 305 310 315 320

G u Tyr Lys Cys Lys Val Ser Asn Lys Al a Leu Pro Al a Pro Il e G u
 325 330 335

Lys Thr Il e Ser Lys Al a Lys G y G n Pro Arg G u Pro G n Val Tyr
 340 345 350

Thr Leu Pro Pro Ser Arg Asp G u Leu Thr Lys Asn G n Val Ser Leu
 355 360 365

Thr Cys Leu Val Lys G y Phe Tyr Pro Ser Asp Il e Al a Val G u Trp
 370 375 380

G u Ser Asn G y G n Pro G u Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400

Leu Asp Ser Asp G y Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415

Lys Ser Arg Trp G n G n G y Asn Val Phe Ser Cys Ser Val Met Hi s
 420 425 430

G u Al a Leu Hi s Asn Hi s Tyr Thr G n Lys Ser Leu Ser Leu Ser Pro
 435 440 445

G y

<210> 96
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> huCD37-38

<400> 96

G n Val G n Leu G n G u Ser G y Pro G y Leu Val Lys Pro Ser G n
 1 5 10 15

Ser Leu Ser Leu Thr Cys Thr Val Ser G y Tyr Ser Il e Thr Ser G y
 20 25 30

2921032PC01SequenceLi st i ng. t xt

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

Met Ala Tyr Ile Leu Tyr Ser Gly Gly Thr Asp Tyr Asn Pro Ser Leu
50 55 60

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

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

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

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
290 295 300

2921032PC01SequenceLi st i ng. t xt

Val Val Ser Val Leu Thr Val Leu His G n Asp Trp Leu Asn Gly Lys
305 310 315 320

G u Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile G u
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly G n Pro Arg G u Pro G n Val Tyr
340 345 350

Thr Leu Pro Pro Ser Arg Asp G u Leu Thr Lys Asn G n Val Ser Leu
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val G u Trp
370 375 380

G u Ser Asn Gly G n Pro G u Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp G n G n Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

G u Ala Leu His Asn His Tyr Thr G n Lys Ser Leu Ser Leu Ser Pro
435 440 445

G y

<210> 97
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<212> PRT
<213> Artificial Sequence

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<400> 97

Asp Val G n Leu G n G u Ser Gly Pro Asp Leu Leu Lys Pro Ser G n
1 5 10 15

Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Gly
20 25 30

Phe Ala Trp His Trp Ile Arg G n Phe Pro Gly Asn Lys Leu G u Trp
35 40 45

Met Gly Tyr Ile Leu Tyr Ser Gly Ser Thr Val Tyr Ser Pro Ser Leu
50 55 60

Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn His Phe Phe

	70						75						80					
Leu	G n	Leu	Asn	Ser 85	Val	Thr	Thr	G u	Asp 90	Thr	Al a	Thr	Tyr	Tyr 95	Oys			
Al a	Arg	G y	Tyr 100	Tyr	G y	Tyr	G y	Al a 105	Tr p	Phe	Al a	Tyr	Tr p 110	G y	G n			
G y	Thr	Leu 115	Val	Thr	Val	Ser	Al a 120	Al a	Lys	Thr	Thr	Al a 125	Pro	Ser	Val			
Tyr	Pro 130	Leu	Al a	Pro	Val	Oys 135	G y	Asp	Thr	Thr	G y 140	Ser	Ser	Val	Thr			
Leu 145	G y	Oys	Leu	Val	Lys 150	G y	Tyr	Phe	Pro	G u 155	Pro	Val	Thr	Leu	Thr 160			
Tr p	Asn	Ser	G y	Ser 165	Leu	Ser	Ser	G y	Val 170	Hi s	Thr	Phe	Pro	Al a 175	Val			
Leu	G n	Ser	Asp 180	Leu	Tyr	Thr	Leu	Ser 185	Ser	Ser	Val	Thr	Val 190	Thr	Ser			
Ser	Thr	Tr p 195	Pro	Ser	G n	Ser	Ile 200	Thr	Oys	Asn	Val	Al a 205	Hi s	Pro	Al a			
Ser	Ser 210	Thr	Lys	Val	Asp	Lys 215	Lys	Ile	G u	Pro	Arg 220	G y	Pro	Thr	Ile			
Lys 225	Pro	Oys	Pro	Pro	Oys 230	Lys	Oys	Pro	Al a	Pro 235	Asn	Leu	Leu	G y	G y 240			
Pro	Ser	Val	Phe	Ile 245	Phe	Pro	Pro	Lys	Ile 250	Lys	Asp	Val	Leu	Met 255	Ile			
Ser	Leu	Ser	Pro 260	Ile	Val	Thr	Oys	Val 265	Val	Val	Asp	Val	Ser 270	G u	Asp			
Asp	Pro	Asp 275	Val	G n	Ile	Ser	Tr p 280	Phe	Val	Asn	Asn	Val 285	G u	Val	Hi s			
Thr	Al a 290	G n	Thr	G n	Thr	Hi s 295	Arg	G u	Asp	Tyr	Asn 300	Ser	Thr	Leu	Arg			
Val 305	Val	Ser	Al a	Leu	Pro 310	Ile	G n	Hi s	G n	Asp 315	Tr p	Met	Ser	G y	Lys 320			
G u	Phe	Lys	Oys	Lys 325	Val	Asn	Asn	Lys	Asp 330	Leu	Pro	Al a	Pro	Ile 335	G u			
Arg	Thr	Ile	Ser	Lys	Pro	Lys	G y	Ser	Val	Arg	Al a	Pro	G n	Val	Tyr			

340

345

350

Val Leu Pro Pro Pro Gl u Gl u Gl u Met Thr Lys Lys Gl n Val Thr Leu
355 360 365

Thr Cys Met Val Thr Asp Phe Met Pro Gl u Asp Ile Tyr Val Gl u Trp
370 375 380

Thr Asn Asn Gl y Lys Thr Gl u Leu Asn Tyr Lys Asn Thr Gl u Pro Val
385 390 395 400

Leu Asp Ser Asp Gl y Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Gl u
405 410 415

Lys Lys Asn Trp Val Gl u Arg Asn Ser Tyr Ser Cys Ser Val Val Hi s
420 425 430

Gl u Gl y Leu Hi s Asn Hi s Hi s Thr Thr Lys Ser Phe Ser Arg Thr Pro
435 440 445

Gl y Lys
450

<210> 98

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> huCD37-50

<400> 98

Gl n Val Gl n Leu Gl n Gl u Ser Gl y Pro Gl y Leu Leu Lys Pro Ser Gl n
1 5 10 15

Ser Leu Ser Leu Thr Cys Thr Val Ser Gl y Tyr Ser Ile Thr Ser Gl y
20 25 30

Phe Ala Trp Hi s Trp Ile Arg Gl n Hi s Pro Gl y Asn Lys Leu Gl u Trp
35 40 45

Met Gl y Tyr Ile Leu Tyr Ser Gl y Ser Thr Val Tyr Ser Pro Ser Leu
50 55 60

Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Hi s Phe Phe
65 70 75 80

Leu Gl n Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Gl y Tyr Tyr Gl y Tyr Gl y Ala Trp Phe Ala Tyr Trp Gl y Gl n
100 105 110

2921032PC01SequenceLi st i ng. t xt

G y Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys G y Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser G y G y Thr Ala Ala
 130 135 140
 Leu G y Cys Leu Val Lys Asp Tyr Phe Pro G u Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser G y Ala Leu Thr Ser G y Val Hi s Thr Phe Pro Ala Val
 165 170 175
 Leu G n Ser Ser G y Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu G y Thr G n Thr Tyr Ile Cys Asn Val Asn Hi s Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Lys Val G u Pro Lys Ser Cys Asp
 210 215 220
 Lys Thr Hi s Thr Cys Pro Pro Cys Pro Ala Pro G u Leu Leu G y G y
 225 230 235 240
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 245 250 255
 Ser Arg Thr Pro G u Val Thr Cys Val Val Val Asp Val Ser Hi s G u
 260 265 270
 Asp Pro G u Val Lys Phe Asn Trp Tyr Val Asp G y Val G u Val Hi s
 275 280 285
 Asn Ala Lys Thr Lys Pro Arg G u G u G n Tyr Asn Ser Thr Tyr Arg
 290 295 300
 Val Val Ser Val Leu Thr Val Leu Hi s G n Asp Trp Leu Asn G y Lys
 305 310 315 320
 G u Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile G u
 325 330 335
 Lys Thr Ile Ser Lys Ala Lys G y G n Pro Arg G u Pro G n Val Tyr
 340 345 350
 Thr Leu Pro Pro Ser Arg Asp G u Leu Thr Lys Asn G n Val Ser Leu
 355 360 365
 Thr Cys Leu Val Lys G y Phe Tyr Pro Ser Asp Ile Ala Val G u Trp
 370 375 380

2921032PC01SequenceLi st i ng. t xt

Gl u Ser Asn Gl y G n Pro Gl u Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gl y Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp G n G n Gl y Asn Val Phe Ser Cys Ser Val Met Hi s
420 425 430

Gl u Al a Leu Hi s Asn Hi s Tyr Thr G n Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gl y

<210> 99
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD37- 51

<400> 99

Asp Val G n Leu G n Gl u Ser Gl y Pro Asp Leu Leu Lys Pro Ser G n
1 5 10 15

Ser Leu Ser Leu Thr Cys Thr Val Thr Gl y Tyr Ser Ile Ser Ser Gl y
20 25 30

Phe Al a Trp Hi s Trp Ile Arg G n Phe Pro Gl y Asn Lys Leu Gl u Trp
35 40 45

Met Gl y Tyr Ile Hi s Tyr Ser Gl y Ser Thr Asn Tyr Ser Pro Ser Leu
50 55 60

Lys Ser Arg Ile Ser Ile Thr Arg Asp Ser Ser Lys Asn G n Phe Phe
65 70 75 80

Leu G n Leu Asn Ser Val Thr Thr Gl u Asp Thr Al a Thr Tyr Tyr Cys
85 90 95

Al a Arg Gl y Tyr Tyr Gl y Phe Gl y Al a Trp Phe Val Tyr Trp Gl y G n
100 105 110

Gl y Thr Leu Val Thr Val Ser Al a Al a Lys Thr Thr Al a Pro Ser Val
115 120 125

Tyr Pro Leu Al a Pro Val Cys Gl y Asp Thr Thr Gl y Ser Ser Val Thr
130 135 140

Leu Gl y Cys Leu Val Lys Gl y Tyr Phe Pro Gl u Pro Val Thr Leu Thr

145 150 155 160
 Trp Asn Ser Gly Ser₁₆₅ Leu Ser Ser Gly Val₁₇₀ His Thr Phe Pro Ala₁₇₅ Val
 Leu Gln Ser Asp₁₈₀ Leu Tyr Thr Leu Ser₁₈₅ Ser Ser Val Thr Val₁₉₀ Thr Ser
 Ser Thr Trp₁₉₅ Pro Ser Gln Ser Ile₂₀₀ Thr Cys Asn Val Ala₂₀₅ His Pro Ala
 Ser Ser₂₁₀ Thr Lys Val Asp Lys₂₁₅ Lys Ile Gu Pro Arg₂₂₀ Gly Pro Thr Ile
 Lys Pro Cys Pro Pro Cys₂₃₀ Lys Cys Pro Ala Pro₂₃₅ Asn Leu Leu Gly Gly₂₄₀
 Pro Ser Val Phe Ile₂₄₅ Phe Pro Pro Lys Ile₂₅₀ Lys Asp Val Leu Met₂₅₅ Ile
 Ser Leu Ser Pro₂₆₀ Ile Val Thr Cys Val₂₆₅ Val Val Asp Val Ser₂₇₀ Gu Asp
 Asp Pro Asp₂₇₅ Val Gln Ile Ser Trp₂₈₀ Phe Val Asn Asn Val₂₈₅ Gu Val His
 Thr Ala₂₉₀ Gln Thr Gln Thr His₂₉₅ Arg Gu Asp Tyr Asn₃₀₀ Ser Thr Leu Arg
 Val Val Ser Ala Leu Pro₃₁₀ Ile Gln His Gln Asp₃₁₅ Trp Met Ser Gly Lys₃₂₀
 Gu Phe Lys Cys Lys₃₂₅ Val Asn Asn Lys Asp₃₃₀ Leu Pro Ala Pro Ile₃₃₅ Gu
 Arg Thr Ile Ser₃₄₀ Lys Pro Lys Gly Ser₃₄₅ Val Arg Ala Pro Gln₃₅₀ Val Tyr
 Val Leu Pro₃₅₅ Pro Pro Gu Gu₃₆₀ Gu Met Thr Lys Lys Gln₃₆₅ Val Thr Leu
 Thr Cys₃₇₀ Met Val Thr Asp Phe₃₇₅ Met Pro Gu Asp Ile₃₈₀ Tyr Val Gu Trp
 Thr₃₈₅ Asn Asn Gly Lys Thr₃₉₀ Gu Leu Asn Tyr Lys₃₉₅ Asn Thr Gu Pro Val₄₀₀
 Leu Asp Ser Asp Gly₄₀₅ Ser Tyr Phe Met Tyr₄₁₀ Ser Lys Leu Arg Val₄₁₅ Gu
 Lys Lys Asn Trp Val Gu Arg Asn Ser Tyr Ser Cys Ser Val Val His
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420

425

430

G u G y Leu H i s A s n H i s H i s T h r T h r L y s S e r P h e S e r A r g T h r P r o
 435 440 445

G y L y s
 450

<210> 100
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 <212> PRT
 <213> A r t i f i c i a l S e q u e n c e

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 <223> h u C D 3 7 - 5 1

<400> 100

G u V a l G n L e u V a l G u S e r G y P r o G u V a l L e u L y s P r o G y G u
 1 5 10 15

S e r L e u S e r L e u T h r C y s T h r V a l S e r G y T y r S e r I l e S e r S e r G y
 20 25 30

P h e A l a T r p H i s T r p I l e A r g G n P h e P r o G y L y s G y L e u G u T r p
 35 40 45

M e t G y T y r I l e H i s T y r S e r G y S e r T h r A s n T y r S e r P r o S e r L e u
 50 55 60

G n G y A r g I l e S e r I l e T h r A r g A s p S e r S e r I l e A s n G n P h e P h e
 65 70 75 80

L e u G n L e u A s n S e r V a l T h r A l a S e r A s p T h r A l a T h r T y r T y r C y s
 85 90 95

A l a A r g G y T y r T y r G y P h e G y A l a T r p P h e V a l T y r T r p G y G n
 100 105 110

G y T h r L e u V a l T h r V a l S e r A l a A l a S e r T h r L y s G y P r o S e r V a l
 115 120 125

P h e P r o L e u A l a P r o S e r S e r L y s S e r T h r S e r G y G y T h r A l a A l a
 130 135 140

L e u G y C y s L e u V a l L y s A s p T y r P h e P r o G u P r o V a l T h r V a l S e r
 145 150 155 160

T r p A s n S e r G y A l a L e u T h r S e r G y V a l H i s T h r P h e P r o A l a V a l
 165 170 175

L e u G n S e r S e r G y L e u T y r S e r L e u S e r S e r V a l V a l T h r V a l P r o
 180 185 190

2921032PC01SequenceLi st i ng. t xt

Ser Ser Ser Leu Gly Thr G n Thr Tyr Ile Oys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Gu Pro Lys Ser Oys Asp
210 215 220

Lys Thr His Thr Oys Pro Pro Oys Pro Ala Pro Gu Leu Leu Gly Gly
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255

Ser Arg Thr Pro Gu Val Thr Oys Val Val Val Asp Val Ser His Gu
260 265 270

Asp Pro Gu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Gu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Arg Gu Gu G n Tyr Asn Ser Thr Tyr Arg
290 295 300

Val Val Ser Val Leu Thr Val Leu His G n Asp Trp Leu Asn Gly Lys
305 310 315 320

Gu Tyr Lys Oys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Gu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly G n Pro Arg Gu Pro G n Val Tyr
340 345 350

Thr Leu Pro Pro Ser Arg Asp Gu Leu Thr Lys Asn G n Val Ser Leu
355 360 365

Thr Oys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Gu Trp
370 375 380

Gu Ser Asn Gly G n Pro Gu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp G n G n Gly Asn Val Phe Ser Oys Ser Val Met His
420 425 430

Gu Ala Leu His Asn His Tyr Thr G n Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly

2921032PC01SequenceLi st i ng. t xt

<210> 101
 <211> 444
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> muCD37-56

<400> 101

Asp Val G n Leu G n G u Ser G y Pro Asp Leu Val Lys Pro Ser G n
 1 5 10 15

Ser Leu Ser Leu Thr Cys Thr Val Thr G y Tyr Ser Ile Thr Ser G y
 20 25 30

Phe Ala Trp His Trp Ile Arg G n Phe Pro G y Asn Lys Leu G u Trp
 35 40 45

Met G y Tyr Ile His Tyr Ser G y G y Thr Asn Tyr Asn Pro Ser Leu
 50 55 60

Lys Ser Arg Val Ser Ile Thr Arg Asp Thr Ser Lys Asn G n Phe Phe
 65 70 75 80

Leu G n Leu Asn Ser Val Thr Thr G u Asp Thr Ala Thr Tyr Tyr Cys
 85 90 95

Ala Arg G y Tyr Tyr G y Phe G y Ala Trp Phe Ala Tyr Trp G y G n
 100 105 110

G y Thr Leu Val Pro Val Ser Ala Ala Lys Thr Thr Pro Pro Ser Val
 115 120 125

Tyr Pro Leu Ala Pro G y Ser Ala Ala G n Thr Asn Ser Met Val Thr
 130 135 140

Leu G y Cys Leu Val Lys G y Tyr Phe Pro G u Pro Val Thr Val Thr
 145 150 155 160

Trp Asn Ser G y Ser Leu Ser Ser G y Val His Thr Phe Pro Ala Val
 165 170 175

Leu G u Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser
 180 185 190

Ser Met Arg Pro Ser G u Thr Val Thr Cys Asn Val Ala His Pro Ala
 195 200 205

Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys G y Cys
 210 215 220

Lys Pro Cys Ile Cys Thr Val Pro G u Val Ser Ser Val Phe Ile Phe

225 230 235 240

Pro Pro Lys Pro Lys₂₄₅ Asp Val Leu Thr Ile₂₅₀ Thr Leu Thr Pro Lys₂₅₅ Val

Thr Cys Val Val₂₆₀ Val Asp Ile Ser Lys₂₆₅ Asp Asp Pro Glu Val₂₇₀ Gl n Phe

Ser Trp Phe₂₇₅ Val Asp Asp Val Glu₂₈₀ Val His Thr Ala Gl n₂₈₅ Thr Gl n Pro

Arg Glu₂₉₀ Glu Gl n Phe Asn Ser₂₉₅ Thr Phe Arg Ser Val₃₀₀ Ser Glu Leu Pro

Ile₃₀₅ Met His Gl n Asp Trp₃₁₀ Leu Asn Gly Lys Glu₃₁₅ Phe Lys Cys Arg Val₃₂₀

Asn Ser Ala Ala Phe₃₂₅ Pro Ala Pro Ile Glu₃₃₀ Lys Thr Ile Ser Lys₃₃₅ Thr

Lys Gly Arg Pro₃₄₀ Lys Ala Pro Gl n Val₃₄₅ Tyr Thr Ile Pro Pro₃₅₀ Pro Lys

Glu Gl n Met₃₅₅ Ala Lys Asp Lys Val₃₆₀ Ser Leu Thr Cys Met₃₆₅ Ile Thr Asp

Phe Phe₃₇₀ Pro Glu Asp Ile Thr₃₇₅ Val Glu Trp Gl n Trp₃₈₀ Asn Gly Gl n Pro

Ala Glu₃₈₅ Asn Tyr Lys Asn Thr Gl n Pro Ile Met₃₉₅ Asn Thr Asn Gly Ser₄₀₀

Tyr Phe Val Tyr Ser₄₀₅ Lys Leu Asn Val Gl n₄₁₀ Lys Ser Asn Trp Glu₄₁₅ Ala

Gly Asn Thr Phe₄₂₀ Thr Cys Ser Val Leu₄₂₅ His Glu Gly Leu His₄₃₀ Asn His

His Thr Glu₄₃₅ Lys Ser Leu Ser His₄₄₀ Ser Pro Gly Lys

<210> 102
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> huCD37-56

<400> 102

Gl n Val Gl n Leu Gl n Glu Ser Gly Pro Gly₁₀ Leu Val Lys Pro Ser₁₅ Gl n

2921032PC01SequenceLi st i ng. t xt

Ser Leu Ser Leu Thr Oys Thr Val Ser Gly Tyr Ser Ile Thr Ser Gly
20 25 30

Phe Ala Trp His Trp Ile Arg Gln Phe Pro Gly Lys Gly Leu Glu Trp
35 40 45

Met Gly Tyr Ile His Tyr Ser Gly Gly Thr Asn Tyr Asn Pro Ser Leu
50 55 60

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

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

Ala Arg Gly Tyr Tyr Gly Phe Gly Ala Trp Phe Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Pro Val Ser Ala Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Oys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Oys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Oys Asp
210 215 220

Lys Thr His Thr Oys Pro Pro Oys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255

Ser Arg Thr Pro Glu Val Thr Oys Val Val Val Asp Val Ser His Glu
260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

2921032PC01SequenceLi st i ng. t xt

Asn Ala Lys Thr Lys Pro Arg Gu Gu Gn Tyr Asn Ser Thr Tyr Arg
 290 295 300

Val Val Ser Val Leu Thr Val Leu His Gn Asp Trp Leu Asn Gly Lys
 305 310 315 320

Gu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Gu
 325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gn Pro Arg Gu Pro Gn Val Tyr
 340 345 350

Thr Leu Pro Pro Ser Arg Asp Gu Leu Thr Lys Asn Gn Val Ser Leu
 355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Gu Trp
 370 375 380

Gu Ser Asn Gly Gn Pro Gu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415

Lys Ser Arg Trp Gn Gn Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430

Gu Ala Leu His Asn His Tyr Thr Gn Lys Ser Leu Ser Leu Ser Pro
 435 440 445

Gly

<210> 103
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> muCD37-57

<400> 103

Asp Val Gn Leu Gn Gu Ser Gly Pro Asp Leu Leu Lys Pro Ser Gn
 1 5 10 15

Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Gly
 20 25 30

Phe Ala Trp His Trp Ile Arg Gn Phe Pro Gly Asn Lys Leu Gu Trp
 35 40 45

Met Gly Tyr Ile Leu Tyr Ser Gly Ser Thr Val Tyr Ser Pro Ser Leu

50

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

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

Ala Arg Gly Tyr Tyr Gly Tyr Gly Ala Trp Phe Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ala Ala Lys Thr Thr Ala Pro Ser Val
115 120 125

Tyr Pro Leu Ala Pro Val Cys Gly Asp Thr Thr Gly Ser Ser Val Thr
130 135 140

Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Gu Pro Val Thr Leu Thr
145 150 155 160

Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Thr Ser
180 185 190

Ser Thr Trp Pro Ser Gln Ser Ile Thr Cys Asn Val Ala His Pro Ala
195 200 205

Ser Ser Thr Lys Val Asp Lys Lys Ile Gu Pro Arg Gly Pro Thr Ile
210 215 220

Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly
225 230 235 240

Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile
245 250 255

Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser Gu Asp
260 265 270

Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Gu Val His
275 280 285

Thr Ala Gln Thr Gln Thr His Arg Gu Asp Tyr Asn Ser Thr Leu Arg
290 295 300

Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys
305 310 315 320

Gu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Gu
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330

335

Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr
 340 345 350
 Val Leu Pro Pro Pro Gu Gu Gu Met Thr Lys Lys Gln Val Thr Leu
 355 360 365
 Thr Cys Met Val Thr Asp Phe Met Pro Gu Asp Ile Tyr Val Gu Trp
 370 375 380
 Thr Asn Asn Gly Lys Thr Gu Leu Asn Tyr Lys Asn Thr Gu Pro Val
 385 390 395 400
 Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Gu
 405 410 415
 Lys Lys Asn Trp Val Gu Arg Asn Ser Tyr Ser Cys Ser Val Val His
 420 425 430
 Gu Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro
 435 440 445
 Gly Lys
 450

<210> 104
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> huCD37-57

<400> 104

Gln Val Gln Leu Gln Gu Ser Gly Pro Gly Leu Leu Lys Pro Ser Gln
 1 5 10 15
 Ser Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Gly
 20 25 30
 Phe Ala Trp His Trp Ile Arg Gln Phe Pro Gly Lys Gly Leu Gu Trp
 35 40 45
 Met Gly Tyr Ile Leu Tyr Ser Gly Ser Thr Val Tyr Ser Pro Ser Leu
 50 55 60
 Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
 65 70 75 80
 Leu Gln Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Thr Tyr Tyr Cys
 85 90 95

2921032PC01SequenceLi st i ng. t xt

Al a Arg Gly Tyr Tyr Gly Tyr Gly Ala Trp Phe Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Gu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Gu Pro Lys Ser Cys Asp
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Gu Leu Leu Gly Gly
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255

Ser Arg Thr Pro Gu Val Thr Cys Val Val Val Asp Val Ser His Gu
260 265 270

Asp Pro Gu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Gu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Arg Gu Gu Gln Tyr Asn Ser Thr Tyr Arg
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Gu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Gu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Gu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Ser Arg Asp Gu Leu Thr Lys Asn Gln Val Ser Leu
355 360 365

2921032PC01SequenceLi st i ng. t xt

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly

<210> 105
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> muCD37-3

<400> 105

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

Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Arg Ser Asn
20 25 30

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

Asn Val Ala Thr Asn Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Gly Thr Tyr Tyr Cys Gln His Tyr Trp Gly Thr Thr Trp
85 90 95

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

Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly
115 120 125

Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile

130

Asn Val Lys Trp Lys Ile Asp Gly Ser Gu Arg Gn Asn Gly Val Leu
145 150 155 160

Asn Ser Trp Thr Asp Gn Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
165 170 175

Ser Thr Leu Thr Leu Thr Lys Asp Gu Tyr Gu Arg His Asn Ser Tyr
180 185 190

Thr Cys Gu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser
195 200 205

Phe Asn Arg Asn Gu Cys
210

<210> 106
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> chCD37-3

<400> 106

Asp Ile Gn Met Thr Gn Ser Pro Ala Ser Leu Ser Val Ser Val Gly
1 5 10 15

Gu Thr Val Thr Ile Thr Cys Arg Ala Ser Gu Asn Ile Arg Ser Asn
20 25 30

Leu Ala Trp Tyr Gn Gn Lys Gn Gly Lys Ser Pro Gn Leu Leu Val
35 40 45

Asn Val Ala Thr Asn Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Gn Tyr Ser Leu Lys Ile Asn Ser Leu Gn Ser
65 70 75 80

Gu Asp Phe Gly Thr Tyr Tyr Cys Gn His Tyr Trp Gly Thr Thr Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Gu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Gu Gn Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Gu Ala
130 135 140

2921032PC01SequenceLi st i ng. t xt

Lys Val G n Trp Lys Val Asp Asn Al a Leu G n Ser G y Asn Ser G n
145 150 155 160

G u Ser Val Thr G u G n Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Al a Asp Tyr G u Lys Hi s Lys Val Tyr
180 185 190

Al a Cys G u Val Thr Hi s G n G y Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg G y G u Cys
210

<210> 107

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> huCD37-3 (1.0 and 1.1)

<400> 107

Asp Ile G n Met Thr G n Ser Pro Ser Ser Leu Ser Val Ser Val G y
1 5 10 15

G u Arg Val Thr Ile Thr Cys Arg Al a Ser G u Asn Ile Arg Ser Asn
20 25 30

Leu Al a Trp Tyr G n G n Lys Pro G y Lys Ser Pro Lys Leu Leu Val
35 40 45

Asn Val Al a Thr Asn Leu Al a Asp G y Val Pro Ser Arg Phe Ser G y
50 55 60

Ser G y Ser G y Thr Asp Tyr Ser Leu Lys Ile Asn Ser Leu G n Pro
65 70 75 80

G u Asp Phe G y Thr Tyr Tyr Cys G n Hi s Tyr Trp G y Thr Thr Trp
85 90 95

Thr Phe G y G n G y Thr Lys Leu G u Ile Lys Arg Thr Val Al a Al a
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp G u G n Leu Lys Ser G y
115 120 125

Thr Al a Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg G u Al a
130 135 140

Lys Val G n Trp Lys Val Asp Asn Al a Leu G n Ser G y Asn Ser G n

145 150 155 160

G u Ser Val Thr G u G n Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Al a Asp Tyr G u Lys Hi s Lys Val Tyr
180 185 190

Al a Cys G u Val Thr Hi s G n G y Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg G y G u Cys
210

<210> 108

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> muCD37-12

<400> 108

Asp Ile Val Leu Thr G n Ser Pro Al a Ser Leu Al a Val Ser Leu G y
1 5 10 15

G n Arg Al a Thr Ile Ser Cys Arg Al a Ser G n Ser Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Leu Tyr Trp Phe G n G n Lys Pro G y G n Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Al a Ser Asn Leu Al a Ser G y Val Pro Al a
50 55 60

Arg Phe Ser G y Ser G y Ser G y Thr Asp Phe Thr Leu Asn Ile Hi s
65 70 75 80

Pro Val G u G u G u Asp Thr Al a Thr Tyr Tyr Cys G n Hi s Ser Trp
85 90 95

G u Ile Pro Tyr Thr Phe G y G y G y Thr Lys Leu G u Ile Lys Arg
100 105 110

Al a Asp Al a Al a Pro Thr Val Ser Ile Phe Pro Pro Ser Ser G u G n
115 120 125

Leu Thr Ser G y G y Al a Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
130 135 140

Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp G y Ser G u Arg G n
145 150 155 160

2921032PC01SequenceLi st i ng. t xt

Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
165 170 175

Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
180 185 190

His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
195 200 205

Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
210 215

<210> 109
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> chCD37-12

<400> 109

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

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

Ser Tyr Ser Tyr Leu Tyr Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

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

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

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

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115 120 125

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr

165

170

175

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
180 185 190

His Lys Val Tyr Ala Cys Gu Val Thr His G n Gly Leu Ser Ser Pro
195 200 205

Val Thr Lys Ser Phe Asn Arg Gly Gu Cys
210 215

<210> 110

<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<223> muCD37-38

<400> 110

G n Ile Val Leu Thr G n Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
1 5 10 15

G u Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met
20 25 30

His Trp Tyr G n G n Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
35 40 45

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys G n G n Trp Ile Ser Asn Pro Pro Thr
85 90 95

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

Thr Val Ser Ile Phe Pro Pro Ser Ser Gu G n Leu Thr Ser Gly Gly
115 120 125

Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn
130 135 140

Val Lys Trp Lys Ile Asp Gly Ser Gu Arg G n Asn Gly Val Leu Asn
145 150 155 160

Ser Trp Thr Asp G n Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser
165 170 175

2921032PC01SequenceLi st i ng. t xt

Thr Leu Thr Leu Thr Lys Asp G u Tyr G u Arg Hi s Asn Ser Tyr Thr
180 185 190

Oys G u Al a Thr Hi s Lys Thr Ser Thr Ser Pro Il e Val Lys Ser Phe
195 200 205

Asn Arg Asn G u Oys
210

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

<220>
<223> chCD37-38

<400> 111

G n Il e Val Leu Thr G n Ser Pro Al a Il e Met Ser Al a Ser Pro Gly
1 5 10 15

G u Lys Val Thr Met Thr Oys Ser Al a Ser Ser Ser Val Thr Tyr Met
20 25 30

Hi s Trp Tyr G n G n Lys Ser Gly Thr Ser Pro Lys Arg Trp Il e Tyr
35 40 45

Asp Thr Ser Lys Leu Al a Ser Gly Val Pro Al a Arg Phe Ser Gly Gly
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Il e Ser Ser Met Gl u Al a Gl u
65 70 75 80

Asp Al a Al a Thr Tyr Tyr Oys G n G n Trp Il e Ser Asn Pro Pro Thr
85 90 95

Phe Gly Gly Gly Thr Lys Leu G u Il e Lys Arg Thr Val Al a Al a Pro
100 105 110

Ser Val Phe Il e Phe Pro Pro Ser Asp G u G n Leu Lys Ser Gly Thr
115 120 125

Al a Ser Val Val Oys Leu Leu Asn Asn Phe Tyr Pro Arg Gl u Al a Lys
130 135 140

Val G n Trp Lys Val Asp Asn Al a Leu G n Ser Gly Asn Ser G n Gl u
145 150 155 160

Ser Val Thr G u G n Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Al a Asp Tyr G u Lys Hi s Lys Val Tyr Al a
Page 71

180

185

190

Oys G u Val Thr His G n G y Leu Ser Ser Pro Val Thr Lys Ser Phe
 195 200 205

Asn Arg G y G u Oys
 210

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

<220>
 <223> huCD37-38

<400> 112

Asp Ile Val Leu Thr G n Ser Pro Ala Ser Met Ser Ala Ser Pro Gly
 1 5 10 15

G u Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met
 20 25 30

His Trp Tyr G n G n Lys Pro Gly Thr Ser Pro Lys Arg Trp Ile Tyr
 35 40 45

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys G n G n Trp Ile Ser Asn Pro Pro Thr
 85 90 95

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

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu G n Leu Lys Ser Gly Thr
 115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
 130 135 140

Val G n Trp Lys Val Asp Asn Ala Leu G n Ser Gly Asn Ser G n Glu
 145 150 155 160

Ser Val Thr Glu G n Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
 165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
 180 185 190

2921032PC01SequenceLi st i ng. t xt

Oys G u Val Thr His G n G y Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg G y G u Oys
210

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

<220>
<223> muCD37-50

<400> 113

G n Ile Val Leu Thr G n Ser Pro Ala Ile Met Ser Ala Ser Pro G y
1 5 10 15

G u Lys Val Thr Met Thr Oys Ser Ala Thr Ser Ser Val Thr Tyr Met
20 25 30

His Trp Tyr G n G n Lys Ser G y Thr Ser Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Lys Leu Pro Tyr G y Val Pro G y Arg Phe Ser G y Ser
50 55 60

G y Ser G y Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Oys G n G n Trp Ser Asp Asn Pro Pro Thr
85 90 95

Phe G y Ser G y Thr Lys Leu G u Ile Lys Arg Ala Asp Ala Ala Pro
100 105 110

Thr Val Ser Ile Phe Pro Pro Ser Ser G u G n Leu Thr Ser G y G y
115 120 125

Ala Ser Val Val Oys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn
130 135 140

Val Lys Trp Lys Ile Asp G y Ser G u Arg G n Asn G y Val Leu Asn
145 150 155 160

Ser Trp Thr Asp G n Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser
165 170 175

Thr Leu Thr Leu Thr Lys Asp G u Tyr G u Arg His Asn Ser Tyr Thr
180 185 190

Oys G u Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe

195

Asn Arg Asn Gl u Cys
210

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

<220>
<223> huCD37- 50

<400> 114

Gl u Ile Val Leu Thr Gl n Ser Pro Ala Thr Met Ser Ala Ser Pro Gly
1 5 10 15

Gl u Arg Val Thr Met Thr Cys Ser Ala Thr Ser Ser Val Thr Tyr Met
20 25 30

His Trp Tyr Gl n Gl n Lys Pro Gly Gl n Ser Pro Lys Arg Trp Ile Tyr
35 40 45

Asp Thr Ser Asn Leu Pro Tyr Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Gl u Ala Gl u
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gl n Gl n Trp Ser Asp Asn Pro Pro Thr
85 90 95

Phe Gly Gl n Gly Thr Lys Leu Gl u Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Gl u Gl n Leu Lys Ser Gly Thr
115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Gl u Ala Lys
130 135 140

Val Gl n Trp Lys Val Asp Asn Ala Leu Gl n Ser Gly Asn Ser Gl n Gl u
145 150 155 160

Ser Val Thr Gl u Gl n Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Gl u Lys His Lys Val Tyr Ala
180 185 190

Cys Gl u Val Thr His Gl n Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

2921032PC01SequenceLi st i ng. t xt

Asn Arg Gly Gu Oys
210

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

<220>
<223> muCD37-51

<400> 115

G n I l e Val Leu Thr G n Ser Pro Al a I l e Met Ser Al a Ser Pro Gly
1 5 10 15

G u Lys Val Thr Met Thr Cys Ser Al a Thr Ser Ser Val Thr Tyr Met
20 25 30

Hi s Trp Tyr G n G n Lys Ser Gly Thr Ser Pro Lys Arg Trp I l e Tyr
35 40 45

Asp Thr Ser Lys Leu Al a Ser Gly Val Pro Al a Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr I l e Ser Asn Met Gl u Al a Gl u
65 70 75 80

Asp Al a Al a Thr Tyr Tyr Cys G n G n Trp Ser Ser Asn Pro Pro Thr
85 90 95

Phe Gly Ser Gly Thr Lys Leu Gl u I l e Lys Arg Al a Asp Al a Al a Pro
100 105 110

Thr Val Ser I l e Phe Pro Pro Ser Ser Gl u G n Leu Thr Ser Gly Gly
115 120 125

Al a Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp I l e Asn
130 135 140

Val Lys Trp Lys I l e Asp Gly Ser Gl u Arg G n Asn Gly Val Leu Asn
145 150 155 160

Ser Trp Thr Asp G n Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser
165 170 175

Thr Leu Thr Leu Thr Lys Asp Gl u Tyr Gl u Arg Hi s Asn Ser Tyr Thr
180 185 190

Oys Gl u Al a Thr Hi s Lys Thr Ser Thr Ser Pro I l e Val Lys Ser Phe
195 200 205

Asn Arg Asn Gl u Oys

210

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

<220>
 <223> huCD37-51

<400> 116

G u I l e Val Leu Thr G n Ser Pro Al a Thr Met Ser Al a Ser Pro G y
 1 5 10 15

G u Arg Val Thr Met Thr Oys Ser Al a Thr Ser Ser Val Thr Tyr Met
 20 25 30

Hi s Trp Tyr G n G n Lys Pro G y G n Ser Pro Lys Arg Trp I l e Tyr
 35 40 45

Asp Thr Ser Lys Leu Al a Ser G y Val Pro Al a Arg Phe Ser G y Ser
 50 55 60

G y Ser G y Thr Ser Tyr Ser Leu Thr I l e Ser Ser Met G u Al a G u
 65 70 75 80

Asp Al a Al a Thr Tyr Tyr Oys G n G n Trp Ser Ser Asn Pro Pro Thr
 85 90 95

Phe G y G n G y Thr Lys Leu G u I l e Lys Arg Thr Val Al a Al a Pro
 100 105 110

Ser Val Phe I l e Phe Pro Pro Ser Asp G u G n Leu Lys Ser G y Thr
 115 120 125

Al a Ser Val Val Oys Leu Leu Asn Asn Phe Tyr Pro Arg G u Al a Lys
 130 135 140

Val G n Trp Lys Val Asp Asn Al a Leu G n Ser G y Asn Ser G n G u
 145 150 155 160

Ser Val Thr G u G n Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
 165 170 175

Thr Leu Thr Leu Ser Lys Al a Asp Tyr G u Lys Hi s Lys Val Tyr Al a
 180 185 190

Oys G u Val Thr Hi s G n G y Leu Ser Ser Pro Val Thr Lys Ser Phe
 195 200 205

Asn Arg G y G u Oys
 210

2921032PC01SequenceLi st i ng. t xt

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

<220>
 <223> muCD37-56

<400> 117

G n I l e Val Leu Thr G n Ser Pro Al a Phe Met Ser Al a Ser Pro G y
 1 5 10 15

Asp Lys Val Thr Met Thr Cys Ser Al a Ser Ser Ser Val Thr Tyr Met
 20 25 30

Hi s Trp Tyr G n G n Lys Ser G y Thr Ser Pro Lys Arg Trp I l e Tyr
 35 40 45

Asp Thr Ser Lys Leu Al a Ser G y Val Pro Al a Arg Phe Ser G y G y
 50 55 60

G y Ser G y Thr Ser Tyr Ser Leu Thr I l e Ser Thr Met Gl u Al a Gl u
 65 70 75 80

Asp Al a Al a Thr Tyr Tyr Cys G n G n Trp I l e Ser Asp Pro Pro Thr
 85 90 95

Phe G y G y G y Thr Lys Leu Gl u I l e Lys Arg Al a Asp Al a Al a Pro
 100 105 110

Thr Val Ser I l e Phe Pro Pro Ser Ser Gl u G n Leu Thr Ser G y G y
 115 120 125

Al a Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp I l e Asn
 130 135 140

Val Lys Trp Lys I l e Asp G y Ser Gl u Arg G n Asn G y Val Leu Asn
 145 150 155 160

Ser Trp Thr Asp G n Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser
 165 170 175

Thr Leu Thr Leu Thr Lys Asp Gl u Tyr Gl u Arg Hi s Asn Ser Tyr Thr
 180 185 190

Cys Gl u Al a Thr Hi s Lys Thr Ser Thr Ser Pro I l e Val Lys Ser Phe
 195 200 205

Asn Arg Asn Gl u Cys
 210

<210> 118

2921032PC01SequenceLi st i ng. t xt

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

<220>
 <223> huCD37-56

<400> 118

Asp Ile Val Leu Thr Gln Ser Pro Ala Phe Met Ser Ala Ser Pro Gly
 1 5 10 15

Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met
 20 25 30

His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Arg Trp Ile Tyr
 35 40 45

Asp Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Gly
 50 55 60

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

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ile Ser Asp Pro Pro Thr
 85 90 95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
 100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
 115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
 130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
 145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
 165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
 180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
 195 200 205

Asn Arg Gly Glu Cys
 210

<210> 119
 <211> 213
 <212> PRT

<213> Artificial Sequence

<220>

<223> muCD37-57

<400> 119

G n I l e Val Leu Thr G n Ser Pro Al a I l e Met Ser Al a Ser Pro Gly
1 5 10 15

G u Lys Val Thr Met Thr Oys Ser Al a Thr Ser Ser Val Thr Tyr Met
20 25 30

Hi s Trp Tyr G n G n Lys Ser Gly Thr Ser Pro Lys Arg Trp I l e Tyr
35 40 45

Asp Thr Ser Lys Leu Al a Ser Gly Val Pro Al a Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr I l e Ser Ser Met Gl u Al a Gl u
65 70 75 80

Asp Al a Al a Thr Tyr Tyr Oys G n G n Trp Ser Asp Asn Pro Pro Thr
85 90 95

Phe Gly Ser Gly Thr Lys Leu Gl u I l e Lys Arg Al a Asp Al a Al a Pro
100 105 110

Thr Val Ser I l e Phe Pro Pro Ser Ser Gl u G n Leu Thr Ser Gly Gly
115 120 125

Al a Ser Val Val Oys Phe Leu Asn Asn Phe Tyr Pro Lys Asp I l e Asn
130 135 140

Val Lys Trp Lys I l e Asp Gly Ser Gl u Arg G n Asn Gly Val Leu Asn
145 150 155 160

Ser Trp Thr Asp G n Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser
165 170 175

Thr Leu Thr Leu Thr Lys Asp Gl u Tyr Gl u Arg Hi s Asn Ser Tyr Thr
180 185 190

Oys Gl u Al a Thr Hi s Lys Thr Ser Thr Ser Pro I l e Val Lys Ser Phe
195 200 205

Asn Arg Asn Gl u Oys
210

<210> 120

<211> 212

<212> PRT

<213> Artificial Sequence

2921032PC01SequenceLi st i ng. t xt

<220>

<223> huCD37- 57

<400> 120

G u I l e Val Leu Thr G n Ser Pro Al a Thr Met Ser Al a Ser Pro G y
1 5 10 15

G u Arg Val Thr Met Thr Cys Ser Al a Thr Ser Ser Val Thr Tyr Met
20 25 30

Hi s Trp Tyr G n G n Lys Pro G y G n Ser Pro Arg Arg Trp I l e Tyr
35 40 45

Asp Thr Ser Asn Leu Al a Ser G y Val Pro Al a Arg Phe Ser G y Ser
50 55 60

G y Ser G y Thr Ser Tyr Ser Leu Thr I l e Ser Ser Met G u Al a G u
65 70 75 80

Asp Al a Al a Thr Tyr Tyr Cys G n G n Trp Ser Asp Asn Pro Pro Thr
85 90 95

Phe G y G n G y Thr Lys Leu G u I l e Lys Arg Thr Val Al a Al a Pro
100 105 110

Ser Val Phe I l e Phe Pro Pro Ser Asp G u G n Leu Lys Ser G y Thr
115 120 125

Al a Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg G u Al a Lys
130 135 140

Val G n Trp Lys Val Asp Asn Al a Leu G n Ser G y Asn Ser G n G u
145 150 155 160

Ser Val Thr G u G n Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Al a Asp Tyr G u Lys Hi s Lys Val Tyr Al a
180 185 190

Cys G u Val Thr Hi s G n G y Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg G y G u
210

<210> 121

<211> 345

<212> DNA

<213> Artificial Sequence

<220>

<223> muCD37- 3

2921032PC01SequenceLi st i ng. t xt

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<400> 121
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acat gact g t ct cagggt t ct cat t aacc acct ct ggt g t aagct gggt t cgccagcct      120
ccaggaaagg gt ct ggagt g gct gggagt a at at ggggt g acgggagcac aaact at cat      180
t cagct ct ca aat ccagact gagcat caag aaggat cact ccaagagcca agt t t t ct t a      240
aaact gaaca gt ct gcaaac t gat gacaca gccacgt act act gt gccaa aggaggct ac      300
t cgt t ggct c act ggggccca agggact ct g gt cacagt ct ct gca                        345
```

```
<210> 122
<211> 431
<212> DNA
<213> Artificial Sequence
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```
<220>
<223> chCD37- 3
```

```
<400> 122
aagct t gcca ccat ggct gt cct ggcact g ct cct ct gcc t ggt gacat a cccaagct gt      60
gt cct at cac aggt gcaggt gaaggagt ca ggacct ggcc t ggt ggcgcc ct cacagagc      120
ct gt ccat t a cat gact gt ct cagggt t c t cat t aacca cct ct ggt gt aagct gggt t      180
cgccagcct c caggaaagg t ct ggagt gg ct gggagt aa t at ggggt ga cgggagcaca      240
aact at cat t cagct ct caa at ccagact g agcat caaga aggat cact c caagagccaa      300
gt t t t ct t aa aact gaacag t ct gcaaact gat gacacag ccacgt act a ct gt gccaaa      360
ggaggct act cgt t ggct ca ct ggggccaa gggact ct gg t cacagt ct c t gcagcct ct      420
acgaagggcc c                                                                431
```

```
<210> 123
<211> 431
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> huCD37- 3v1. 0
```

```
<400> 123
aagct t gcca ccat gggt t g gagct gcatt at t ct gtt t c t ggt ggccac cgccaccggt      60
gt gact cac aagt ccaagt ccaagaat ct ggt ccaggt c t ggt ggcccc t t cccaaact      120
ct gagcat ca cct gt accgt t t ct ggt t t t agcct t acca cct ct ggt gt gagt t gggt a      180
cgccaaccac ccggt aagg t ct cgaat gg ct ggggt gt aa t ct ggggt ga t ggt t ccaca      240
aat t accat c ct t ccct caa gt cccgcct t agcat caaaa aggat cacag caaaagt caa      300
gt t t t cct ga aact gaat ag t ct gacagca gccgat acag ccacct act a t t gcgccaaag      360
ggg ggt t at a gt ct t gcaca ct ggggt caa ggt accct cg t t accgt ct c ct cagct agt      420
accaagggcc c                                                                431
```

```
<210> 124
```

2921032PC01SequenceLi st i ng. t xt

<211> 431
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD37-3v1.1

<400> 124
aagcttgcca ccatgggctg gagctgtatc attctgtttc tggcggcgac agctactggg 60
gtccactccc aagtgcaggt acaagagtcc gggcctggat tggcgcacc aagccagacc 120
ctctctatca ctgtaccgt tagcgggttc tctctgacaa ccagtgagtg aggtgggtg 180
aggcagccac caggaaaggg actggagtggt ctgggggtga tttggggcga cggcagcaca 240
aactatcatt ccagctctaa atctcggttg tccattaaaa aagaccatag taaatctcaa 300
gttttcctga aactcaatag cctgacagcc gcagacactg ctacgtatta ctgcgcaaaa 360
ggaggataca gtctggctca ctggggacag gggaccctgg tgaccgtgtc atccgcatca 420
acaaagggcc c 431

<210> 125
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<223> muCD37-12

<400> 125
cagatccagt tggcgcagt tggacctgag ctgaagaagc ctggagagac agtcaagatc 60
tcctgcaagg ctctgggtat accttcaca aagtatggaa tgaactgggt gaagcaggct 120
caaggaaagg gtttaagt g gatgggctgg ataaacacca aactggaga gtcaagaaat 180
gctgaagaat tcaaggagc gtttgccttc tctttggaaa cctctgccag cactgcctat 240
ttgcagatca acaacctcaa atatgaggac acggctacat attctgtgg aaggggcacg 300
gtagtgcgg actggggcca aggcaccact ctcacagtct cctca 345

<210> 126
<211> 431
<212> DNA
<213> Artificial Sequence

<220>
<223> chCD37-12

<400> 126
aagcttgcca ccatggggtg gtcattgcata atcctctttc tggcgcctac tgcctaccggt 60
gtgcaactcac agattcagct ggttcaaagt ggcccagagc taaaaagcc aggggaaaca 120
gtgaaaataa gttgcaaggc atccggttac actttcacia agtacggcat gaactgggtc 180
aagcaggccc agggcaagg gctcaaatgg atgggttgg tcaatacca cactggcgag 240
tctaggaatg ctgaggagt taaaggcccg tttgccttca gcctggagac aagtgccagc 300
acagcttacc tgcaaatcaa caatctgaag tataggatg cagcaacct atttctgcggc 360

cgcgggcact g t cgt tgcaga ct ggggacaa ggt accacct t gact gt at c cagt gccagc 420
act aagggcc c 431

<210> 127
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> muCD37-38

<400> 127
gat gt gcagc t t caggagt c aggacct gac ct ggt gaaac ct t ct cagt c act t t cact c 60
acct gact g t cact ggct a ct ccat cacc agt ggt t t t g gct ggact g gat ccggcag 120
t t t ccaggaa acaagct gga at ggat ggcc t acat act ct acagt ggt gg cact gact ac 180
aaccat ct c t caaaagt cg aat ct ct at c act cgagaca ct t ccaagaa ccagt t ct t c 240
ct gcggt t ga gt t ct gt gac t act gaggac acagccacat at t act gt gc aagaggct ac 300
t at ggt t acg gggcct ggt t t gt t t act gg ggccaagga ct ct ggt cac t gt ct ct gca 360

<210> 128
<211> 446
<212> DNA
<213> Artificial Sequence

<220>
<223> chCD37-38

<400> 128
aagct t gcca ccat gggct g gagt t gt at c at t ct gt t t t t ggt ggccac cgccact gga 60
gt ccat t ccc aagt gcaact ccaggaat ct ggccct gacc t ggt t aagcc at ct cagagc 120
ct ct ccct ga cct gact gt t acaggat ac t caat cacat caggct t t gg ct ggact gg 180
at cagacaat t t cccgggaa caagt t ggaa t ggat ggct t acat t ct gt a t agcgggggt 240
accgat t aca at cct t ccct caagagccga at ct ct at ca ccagggat ac aagcaagaac 300
caat t t t t t c t ccgcct cag ct ct gt gact accgaagat a ccgct act t a ct at t gt gcc 360
aggggct act at ggat at gg t gcat ggt t c gt ct at t ggg gccaggaac cct ggt gact 420
gt gagcgct g cct ct accaa gggccc 446

<210> 129
<211> 446
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD37-38

<400> 129
aagct t gcca ccat ggg t g gact gcat c at t ct t t t cc t ggt cgct ac t gcaact gga 60
gt ccaact cac aggt ccagct gcaagagt cc ggt cct gggc t t gt gaaacc cagccagt cc 120
ct cagt ct ca cct gt act gt ct ct ggct ac t ct at t acca gt ggg t t cgg ct ggcat t gg 180

2921032PC01SequenceLi st i ng. t xt

att aggcagt t t cccggt aa ggggct ggag t ggat ggc at at cct gt a cagcggagga 240
accgatt aca acccaagt ct gaagagcagg at cagcat t a cccgggacac aagcaaaaac 300
cagtttttcc t t cggct gt c tagt gtt aca gct gcagaca ccgct act t a ct at t gt gct 360
cgggggtt act at ggct at gg ggct t ggt t t gt gt at t ggg gacaaggcac t ct t gt gacc 420
gt gagcagcg cct caacaaa gggccc 446

<210> 130
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> muCD37- 50

<400> 130
gat gt gcagc t t caggagt c aggacct gac ct gtt gaaac ct t ct cagt c act t t cact c 60
acct gcact g t cact ggct a ct ccat cacc agt ggt t t t g cct ggcact g gat ccggcag 120
t t t ccaggaa acaaact gga at ggat gggc t acat act ct acagt ggt ag cact gt ct ac 180
agcccat ct c t caaaagt cg aat ct ct at c act cgagaca cat ccaagaa ccact t ct t c 240
ct gcagt t ga at t ct gt gac t act gaggac acagccacat at t act gt gc aagagggt ac 300
t at ggt t acg gcgcct ggt t t gct t act gg ggccaaggga ct ct ggt cac t gt ct ct gca 360

<210> 131
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> muCD37- 51

<400> 131
gat gt gcagc t t caggagt c aggacct gac ct gtt gaaac ct t ct cagt c act t t cact c 60
acct gcact g t cact ggct a ct ccat ct cc agt ggt t t t g cct ggcact g gat ccggcag 120
t t t ccaggaa acaaact gga at ggat gggc t acat acact acagt ggt ag cact aact ac 180
agcccat ct c t caaaagt cg aat ct ct at c act cgagact cat ccaagaa ccagt t ct t c 240
ct gcagt t ga at t ct gt gac t act gaggac acagccacat at t act gt gc aagaggat ac 300
t at ggt t t cg gcgcct ggt t t gtt t act gg ggccaaggga ct ct ggt cac t gt ct ct gca 360

<210> 132
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> muCD37- 56

<400> 132
gat gt gcagc t t caggagt c aggacct gac ct ggt gaaac ct t ct cagt c act t t cact c 60
acct gcact g t cact ggct a ct ccat cacc agt ggt t t t g cct ggcact g gat ccggcag 120

2921032PC01SequenceLi st i ng. t xt

t t t ccaggaa acaaact gga at ggat gggc t acat acact acagt ggt gg cact aact ac	180
aacccat ct c t caaaagt cg agt ct ct at c act cgagaca cat ccaagaa ccagt t ct t c	240
ct gcagt t ga at t ct gt gac t act gaggac acagccacat at t act gt gc aagaggct ac	300
t at ggt t t cg gggcct ggt t t gct t act gg ggccaaggga ct ct ggt ccc t gt ct ct gca	360

<210> 133
 <211> 446
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> huCD37-56

<400> 133 aagct t gcca ccat ggggt g gagct gcat t at cct gt t cc t cgt cgccac cgcaaccggc	60
gt ccaact ccc aggt gcagct gcaagaaagc gggccaggat t ggt aaaacc t t cccagt ct	120
ct gagt ct t a ct t gt accgt at ct ggat ac agt at cacat ct ggct t cgc ct ggcat t gg	180
at t cgccagt t t cccggcaa ggggct t gag t ggat ggggt at at t cat t a t t ct ggaggt	240
accaaact aca accct t cct gaagagt cga gt ct caat t a ccagggacac t t ccaagaac	300
caat t ct t t t t gcagct t aa t t cagt gacc gct gccgaca ccgct act t a ct act gcgcc	360
cggggct act at ggggt t t gg t gcct ggt t c gcct act ggg gccaggggac cct ggt gccc	420
gt gt ct gct g cct ccacaaa gggccc	446

<210> 134
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> muCD37-57

<400> 134 gat gt gcagc t t caggagt c aggacct gac ct gt t gaaac ct t ct cagt c act t t cact c	60
acct gcaact g t cact ggct a ct ccat cacc agt ggt t t t g cct ggcaact g gat ccggcag	120
t t t ccaggaa acaaact gga at ggat gggc t acat act ct acagt ggt ag cact gt ct ac	180
agcccat ct c t caaaagt cg aat ct ct at c act cgagaca cat ccaagaa ccagt t ct t c	240
ct gcagt t ga at t ct gt gac t act gaggac acagccacat at t act gt gc aagagggt ac	300
t at ggt t acg ggcct ggt t t gct t act gg ggccaaggga ct ct ggt cac t gt ct ct gca	360

<210> 135
 <211> 446
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> huCD37-57

<400> 135 aagct t gcca ccat gggct g gagct gcat c at t ct gt t t c t ggt ggccac agcaact ggc	60
---	----

2921032PC01SequenceLi st i ng. t xt

gt t cacagt c aagt ccaact gcaggagagc ggccccggac t cct gaaacc at ct cagt ca 120
ct cagt ct ga cat gt act gt gagcggct ac agcat t acct caggct t cgc t t ggcat t gg 180
at caggcagt t ccccgga a aggt ct ggag t ggat ggggt acat t ct gt a cagcggcagt 240
acagt gt at t caccct cct t gaaat ct agg at at caat ca cacgt gat ac aagcaaaaat 300
cagt t ct t cc t ccagct gaa ct ccgt cacc gccgcagaca cagcaacct a t t at t gt gct 360
cgcggt act acggat at gg cgcat ggt t c gcct at t ggg gccagggggac act cgt gacc 420
gt t t ccgccg cct ccacaaa gggccc 446

<210> 136
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> muCD37-3

<400> 136
gacat ccaga t gact cagt c t ccagcct cc ct t t ct gt at ct gt gggaga aact gt cacc 60
at cacat gt c gagcaagt ga gaat at t cgc agt aat t t ag cat ggt at ca gcagaaacag 120
ggaaaat ct c ct cagct cct ggt caat gt t gcaacaaact t agcagat gg t gt gccat ca 180
aggt t cagt g gcagt ggat c aggcacacag t at t ccct ca agat caacag cct gcagt ct 240
gaagat t t t g ggact t at t a ct gt caacat t at t ggggt a ct acgt ggac gt t cggt gga 300
ggcaccaagc t ggaaat caa acgt 324

<210> 137
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> chCD37-3

<400> 137
gaat t cgcca ccat gagt gt gccact cag gt cct ggggt t gct gct gct gt ggct t aca 60
gat gccagat gt gacat cca gat gact cag t ct ccagcct ccct t t ct gt at ct gt ggga 120
gaaact gt ca ccat cacat g t cgagcaagt gagaat at t c gcagt aat t t agcat ggt at 180
cagcagaaac agggaaaat c t cct cagct c ct ggt caat g t t gcaacaaa ct t agcagat 240
gggt gt gccat caaggt t cag t ggaggt gga t caggcacac agt at t ccct caagat caac 300
agcct gcagt ct gaagat t t t gggact t at t act gt caac at t at t gggg t act acgt gg 360
acgt t cggt g gaggcaccaa gct ggaaat c aaacgt acg 399

<210> 138
<211> 396
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD37-3 (1.0 and 1.1)

2921032PC01SequenceLi st i ng. t xt

```
<400> 138
gaat t cgcca ccat gggt t g gt cct gcat c at ct t gt t t c t cgt ggccac agccaccggt 60
gt t cact ct g at at acaaat gact caaagc cct t ccagt t t gagcgt aag t gt gggt gaa 120
cgcgt aacaa t cacct gt ag agct agt gaa aacat ccgca gt aat ct cgc at ggt accaa 180
caaaagccag gt aagt cacc t aagct cct c gt gaat gt t g ct accaacct cgct gat ggt 240
gt gcct t cac gat t ct ct gg t t caggt t cc ggt accgat t at t cact t aa gat caact ca 300
ct ccaaccag aagat t t cgg t acat at t ac t gt caacact act ggggt ac gacct ggaca 360
t t cgggt caag gt act aagct ggaaat caag cgt acg 396
```

```
<210> 139
<211> 336
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> muCD37-12
```

```
<400> 139
gacat t gt gc t aacacagt c t cct gct t cc t t agct gt at ct ct ggggca gagggccacc 60
at ct cat gca gggccagcca aagt gt cagt acat ct agct at agt t at t t gt act ggt t c 120
cagcagaaac caggacagcc acccaaact c ct cat caagt at gcat ccaa cct agcat ct 180
ggggt ccct g ccaggt t cag t ggcagt ggg t ct gggacag act t caccct caacat ccat 240
cct gt ggagg aggaggat ac t gcaacat at t act gt caac acagt t ggga gat t ccgt ac 300
acgt t cggag gggggaccaa act ggaaat a aaacgg 336
```

```
<210> 140
<211> 408
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> chCD37-12
```

```
<400> 140
gaat t cgcca ccat gggt t g gt cct gt at a at cct gt t ct t ggt ggccac cgct act ggc 60
gt t cat agt g at at t gt act cact cagt ca ccagccagt c t ggcagt gt c cct gggccag 120
cgt gccacca t ct cct gccg ggcct cacag t ccgt gagca ct agct ct t a t t cct at ct c 180
t act ggt t t c aacagaagcc aggacagccc cct aagct gc t gat caagt a cgcct ccaac 240
ct cgccagcg gcgt t cccgc tagat t ct ct ggt t ccggt a gcggaact ga t t t cact t t g 300
aacat ccacc ccgt t gagga agaggat acc gccact t act at t gt caaca ct ct t gggag 360
at t cct t aca cct t t ggagg aggaacaaag ct cgaaat t a agcgt acg 408
```

```
<210> 141
<211> 321
<212> DNA
<213> Artificial Sequence
```

2921032PC01SequenceLi st i ng. t xt

<220>

<223> muCD37-38

<400> 141

caaat t g t t c t c a c c c a g t c t c c a g c a a t c a t g t c t g c a t c t c c a g g g g a g a a g g t c a c c	60
a t g a c c t g c a g t g c c a g c t c a a g t g t a a c t t a c a t g c a c t g g t a c c a g c a g a a g t c a g g c	120
a c c t c c c c c a a a a g a t g g a t t t a t g a c a c a t c c a a a c t g g c t t c t g g a g t c c c t g c t c g c	180
t t c a g t g g c g g t g g g t c t g g g a c c t c t t a c t c t c t c a c a a t c a g c a g c a t g g a g g c t g a a	240
g a t g c t g c c a c t t a t t a c t g c c a g c a g t g g a t t a g t a a c c c a c c c a c g t t c g g a g g g g g g	300
a c c a a g c t g g a a a t t a a a c g g	321

<210> 142

<211> 393

<212> DNA

<213> Artificial Sequence

<220>

<223> chCD37-38

<400> 142

g a a t t c g c c a c c a t g g g c t g g t c c t g t a t c a t c c t g t t t c t c g t g g c c a c a g c t a c a g g t	60
g t t c a t t c t c a g a t t g t g c t g a c c c a a t c a c c a g c t a t t a t g t c c g c t a g c c c c g g c g a g	120
a a a g t g a c a a t g a c a t g t a g c g c t a g c t c t t c t g t g a c t t a c a t g c a t t g g t a t c a a c a g	180
a a g t c a g g t a c c a g t c c c a a g c g t t g g a t c t a c g a c a c a t c c a a a c t g g c c t c c g g a g t c	240
c c t g c c a g g t t c a g c g g a g g t g g g t c c g g c a c c a g t t a t t c a c t g a c c a t a t c c t c t a t g	300
g a a g c t g a a g a t g c t g c t a c t t a t t a t t g t c a a c a a t g g a t t t c t a a c c c c c c a c c t t t	360
g g t g g c g g a a c a a g c t g g a g a t c a a g c g t a c g	393

<210> 143

<211> 393

<212> DNA

<213> Artificial Sequence

<220>

<223> huCD37-38

<400> 143

g a a t t c g c c a c c a t g g g a t g g t c c t g c a t t a t t c t g t t c t t g g t c g c c a c t g c t a c t g g c	60
g t t c a c t c t g a c a t t g t g c t c a c a c a g t c t c c a g c c t c a a t g t c t g c t t c c c c g g t g a g	120
c g g g t g a c c a t g a c a t g c t c t g c c a g t t c c t c c g t g a c a t a t a t g c a t t g g t a t c a g c a a	180
a a a c c c g g t a c c t c t c c a a a a a g a t g g a t c t a c g a c a c t t c a a a g c t t g c a t c a g g c g t t	240
c c t g c c a g a t t t t c c g g g t c t g g g t c t g g c a c t t c a t a c a g t c t g a c c a t t a g t t c c a t g	300
g a a g c t g a a g a t g c a g c c a c c t a t t a c t g t c a g c a g t g g a t t t c a a a t c c t c c t a c c t t c	360
g g c g g c g g a a c c a a a c t g g a g a t a a a g c g t a c g	393

<210> 144

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> muCD37-50

<400> 144

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caaat t g t t c t c a c c c a g t c t c c a g c a a t c a t g t c t g c a t c t c c a g g g g a g a a g g t c a c c      60
a t g a c c t g c a g t g c c a c c t c a a g t g t g a c t t a c a t g c a c t g g t a c c a g c a g a a g t c a g g c      120
a c c t c c c c c a a a a g a t g g a t t t a t g a c a c a t c c a a a c t g c t t a t g g a g t c c c t g g t c g t      180
t t c a g t g g t a g t g g g t c t g g g a c c t c t t a c t c t c t c a c a a t c a g c a g c a t g g a g g c t g a a      240
g a t g c t g c c a c t t a t t a c t g c c a g c a g t g g a g t g a t a a c c c a c c c a c g t t c g g c t c g g g g      300
a c a a a g t t g g a a a t a a a g c g g      321

```

<210> 145

<211> 393

<212> DNA

<213> Artificial Sequence

<220>

<223> huCD37-50

<400> 145

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g a a t t c g c c a c c a t g g g t t g g t c a t g c a t t a t t c t g t t c c t g g t t g c t a c c g c a a c a g g a      60
g t a c a t a g t g a g a t a g t c c t c a c c c a a a g t c c t g c t a c t a t g t c t g c c a g c c c a g g a g a g      120
c g t g t g a c c a t g a c t t g c t c t g c a a c c t c a a g t g t g a c a t a c a t g c a t t g g t a t c a g c a a      180
a a g c c t g g c c a a t c c c c t a a a a g g t g g a t c t a c g a t a c t t c t a a t c t g c c a t a c g g t g t g      240
c c c g c a a g g t t c t c c g g g a g t g g c a g t g g c a c c a g t t a t a g t c t g a c c a t c a g t t c a a t g      300
g a a g c a g a g g a t g c a g c a a c c t a t t a t t g t c a g c a g t g g t c c g a t a a t c c c c c t a c t t t t      360
g g t c a g g g t a c a a g c t g g a g a t t a a g c g t a c g      393

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<210> 146

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> muCD37-51

<400> 146

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c a a a t t g t t c t c a c c c a g t c t c c a g c a a t c a t g t c t g c a t c t c c a g g g g a g a a g g t c a c c      60
a t g a c c t g c a g t g c c a c c t c a a g t g t g a c t t a c a t g c a c t g g t a c c a g c a g a a g t c a g g c      120
a c c t c c c c c a a a a g a t g g a t t t a t g a c a c a t c c a a a c t g g c t t c t g g a g t c c c t g c t c g c      180
t t c a g t g g c a g t g g g t c t g g g a c c t c t t a c t c t c t c a c a a t c a g c a a c a t g g a g g c t g a a      240
g a t g c t g c c a c t t a t t a c t g c c a g c a g t g g a g t a g t a a c c c a c c c a c g t t c g g c t c g g g g      300
a c a a a g t t g g a a a t a a a g c g g      321

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<210> 147

<211> 393

<212> DNA

<213> Artificial Sequence

<220>

<223> huCD37- 51

<400> 147

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gtccattccg agatagtcct caccagagc cccgcaacca t gagtgcctc ccctggggag      120
cgagtgacta tgacttgttc cgccacttct tcagttacct atatgcattg gtatcagcag      180
aaacctggac agtctccaaa gcgttggatt tacgacacct ccaacctggc ttcaggagtt      240
cctgctaggt tcagcggatc tgggtctggc acaagttatt cactcaccat tagttccatg      300
gaggccgaag atgccgtac ttactactgt cagcagt gga gcagcaaccc ccctacattc      360
gggcagggaa ctaagctgga gatcaaactg acg                                     393

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<210> 148

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> muCD37- 56

<400> 148

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atgacctgca gtgccagttc aagtgttact t acatgcact ggtatcagca gaagtcaggc      120
acctccccca aaagatggat ttatgacaca tccaaactgg ctctctggagt ccctgctcgc      180
ttcagtggcg gtgggtctgg gacctcttac tctctcacia tcagcaccat ggaggctgaa      240
gatgctgcca cttattactg ccagcagtgg attagtgacc caccacgtt cggagggggg      300
accaagctgg aaataaaacg g                                     321

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<210> 149

<211> 393

<212> DNA

<213> Artificial Sequence

<220>

<223> huCD37- 56

<400> 149

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gttcactctg atattgtcct gacacagagt ccagccttca tgagtgttct tcccggagaa      120
aaggtcacia tgacttgttc agcttcctcc tccgtcacat acatgcattg gtaccagcag      180
aagcctgacc agagtcctaa gaggtggatc tatgatcaa gcaatctggc ttcgggtgtc      240
ccctcccgtc tttcaggcgg cggaagcggg actgactata gccttaccat ct cctcaatg      300
gaagccgagg acgctgctac atattactgc cagcaatgga tcagcgaccc tctactttc      360
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<210> 150

2921032PC01SequenceLi st i ng. t xt

<211> 321
<212> DNA
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<220>
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acctccccca aaagatggat ttatgacaca tccaaactgg ctctctggagt ccctgctcgc 180
ttcagtgcca gtgggtctgg gacctcttac tctctcacia t cagcagcat ggaggctgaa 240
gatgctgcca ctctattactg ccagcagtgga agtgataacc caccacgtt cggctcgggg 300
acaaagttgg aaataaagcg g 321

<210> 151
<211> 393
<212> DNA
<213> Artificial Sequence

<220>
<223> huCD37-57

<400> 151
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gttcaactccg agatcgtgtt gactcagagc ccagccacca tgtccgcttc ccccggggag 120
agagt gacaa tgacttgttc cgccacaagt tctgtaacct acatgcattg gtaccagcaa 180
aaaccaggac agagtccccg tcgttggatt tatgatacct ct aacctggc ttcaggcgtt 240
cctgcccgt tttctggtag tggatctggg acttctat a gccttaccat aagctctatg 300
gaagccgagg acgccgtac atactactgc cagcagtgga gtgat aacct cccaccttc 360
gggcaggga ccaaat tga gatcaaact acg 393

<210> 152
<211> 1410
<212> DNA
<213> Artificial Sequence

<220>
<223> chCD37-3

<400> 152
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ctgtccatt a catgcactgt ct cagggttc tcat taacca cctctggtgt aagctgggtt 180
cgccagcctc caggaaaggg tctggagtgg ctgggagt aa tatggggtga cgggagcaca 240
aactatcat t cagctctcaa atccagactg agcatcaaga aggatcactc caagagccaa 300
gttttcttaa aactgaacag tctgcaaact gatgacacag ccacgtacta ctgtgccaaa 360
ggaggctact cgttggctca ctggggccaa gggactctgg t cagactctc tgcagcctct 420

2921032PC01SequenceLi st i ng. t xt

acgaagggcc cat cagt t t t cccct t ggct ccaagt t ct a aat ccacaag cggt ggaaca	480
gct gcact gg gat gcct cgt t aaagat t at t t ccct gage ct gt gacagt gagct ggaat	540
agcggagcat t gact t cagg t gt gcacact t t t cccgct g t gt t gcagt c ct ccggt ct g	600
t act cact gt ccagt gt cgt aaccgt ccct t ct agcagct t gggaaccca gacct acat c	660
t gt aacgt ca accat aaacc at ccaacaca aaggt ggat a agaaggt t ga accaaagagc	720
t gt gat aaga cacat acat g ccct cct t gt cct gcaccag agct cct cgg aggt ccat ct	780
gt gt t cct gt t t ccccccaa acccaaggac act ct t at ga t ct ct cgt ac t ccagaggt c	840
acct gt gt t g t t gt cgacgt gagccat gaa gat cccgagg t t aaat t caa ct ggt acgt g	900
gat ggagt cg aggt t cacia t gccaaagacc aagcccaggg aggagcaat a t aat t ct aca	960
t at cgggt ag t gagcgt t ct gaccgt gct c caccaagat t ggct caat gg aaaagagt ac	1020
aagt gcaagg t gt ccaacaa ggct ct t ccc gct cccat t g agaaaact at ct ccaaagcc	1080
aaggggcagc cacgggaacc ccaggt gt at acat t gcccc cat ct agaga cgagct gacc	1140
aagaaccagg t gagt ct cac t t gt ct ggt c aaggggt t t t accct t ct ga cat t gct gt a	1200
gagt gggagt ct aacggaca gccagaaaac aact acaaga caact ccccc agt gct ggac	1260
agcgacggga gct t ct t cct ct act ccaag t t gact gt ag acaagt ct ag at ggcagcaa	1320
ggaaacgt t t t ct cct gct c agt aat gcat gaggct ct gc acaat cact a t acccagaaa	1380
t cact gt ccc t t agcccagg gt gact cgag	1410

<210> 153
 <211> 1410
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> huCD37- 3v1. 0

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gt gcact cac aagt ccaagt ccaagaat ct ggt ccaggt c t ggt ggcccc t t cccaaact	120
ct gagcat ca cct gt accgt t t ct ggt t t t agcct t acca cct ct ggt gt gagt t ggg t a	180
cgccaaccac ccggt aaggg t ct cgaat gg ct ggg t gt aa t ct ggggt ga t ggt t ccaca	240
aat t accat c ct t ccct caa gt cccgcct t agcat caaaa aggat cacag caaaagt caa	300
gt t t t cct ga aact gaat ag t ct gacagca gccgat acag ccacct act a t t gcgccaag	360
ggg ggt t at a gt ct t gcaca ct ggggt caa ggt accct cg t t accgt ct c ct cagct agt	420
accaagggcc cat cagt t t t cccct t ggct ccaagt t ct a aat ccacaag cggt ggaaca	480
gct gcact gg gat gcct cgt t aaagat t at t t ccct gage ct gt gacagt gagct ggaat	540
agcggagcat t gact t cagg t gt gcacact t t t cccgct g t gt t gcagt c ct ccggt ct g	600
t act cact gt ccagt gt cgt aaccgt ccct t ct agcagct t gggaaccca gacct acat c	660
t gt aacgt ca accat aaacc at ccaacaca aaggt ggat a agaaggt t ga accaaagagc	720

2921032PC01SequenceLi st i ng. t xt

t gt gat aaga cacat acat g ccct cct t gt cct gcaccag agct cct cgg aggt ccat ct	780
gt gt t cct gt t t ccccccaa acccaaggac act ct t at ga t ct ct cgt ac t ccagaggt c	840
acct gt gt t g t t gt cgacgt gagccat gaa gat cccgagg t t aaat t caa ct ggt acgt g	900
gat ggagt cg aggt t cacia t gccaaagacc aagcccaggg aggagcaat a t aat t ct aca	960
t at cgggt ag t gagcgt t ct gaccgt gct c caccaagat t ggct caat gg aaaagagt ac	1020
aagt gcaagg t gt ccaacaa ggct ct t ccc gct cccat t g agaaaact at ct ccaaagcc	1080
aaggggcagc cacgggaacc ccaggt gt at acat t gcccc cat ct agaga cgagct gacc	1140
aagaaccagg t gagt ct cac t t gt ct ggt c aaggggt t t t accct t ct ga cat t gct gt a	1200
gagt gggagt ct aacggaca gccagaaaac aact acaaga caact ccccc agt gct ggac	1260
agcgacggga gct t ct t cct ct act ccaag t t gact gt ag acaagt ct ag at ggcagcaa	1320
ggaaacgt t t t ct cct gct c agt aat gcat gaggct ct gc acaat cact a t acccagaaa	1380
t cact gt ccc t t agcccagg gt gact cgag	1410

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 <212> DNA
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<220>
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ct ct ct at ca ct t gt accgt t agcgggt t c t ct ct gacaa ccagt ggagt gagt t ggggt g	180
aggcagccac caggaaaggg act ggagt gg ct ggggggt ga t t t ggggcga cggcagcaca	240
aact at cat t ccagt ct t aa at ct cgg t t g t ccat t aaaa aagaccat ag t aaat ct caa	300
gt t t t cct ga aact caat ag cct gacagcc gcagacact g ct acgt at t a ct gcgccaaa	360
ggaggat aca gt ct ggct ca ct ggggacag gggaccct gg t gaccgt gt c at ccgcat ca	420
acaaagggcc cat cagt t t t cccct t ggct ccaagt t ct a aat ccacaag cggt ggaaca	480
gct gcact gg gat gcct cgt t aaagat t at t t cctt gage ct gt gacagt gagct ggaat	540
agcggagcat t gact t cagg t gt gcacact t t t cccgct g t gt t gcagt c ct ccggt ct g	600
t act cact gt ccagt gt cgt aaccgt cct t ct agcagct t gggaacca gacct acat c	660
t gt aacgt ca accat aaacc at ccaacaca aaggt ggat a agaaggt t ga accaaagagc	720
t gt gat aaga cacat acat g ccct cct t gt cct gcaccag agct cct cgg aggt ccat ct	780
gt gt t cct gt t t ccccccaa acccaaggac act ct t at ga t ct ct cgt ac t ccagaggt c	840
acct gt gt t g t t gt cgacgt gagccat gaa gat cccgagg t t aaat t caa ct ggt acgt g	900
gat ggagt cg aggt t cacia t gccaaagacc aagcccaggg aggagcaat a t aat t ct aca	960
t at cgggt ag t gagcgt t ct gaccgt gct c caccaagat t ggct caat gg aaaagagt ac	1020

2921032PC01SequenceLi st i ng. t xt

aagt gcaagg t gt ccaacaa ggct ct t ccc gct cccat t g agaaaact at ct ccaaagcc	1080
aaggggcagc cacgggaacc ccaggt gt at acat t gcccc cat ct agaga cgagct gacc	1140
aagaaccagg t gagt ct cac t t gt ct ggt c aaggggt t t t accct t ct ga cat t gct gt a	1200
gagt gggagt ct aacggaca gccagaaaac aact acaaga caact ccccc agt gct ggac	1260
agcgacggga gct t ct t cct ct act ccaag t t gact gt ag acaagt ct ag at ggcagcaa	1320
ggaaacgt t t t ct cct gct c agt aat gcat gaggct ct gc acaat cact a t acccagaaa	1380
t cact gt ccc t t agcccagg gt gact cgag	1410

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 <211> 1410
 <212> DNA
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<220>
 <223> chCD37-12

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gt gcaact cac agat t cagct ggt t caaagt ggcccagagc t gaaaaagcc aggggaaaca	120
gt gaaaaat aa gt t gcaaggc at ccggt t ac act t t cacia agt acggcat gaact ggggt c	180
aagcaggccc agggcaagg gct caaat gg at ggggt t gga t caat accaa cact ggcgag	240
t ct aggaat g ct gaggagt t t aagggccgg t t t gcct t ca gcct ggagac aagt gccagc	300
acagct t acc t gcaaat caa caat ct gaag t at gaggat a cagcaacct a t t t ct gcggc	360
cgcggcact g t cgt t gcaga ct ggggacaa ggt accacct t gact gt at c cagt gccagc	420
act aagggcc cat cagt t t t cccct t ggct ccaagt t ct a aat ccacaag cggt ggaaca	480
gct gcaact gg gat gcct cgt t aaagat t at t t ccct gagc ct gt gacagt gagct ggaat	540
agcggagcat t gact t cagg t gt gcacact t t t cccgct g t gt t gcagt c ct ccggt ct g	600
t act cact gt ccagt gt cgt aaccgt ccct t ct agcagct t gggaacca gacct acat c	660
t gt aacgt ca accat aaacc at ccaacaca aaggt ggat a agaaggt t ga accaaagagc	720
t gt gat aaga cacat acat g ccct cct t gt cct gcaccag agct cct cgg aggt ccat ct	780
gt gt t cct gt t t ccccccaa acccaaggac act ct t at ga t ct ct cgt ac t ccagaggt c	840
acct gt gt t g t t gt cgacgt gagccat gaa gat cccgagg t t aaat t caa ct ggt acgt g	900
gat ggagt cg aggt t cacia t gccaaagacc aagcccaggg aggagcaat a t aat t ct aca	960
t at cgggt ag t gacgt t ct gaccgt gct c caccaagat t ggct caat gg aaaagagt ac	1020
aagt gcaagg t gt ccaacaa ggct ct t ccc gct cccat t g agaaaact at ct ccaaagcc	1080
aaggggcagc cacgggaacc ccaggt gt at acat t gcccc cat ct agaga cgagct gacc	1140
aagaaccagg t gagt ct cac t t gt ct ggt c aaggggt t t t accct t ct ga cat t gct gt a	1200
gagt gggagt ct aacggaca gccagaaaac aact acaaga caact ccccc agt gct ggac	1260
agcgacggga gct t ct t cct ct act ccaag t t gact gt ag acaagt ct ag at ggcagcaa	1320

2921032PC01SequenceLi st i ng. t xt

ggaaacgt t t t c t c c t g c t c a g t a a t g c a t g a g g c t c t g c a c a a t c a c t a t a c c a g a a a 1380
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<210> 156
<211> 1424
<212> DNA
<213> A r t i f i c i a l S e q u e n c e

<220>
<223> c h C D 3 7 - 3 8

<400> 156
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g t c c a t t c c c a a g t g c a a c t c c a g g a a t c t g g c c c t g a c c t g g t t a a g c c a t c t c a g a g c 120
c t c t c c c t g a c c t g c a c t g t t a c a g g a t a c t c a a t c a c a t c a g g c t t t g g c t g g c a c t g g 180
a t c a g a c a a t t t c c c g g g a a c a a g t t g g a a t g g a t g g c t t a c a t t c t g t a t a g c g g g g g t 240
a c c g a t t a c a a t c c t t c c c t c a a g a g c c g a a t c t c t a t c a c c a g g g a t a c a a g c a a g a a c 300
c a a t t t t t t c t c c g c c t c a g c t c t g t g a c t a c c g a a g a t a c c g c t a c t t a c t a t t g t g c c 360
a g g g g c t a c t a t g g a t a t g g t g c a t g g t t c g t c t a t t g g g g c c a g g g a a c c c t g g t g a c t 420
g t g a g c g c t g c c t c t a c c a a g g c c c a t c a g t t t t c c c c t t g g c t c c a a g t t c t a a a t c c 480
a c a a g c g g t g g a a c a g c t g c a c t g g g a t g c c t c g t t a a a g a t t a t t t c c c t g a g c c t g t g 540
a c a g t g a g c t g g a a t a g c g g a g c a t t g a c t t c a g g t g t g c a c a c t t t t c c c g c t g t g t t g 600
c a g t c c t c c g g t c t g t a c t c a c t g t c c a g t g t c g t a a c c g t c c c t t c t a g c a g c t t g g g a 660
a c c c a g a c c t a c a t c t g t a a c g t c a a c c a t a a a c c a t c c a a c a c a a a g g t g g a t a a g a a g 720
g t t g a a c c a a a g a g c t g t g a t a a g a c a c a t a c a t g c c c t c c t t g t c c t g c a c c a g a g c t c 780
c t c g g a g g t c c a t c t g t g t t c c t g t t t c c c c c a a a c c c a a g g a c a c t c t t a t g a t c t c t 840
c g t a c t c c a g a g g t c a c c t g t g t t g t t g t c g a c g t g a g c c a t g a a g a t c c c g a g g t t a a a 900
t t c a a c t g g t a c g t g g a t g g a g t c g a g g t t c a c a a t g c c a a g a c c a a g c c c a g g g a g g a g 960
c a a t a t a a t t c t a c a t a t c g g g t a g t g a g c g t t c t g a c c g t g c t c c a c c a a g a t t g g c t c 1020
a a t g g a a a a g a g t a c a a g t g c a a g g t g t c c a a c a a g g c t c t t c c c g c t c c c a t t g a g a a a 1080
a c t a t c t c c a a a g c c a a g g g g c a g c c a c g g g a a c c c c a g g t g t a t a c a t t g c c c c c a t c t 1140
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t c t g a c a t t g c t g t a g a g t g g a g t c t a a c g g a c a g c c a g a a a c a a c t a c a a g a c a a c t 1260
c c c c c a g t g c t g g a c a g c g a c g g g a g c t t c t t c c t c t a c t c c a a g t t g a c t g t a g a c a a g 1320
t c t a g a t g g c a g c a a g g a a a c g t t t t c t c c t g c t c a g t a a t g c a t g a g g c t c t g c a c a a t 1380
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<211> 1425
<212> DNA
<213> A r t i f i c i a l S e q u e n c e

2921032PC01SequenceLi st i ng. t xt

<220>

<223> huCD37- 38

<400> 157

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ct cagt ct ca cct gt act gt ct ct ggct ac t ct at t acca gt ggggt t cgg ct ggcat t gg      180
at t aggcagt t t cccggt aa ggggct ggag t ggat ggcat at at cct gt a cagcggagga      240
accgat t aca acccaagt ct gaagagcagg at cagcat t a cccgggacac aagcaaaaac      300
cagt t t t t cc t t cggct gt c t agt gt t aca gct gcagaca ccgct act t a ct at t gt gct      360
cgggggt t act at ggct at gg ggct t ggt t t gt gt at t ggg gacaaggcac t ct t gt gacc      420
gt gagcagcg cct caacaaa gggcccat ca gt t t t cccct t ggct ccaag t t ct aaat cc      480
acaagcgggt g gaacagct gc act gggat gc ct cgt t aaag at t at t t ccc t gagcct gt g      540
acagt gagct ggaat agcgg agcat t gact t caggt gt gc aact t t t cc cgct gt gt t g      600
cagt cct ccg gt ct gt act c act gt ccagt gt cgt aaccg t ccct t ct ag cagct t ggga      660
accagacct acat ct gt aa cgt caaccat aaaccat cca acacaaaggt ggat aagaag      720
gt t gaaccaa agagct gt ga t aagacacat acat gccct c ct t gt cct gc accagagct c      780
ct cggaggt c cat ct gt gt t cct gt t t ccc cccaaaccca aggacact ct t at gat ct ct      840
cgt act ccag aggt cacct g t gt t gt t gt c gacgt gagcc at gaagat cc cgaggt t aaa      900
t t caact ggt acgt ggat gg agt cgaggt t cacaat gcca agaccaagcc cagggaggag      960
caat at aat t ct acat at cg ggt agt gage gt t ct gaccg t gct ccacca agat t ggct c      1020
aat ggaaaag agt acaagt g caaggt gt cc aacaaggct c t t cccgct cc cat t gagaaa      1080
act at ct cca aagccaaggg gcagccacgg gaaccccagg t gt at acat t gccccat ct      1140
agagacgagc t gaccaagaa ccaggt gagt ct cact t gt c t ggt caaggg gt t t t accct      1200
t ct gacat t g ct gt agagt g ggagt ct aac ggacagccag aaaacaact a caagacaact      1260
ccccagtg gc t ggacagcga cgggagct t c t t cct ct act ccaagt t gac t gt agacaag      1320
t ct agat ggc agcaaggaaa cgt t t t ct cc t gct cagt aa t gcat gaggc t ct gcacaat      1380
cact at accc agaaat cact gt ccct t agc ccagggt gac t cgag      1425

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<210> 158

<211> 1425

<212> DNA

<213> Artificial Sequence

<220>

<223> huCD37- 50

<400> 158

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aagctt gcca ccat ggggt g gt cct gcat a at cct t t t cc t ggt t gct ac t gct accgga      60
gt ccat t cac aggt gcagct gcaggagt cc ggccccggcc t gct caagcc t t ct cagagt      120
ct gagt ct ga ct t gt act gt t t ct ggct ac agcat aacca gcggt t t cgc t t ggcact gg      180

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2921032PC01SequenceLi st i ng. t xt

at cagacagc at cccggcaa caaact ggag t ggat gggat acat act gt a ct caggct ca	240
act gt ct at t cccct ccct gaaat cccgg at cagt at t a cccgt gacac t t ct aagaac	300
cat t t t t t c t gcagct gaa cagcgt t acc gcagct gaca ct gcaacct a ct act gt gcc	360
cggggat at t at ggat acgg agct t ggt t c gct t act ggg gccaaggcac cct cgt aact	420
gt gagt gct g ct t ccaccaa gggcccat ca gt t t t cccct t ggct ccaag t t ct aaat cc	480
acaagcggg g gaacagct gc act gggat gc ct cgt t aaag at t at t t ccc t gagcct gt g	540
acagt gagct ggaat agcgg agcat t gact t cagggt gt gc acact t t t cc cgct gt gt t g	600
cagt cct ccg gt ct gt act c act gt ccagt gt cgt aaccg t cct t ct ag cagct t ggga	660
accagacct acat ct gt aa cgt caaccat aaaccat cca acacaaagggt ggat aagaag	720
gt t gaaccaa agagct gt ga t aagacacat acat gccct c ct t gt cct gc accagagct c	780
ct cggaggt c cat ct gt gt t cct gt t t ccc cccaaaccca aggacact ct t at gat ct ct	840
cgt act ccag aggt cacct g t gt t gt t gt c gacgt gagcc at gaagat cc cgaggt t aaa	900
t t caact ggt acgt ggat gg agt cgaggt t cacaat gcca agaccaagcc cagggaggag	960
caat at aat t ct acat at cg ggt agt gacg gt t ct gaccg t gct ccacca agat t ggct c	1020
aat ggaaaag agt acaagt g caaggt gt cc aacaaggct c t t cccgct cc cat t gagaaa	1080
act at ct cca aagccaaggg gcagccacgg gaaccccagg t gt at acat t gcccccat ct	1140
agagacgagc t gaccaagaa ccaggt gagt ct cact t gt c t ggt caaggg gt t t t accct	1200
t ct gacat t g ct gt agagt g ggagt ct aac ggacagccag aaaacaact a caagacaact	1260
ccccagt gc t ggacagcga cgggagct t c t t cct ct act ccaagt t gac t gt agacaag	1320
t ct agat ggc agcaaggaaa cgt t t t ct cc t gct cagt aa t gcat gaggc t ct gcacaat	1380
cact at accc agaaat cact gt cct t agc ccagggt gac t cgag	1425

<210> 159
 <211> 1425
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> huCD37- 51

<400> 159	
aagct t gcca ccat ggg t t g gt ct t gcat c at cct gt t cc t ggt ggccac t gccact ggc	60
gt gcat t cag aagt t cagt t ggt ggagt cc ggcccagaag t gct gaaacc cggcgaat ca	120
ct gt cct ga ct t gt accgt gt cagg t t at agcat cagca gcggct t t gc t t ggcact gg	180
at t cggcagt t t ccaggcaa gggact ggaa t ggat gggct acat ccat t a cagt ggct ca	240
accaat t aca gccct agcct gcagggccga at ct ct at t a ccagggat ag t t ct at t aac	300
cagt t t t t cc t gcagct t aa t t ccgt gact gcct ct gaca cagcaact t a ct at t gcgcc	360
cgt ggct act acgggt t cgg agcct ggt t t gt at act ggg gt cagggcac cct ggt cact	420
gt ct cagccg cct ct accaa gggcccat ca gt t t t cccct t ggct ccaag t t ct aaat cc	480

2921032PC01SequenceLi st i ng. t xt

acaagcggg g gaacagct gc act gggat gc ct cgt t aaag at t at t t ccc t gagcct gt g	540
acagt gagct ggaat agcgg agcat t gact t caggt gt gc acact t t t cc cgct gt gt t g	600
cagt cct ccg gt ct gt act c act gt ccagt gt cgt aaccg t ccct t ct ag cagct t ggga	660
accagacct acat ct gt aa cgt caaccat aaaccat cca acacaaaggt ggat aagaag	720
gt t gaaccaa agagct gt ga t aagacacat acat gccct c ct t gt cct gc accagagct c	780
ct cggaggt c cat ct gt gt t cct gt t t ccc cccaaaccca aggacact ct t at gat ct ct	840
cgt act ccag aggt cacct g t gt t gt t gt c gacgt gagcc at gaagat cc cgaggt t aaa	900
t t caact ggt acgt ggat gg agt cgaggt t cacaat gcc a agaccaagcc cagggaggag	960
caat at aat t ct acat at cg ggt agt gagc gt t ct gaccg t gct ccacca agat t ggct c	1020
aat ggaaaag agt acaagt g caaggt gt cc aacaaggct c t t cccgct cc cat t gagaaa	1080
act at ct cca aagccaagg ggcagccacgg gaaccccagg t gt at acat t gccccat ct	1140
agagacgagc t gaccaagaa ccaggt gact ct cact t gt c t ggt caaggg gt t t t accct	1200
t ct gacat t g ct gt agagt g ggagt ct aac ggacagccag aaaacaact a caagacaact	1260
cccccagt gc t ggacagcga cgggagct t c t t cct ct act ccaagt t gac t gt agacaag	1320
t ct agat ggc agcaaggaaa cgt t t t ct cc t gct cagt aa t gcat gaggc t ct gcacaat	1380
cact at accc agaaat cact gt ccct t agc ccagggt gac t cgag	1425

<210> 160
 <211> 1425
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> huCD37- 56

<400> 160	
aagct t gcca ccat ggggt g gagct gcat t at cct gt t cc t cgt cgccac cgcaaccggc	60
gt ccaact ccc aggt gcagct gcaagaaagc gggccaggat t ggt aaaacc t t cccagt ct	120
ct gagt ct t a ct t gt accgt at ct ggat ac agt at cacat ct ggct t cgc ct ggcat t gg	180
at t cgccagt t t cccggcaa ggggct t gag t ggat ggggt at at t cat t a t t ct ggaggt	240
accaact aca accct t ccct gaagagt cga gt ct caat t a ccagggacac t t ccaagaac	300
caat t ct t t t t gcagct t aa t t cagt gacc gct gccgaca ccgct act t a ct act gcgcc	360
cggggct act at ggg t t t gg t gcct ggt t c gcct act ggg gccaggggac cct ggt gccc	420
gt gt ct gct g cct ccacaaa gggcccat ca gt t t t cccct t ggct ccaag t t ct aaat cc	480
acaagcggg g gaacagct gc act gggat gc ct cgt t aaag at t at t t ccc t gagcct gt g	540
acagt gagct ggaat agcgg agcat t gact t caggt gt gc acact t t t cc cgct gt gt t g	600
cagt cct ccg gt ct gt act c act gt ccagt gt cgt aaccg t ccct t ct ag cagct t ggga	660
accagacct acat ct gt aa cgt caaccat aaaccat cca acacaaaggt ggat aagaag	720
gt t gaaccaa agagct gt ga t aagacacat acat gccct c ct t gt cct gc accagagct c	780

2921032PC01SequenceLi st i ng. t xt

ct cggaggt c	cat ct gt gt t	cct gt t t ccc	cccaaacc	aggacact ct	t at gat ct ct	840
cgt act ccag	aggt cacct g	t gt t gt t gt c	gacgt gagcc	at gaagat cc	cgaggt t aaa	900
t t caact ggt	acgt ggat gg	agt cgaggt t	cacaat gcc	agaccaagcc	cagggaggag	960
caat at aat t	ct acat at cg	ggg agt gagc	gt t ct gaccg	t gct ccacca	agat t ggct c	1020
aat ggaaaag	agt acaagt g	caaggt gt cc	aacaaggct c	t t cccgct cc	cat t gagaaa	1080
act at ct cca	aagccaaggg	gcagccacgg	gaaccccagg	t gt at acat t	gcccccat ct	1140
agagacgagc	t gaccaagaa	ccaggt gagt	ct cact t gt c	t ggt caaggg	gt t t t accct	1200
t ct gacat t g	ct gt agagt g	ggagt ct aac	ggacagccag	aaaacaact a	caagacaact	1260
ccccaggt gc	t ggacagcga	cgggagct t c	t t cct ct act	ccaagt t gac	t gt agacaag	1320
t ct agat ggc	agcaaggaaa	cgt t t t ct cc	t gct cagt aa	t gcat gaggc	t ct gcacaat	1380
cact at accc	agaaat cact	gt ccct t agc	ccagggt gac	t cgag		1425

<210> 161
 <211> 1425
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> huCD37-57

<400> 161	
aagct t gcc	ccat gggct g
gagct gcat c	at t ct gt t t c
t ggt ggccac	agcaact ggc
60	
gt t cacagt c	aagt ccaact
gcaggagagc	ggccccggac
t cct gaaacc	at ct cagt ca
120	
ct cagt ct ga	cat gt act gt
gagcggct ac	agcat t acct
caggct t cgc	t t ggcat t gg
180	
at caggcagt	t ccccgga
aggt ct ggag	t ggat ggggt
acat t ct gt a	cagcggcagt
240	
acagt gt at t	caccct cct t
gaaat ct agg	at at caat ca
cacgt gat ac	aagcaaaaat
300	
cagt t ct t cc	t ccagct gaa
ct ccgt cacc	gccgcagaca
cagcaacct a	t t at t gt gct
360	
cgcggat act	acggat at gg
cgcgt ggt t c	gcct at t ggg
gccagggggac	act cgt gacc
420	
gt t t ccgccg	cct ccacaaa
gggcccac ca	gt t t t cccct
t ggct ccaag	t t ct aaat cc
480	
acaagcggg g	gaacagct gc
act gggat gc	ct cgt t aaag
at t at t t ccc	t gagcct gt g
540	
acagt gagct	ggaat agcgg
agcat t gact	t cagggt gt gc
acact t t t cc	cgct gt gt t g
600	
cagt cct ccg	gt ct gt act c
act gt ccagt	gt cgt aaccg
t ccct t ct ag	cagct t ggga
660	
accagacct	acat ct gt aa
cgt caaccat	aaaccat cca
acacaaaggt	ggat aagaag
720	
gt t gaaccaa	agagct gt ga
t aagacacat	acat gccct c
ct t gt cct gc	accagagct c
780	
ct cggaggt c	cat ct gt gt t
cct gt t t ccc	cccaaacc
aggacact ct	t at gat ct ct
840	
cgt act ccag	aggt cacct g
t gt t gt t gt c	gacgt gagcc
at gaagat cc	cgaggt t aaa
900	
t t caact ggt	acgt ggat gg
agt cgaggt t	cacaat gcc
agaccaagcc	cagggaggag
960	
caat at aat t	ct acat at cg
ggg agt gagc	gt t ct gaccg
t gct ccacca	agat t ggct c
1020	
aat ggaaaag	agt acaagt g
caaggt gt cc	aacaaggct c
t t cccgct cc	cat t gagaaa
1080	

2921032PC01SequenceLi st i ng. t xt

act at ct cca aagccaaggg gcagccacgg gaaccccagg t gt at acat t gcccccat ct	1140
agagacgagc t gaccaagaa ccagggt gagg ct cact t gt c t ggt caaggg gt t t t accct	1200
t ct gacat t g ct gt agagt g ggagt ct aac ggacagccag aaaacaact a caagacaact	1260
ccccagtg gc t ggacagcga cgggagct t c t t cct ct act ccaagt t gac t gt agacaag	1320
t ct agat ggc agcaaggaaa cgt t t t ct cc t gct cagt aa t gcat gaggc t ct gcacaat	1380
cact at accc agaaat cact gt ccct t agc ccagggt gac t cgag	1425

<210> 162
 <211> 717
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chCD37-3

<400> 162	
gaat t cgcca ccat gagggt g gcccact cag gt cct ggggt t gct gct gct gt ggct t aca	60
gat gccagat gt gacat cca gat gact cag t ct ccagcct ccct t t ct gt at ct gt ggga	120
gaaact gt ca ccat cacat g t cgagcaagt gagaat at t c gcagt aat t t agcat ggt at	180
cagcagaaac agggaaaat c t cct cagct c ct ggt caat g t t gcaacaaa ct t agcagat	240
gggt gt gccat caaggt t cag t ggcagt gga t caggcacac agt at t ccct caagat caac	300
agcct gcagt ct gaagat t t t gggact t at t act gt caac at t at t gggg t act acgt gg	360
acgt t cggt g gaggcaccaa gct ggaaat c aaacgt acgg t ggct gcacc at ct gt ct t c	420
at ct t cccgc cat ct gat ga gcagt t gaaa t ct ggaact g cct ct gt t gt gt gcct gct g	480
aat aact t ct at cccagaga ggccaaagt a cagt ggaagg t ggat aacgc cct ccaat cg	540
gggt aact ccc aggagagt gt cacagagcag gacagcaagg acagcacct a cagcct cagc	600
agcaccct ga cgct gagcaa agcagact ac gagaaacaca aagt ct acgc ct gcgaagt c	660
acccat cagg gcct gagct c gcccgt caca aagagct t ca acaggggaga gt gt t ag	717

<210> 163
 <211> 714
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> huCD37-3 (1.0 and 1.1)

<400> 163	
gaat t cgcca ccat ggggt t g gt cct gcat c at ct t gt t t c t cgt ggccac agccaccggt	60
gt t cact ct g at at acaaat gact caaagc cct t ccagt t t gagcgt aag t gt ggggt gaa	120
cgcgt aacaa t cacct gt ag agct agt gaa aacat ccgca gt aat ct cgc at ggt accaa	180
caaaagccag gt aagt cacc t aagct cct c gt gaat gt t g ct accaacct cgct gat ggt	240
gt gcct t cac gat t ct ct gg t t cagggt t cc ggt accgat t at t cact t aa gat caact ca	300
ct ccaaccag aagat t t cgg t acat at t ac t gt caacact act ggggt ac gacct ggaca	360

2921032PC01SequenceLi st i ng. t xt

t t cgg t caag g t act aagct g gaaat caag cgt acggt gg ct gcaccat c t gt ct t cat c	420
t t cccgccat ct gat gagca gt t gaaat ct ggaact gcct ct gt t gt gt g cct gct gaat	480
aact t ct at c ccagagaggc caaagt acag t ggaaggt gg at aacgccct ccaat cgggt	540
aact cccagg agagt gt cac agagcaggac agcaaggaca gcacct acag cct cagcagc	600
accct gacgc t gagcaaagc agact acgag aaacacaaag t ct acgcct g cgaagt cacc	660
cat cagggcc t gagct cgcc cgt cacaaag agct t caaca ggggagagt g t t ag	714

<210> 164
 <211> 726
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chCD37- 12

<400> 164 gaat t cgcca ccat ggg t t g gt cct gt at a at cct gt t ct t ggt ggccac cgct act ggc	60
gt t cat agt g at at t gt act cact cagt ca ccagccagt c t ggcagt gt c cct gggccag	120
cgt gccacca t ct cct gccg ggcct cacag t ccgt gagca ct agct ct t a t t cct at ct c	180
t act ggt t t c aacagaagcc aggacagccc cct aagct gc t gat caagt a cgcct ccaac	240
ct cgccagcg gcgt t cccgc t agat t ct ct ggt t ccggt a gcggaact ga t t t cact t t g	300
aacat ccacc ccgt t gagga agaggat acc gccact t act at t gt caaca ct ct t gggag	360
at t cct t aca cct t t ggagg aggaacaaag ct cgaaat t a agcgt acggt ggct gcacca	420
t ct gt ct t ca t ct t cccgcc at ct gat gag cagt t gaaat ct ggaact gc ct ct gt t gt g	480
t gcct gct ga at aact t ct a t cccagagag gccaaagt ac agt ggaaggt ggat aacgcc	540
ct ccaat cgg gt aact ccca ggagagt gt c acagagcagg acagcaagga cagcacct ac	600
agcct cagca gcacct gac gct gagcaaa gcagact acg agaaacacaa agt ct acgcc	660
t gcgaagt ca cccat caggg cct gagct cg cccgt cacia agagct t caa caggggagag	720
t gt t ag	726

<210> 165
 <211> 711
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> chCD37- 38

<400> 165 gaat t cgcca ccat gggct g gt cct gt at c at cct gt t t c t cgt ggccac agct acaggt	60
gt t cat t ct c agat t gt gct gaccaat ca ccagct at t a t gt ccgct ag ccccggcgag	120
aaagt gacaa t gacat gt ag cgct agct ct t ct gt gact t acat gcat t g gt at caacag	180
aagt caggt a ccagt cccaa gcgt t ggat c t acgacacat ccaaact ggc ct ccggagt c	240
cct gccaggt t cagcggagg t ggg t ccggc accagt t at t cact gacct at cct ct at g	300

2921032PC01SequenceLi st i ng. t xt

gaagct gaag at gct gct ac t t at t at t gt caacaat gga t t t ct aaccc cccacct t t	360
ggg ggcggaa caaagct gga gat caagcgt acggg ggct g caccat ct gt ct t cat ct t c	420
ccgccat ct g at gagcagt t gaaat ct gga act gcct ct g t t gt gt gcct gct gaat aac	480
t t ct at ccca gagaggccaa agt acagt gg aagggt ggat a acgccct cca at cgggt aac	540
t cccaggaga gt gt cacaga gcaggacagc aaggacagca cct acagcct cagcagcacc	600
ct gacgct ga gcaaagcaga ct acgagaaa cacaaagt ct acgcct gcga agt cacccat	660
cagggcct ga gct cgccccgt cacaaagagc t t caacaggg gagagt gt t a g	711

<210> 166
 <211> 711
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> huCD37-38

<400> 166	
gaat t cgcca ccat gggat g gt cct gcat t at t ct gt t ct t ggt cgccac t gct act ggc	60
gt t cact ct g acat t gt gct cacacagt ct ccagcct caa t gt ct gct t c ccccggt gag	120
cgggt gacca t gacat gct c t gccagt t cc t ccgt gacat at at gcat t g gt at cagcaa	180
aaacccggt a cct ct ccaaa aagat ggat c t acgacact t caaagct t gc at caggcgt t	240
cct gccagat t t t ccgggt c t ggggt ct ggc act t cat aca gt ct gaccat t agt t ccat g	300
gaagct gaag at gcagccac ct at t act gt cagcagt gga t t t caaat cc t cct acct t c	360
ggcggcgga ccaaact gga gat aaagcgt acggg ggct g caccat ct gt ct t cat ct t c	420
ccgccat ct g at gagcagt t gaaat ct gga act gcct ct g t t gt gt gcct gct gaat aac	480
t t ct at ccca gagaggccaa agt acagt gg aagggt ggat a acgccct cca at cgggt aac	540
t cccaggaga gt gt cacaga gcaggacagc aaggacagca cct acagcct cagcagcacc	600
ct gacgct ga gcaaagcaga ct acgagaaa cacaaagt ct acgcct gcga agt cacccat	660
cagggcct ga gct cgccccgt cacaaagagc t t caacaggg gagagt gt t a g	711

<210> 167
 <211> 711
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> huCD37-50

<400> 167	
gaat t cgcca ccat ggggt t g gt cat gcat t at t ct gt t cc t ggt t gct ac cgcaacagga	60
gt acat agt g agat agt cct caccctaaagt cct gct act a t gt ct gccag cccaggagag	120
cgt gt gacca t gact t gct c t gcaacct ca agt gt gacat acat gcat t g gt at cagcaa	180
aagcct ggcc aat cccct aa aagggt ggat c t acgat act t ct aat ct gcc at acgggt gt g	240
cccgaagggt t ct ccgggag t ggcagt ggc accagt t at a gt ct gaccat cagt t caat g	300

2921032PC01SequenceLi st i ng. t xt

gaagcagagg at gcagcaac ct at t at t gt cagcagt ggt ccgat aat cc ccct act t t t 360
 ggt caggggt a caaagct gga gat t aagcgt acgggt ggct g caccat ct gt ct t cat ct t c 420
 ccgccat ct g at gagcagt t gaaat ct gga act gcct ct g t t gt gt gcct gct gaat aac 480
 t t ct at ccca gagaggccaa agt acagt gg aagggt ggat a acgccct cca at cgggt aac 540
 t cccaggaga gt gt cacaga gcaggacagc aaggacagca cct acagcct cagcagcacc 600
 ct gacgct ga gcaaagcaga ct acgagaaa cacaaagt ct acgcct gcga agt cacccat 660
 cagggcct ga gct cgccccgt cacaaagagc t t caacaggg gagagt gt t a g 711

<210> 168
 <211> 711
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> huCD37-51

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