



US 20090298096A1

(19) **United States**(12) **Patent Application Publication**
Simard(10) **Pub. No.: US 2009/0298096 A1**(43) **Pub. Date: Dec. 3, 2009**(54) **INTERLEUKIN-1 ALPHA ABS AND
METHODS OF USE****Publication Classification**(75) Inventor: **John Simard**, Austin, TX (US)

Correspondence Address:

XBiotech, Inc.**12230 Forest Hill Blvd., Ste 116****Wellington, FL 33414 (US)**(73) Assignee: **XBiotech, Inc.**, Vancouver (CA)(21) Appl. No.: **12/455,458**(22) Filed: **Jun. 1, 2009**(51) **Int. Cl.****G01N 33/53** (2006.01)**C07K 16/00** (2006.01)**C07H 21/00** (2006.01)**C12N 5/00** (2006.01)**C12N 5/08** (2006.01)**G01N 33/68** (2006.01)**G01N 33/543** (2006.01)(52) **U.S. Cl. 435/7.21; 530/388.15; 536/23.53;
435/375; 435/366; 436/86; 436/518****Related U.S. Application Data**

(60) Provisional application No. 61/057,586, filed on May 30, 2008, provisional application No. 61/121,391, filed on Dec. 10, 2008, provisional application No. 61/178,350, filed on May 14, 2009.

(57) **ABSTRACT**Fully human monoclonal Abs includes (i) an antigen-binding variable region that exhibits very high binding affinity for IL-1 α and (ii) a constant region that is effective at both activating the complement system through C1q binding and binding to several different Fc receptors.

INTERLEUKIN-1 ALPHA ABS AND METHODS OF USE

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] The present application claims the priority of U.S. provisional patent applications Ser. Nos. 61/057,586; 61/121,391; and 61/178,350 filed on May 30, 2008; Dec. 10, 2008; and May 14, 2009, respectively.

STATEMENT AS TO FEDERALLY SPONSORED RESEARCH

[0002] Not applicable.

FIELD OF THE INVENTION

[0003] The invention relates generally to the fields of immunology, inflammation, cancer, vascular disorders, and medicine. More particularly, the invention relates to antibodies (Abs) which specifically bind interleukin-1 α (IL-1 α) and methods of using such Abs to treat, prevent, or detect a pathology associated with aberrant IL-1 α expression.

BACKGROUND

[0004] IL-1 α is pro-inflammatory cytokine that plays a role in a number of different activities including inflammation, immune responses, tumor metastasis, and hematopoiesis. IgG autoantibodies against IL-1 α occur naturally in the general human population and are thought to be beneficial in diseases such as atherosclerosis.

SUMMARY

[0005] The invention is based on the development of fully human monoclonal Abs (mAbs) that include (i) an antigen-binding variable region that exhibits very high binding affinity for human IL-1 α and (ii) a constant region that is effective at both activating the complement system through C1q binding and binding to several different Fc receptors. The IL-1 α specific mAbs described herein was made by replacing the constant region of a human IgG4 mAb having a variable region specific for human IL-1 α with the constant region of a human IgG1 mAb.

[0006] Accordingly, the invention features a purified human IgG1 mAb that specifically binds to human IL-1 α , the mAb including a heavy chain covalently joined to a light chain. The heavy chain can include the amino acid sequence of SEQ ID NO: 9 and the light chain can include the amino acid sequence of SEQ ID NO:11.

[0007] Also within the invention is a set of isolated nucleic acids including a first nucleic acid encoding the heavy chain of a human IgG1 mAb that specifically binds to IL-1 α , and a second nucleic acid encoding the light chain of the human IgG1 mAb that specifically binds to human IL-1 α . The first nucleic acid can encode the amino acid sequence of SEQ ID NO: 9 and the second nucleic acid can encode the amino acid sequence of SEQ ID NO:11. The first nucleic acid can include the nucleotide sequence of SEQ ID NO: 10 and the second nucleic acid can include the nucleotide sequence of SEQ ID NO:12.

[0008] In another aspect, the invention features an expression vector including a nucleic acid encoding the amino acid sequence of SEQ ID NO: 9 or SEQ ID NO: 11.

[0009] Another feature of the invention is an isolated host cell (e.g. a mammalian cell such as a CHO cell) including set of isolated nucleic acids including a first nucleic acid encoding the heavy chain of a human IgG1 mAb that specifically binds to IL-1 α , and a second nucleic acid encoding the light chain of the human IgG1 mAb that specifically binds to human IL-1 α . The heavy chain can include the amino acid sequence of SEQ ID NO: 9 and a light chain can include the amino acid sequence of SEQ ID NO:11.

[0010] The invention further features a method of killing a cell expressing human IL-1 α . This method can include the step of contacting the cell with a purified human IgG1 mAb that specifically binds to human IL-1 α .

[0011] A method of inhibiting migration of a human cell through a basement membrane matrix is also within the invention. This method can include the step of adding a purified mAb that specifically binds to human IL-1 α to a mixture including a basement membrane matrix and the human cell.

[0012] Further within the invention is a method of inhibiting an IL-1 α -induced increase in ICAM-1 and/or E-selectin expression on the surface of a human endothelial cell. This method can include the step of adding a purified mAb that specifically binds to human IL-1 α to a mixture including the endothelial cell and IL-1 α .

[0013] The invention additionally includes a method of tracking inflammation in a human subject previously subjected to the steps of: obtaining from the subject a first sample of peripheral blood mononuclear cells at a first time; contacting the first sample with a purified mAb that specifically binds to human IL-1 α ; and determining the percent of cells in the first sample that bind the monoclonal Ab.

[0014] This method can include the steps of: (a) obtaining from the subject a second sample of peripheral blood mononuclear cells at a second time; (b) contacting the second sample with the purified mAb that specifically binds to human IL-1 α ; (c) determining the percent of cells in the second sample that bind the monoclonal Ab; and (d) comparing the percent of cells in the first sample that bind the mAb to the percent of cells in the second sample that bind the monoclonal Ab.

[0015] In the foregoing methods, the purified mAb can be a human IgG1 mAb including a heavy chain covalently joined to a light chain, e.g., wherein the heavy chain includes the amino acid sequence of SEQ ID NO: 9 and the light chain includes the amino acid sequence of SEQ ID NO:11.

[0016] Another method within the invention features the steps of: (a) enriching a biological sample obtained from a human subject using a filter to separate molecules according to molecular weight into a first fraction including intact IgG complexed with IL-1 α and second fraction including molecules less than 100 Kda; and (b) quantifying the amount of IL-1 α in the first fraction.

[0017] Yet another method within the invention features the steps of: (a) enriching a sample of plasma obtained from a human subject using a filter that separates molecules according to molecular weight into a first fraction including intact IgG complexed with IL-1 α and second fraction including molecule less than 100 Kda; (b) adding the first fraction to a substrate including immobilized anti-human IgG Abs under conditions that allow IgG in the first fraction to specifically bind the anti-human IgG Abs immobilized on the substrate; (c) washing the substrate to remove material in the first fraction that does not specifically bind the immobilized anti-human IgG Abs; (d) contacting the substrate washed in step

(c) with an Ab that specifically binds human IL-1 α under conditions that allows the Ab that specifically binds human IL-1 α to specifically bind any human IL-1 α bound to the substrate; (e) washing the substrate to remove any of the Ab that specifically binds human IL-1 α that is not bound to the substrate; and (f) quantifying the amount of Ab that specifically binds human IL-1 α remaining bound to the substrate after step (e).

[0018] Unless otherwise defined, all technical terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Commonly understood definitions of biological terms can be found in Rieger et al., *Glossary of Genetics: Classical and Molecular*, 5th edition, Springer-Verlag: New York, 1991; and Lewin, *Genes V*, Oxford University Press: New York, 1994.

[0019] The term “specifically binds”, as used herein, when referring to a polypeptide (including Abs) or receptor, refers to a binding reaction which is determinative of the presence of the protein or polypeptide or receptor in a heterogeneous population of proteins and other biologics. Thus, under designated conditions (e.g. immunoassay conditions in the case of an Ab), the specified ligand or Ab binds to its particular “target” and does not bind in a significant amount to other proteins present in the sample or to other proteins to which the ligand or Ab may come in contact in an organism. Generally, a first molecule that “specifically binds” a second molecule has an equilibrium affinity constant greater than about 10^5 (e.g., 10^6 , 10^7 , 10^8 , 10^9 , 10^{10} , 10^{11} , and 10^{12} or more) liters/mole for that second molecule.

[0020] When referring to a protein molecule such as an Ab, “purified” means separated from components that naturally accompany such molecules. Typically, an Ab or protein is purified when it is at least about 10% (e.g., 9%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, 99.9%, and 100%), by weight, free from the non-Ab proteins or other naturally-occurring organic molecules with which it is naturally associated. Purity can be measured by any appropriate method, e.g., column chromatography, polyacrylamide gel electrophoresis, or HPLC analysis. A chemically-synthesized protein or other recombinant protein produced in a cell type other than the cell type in which it naturally occurs is “purified.”

[0021] Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions will control. In addition, the particular embodiments discussed below are illustrative only and not intended to be limiting.

DETAILED DESCRIPTION

[0022] The invention encompasses compositions and methods relating to fully human mAbs that include (i) an antigen-binding variable region that exhibits very high binding affinity for IL-1 α and (ii) a constant region that is effective at both activating the complement system through C1q binding and binding to several different Fc receptors. The below described preferred embodiments illustrate adaptation of these compositions and methods. Nonetheless, from the description of these embodiments, other aspects of the invention can be made and/or practiced based on the description provided below.

[0023] Methods involving conventional immunological and molecular biological techniques are described herein. Immunological methods (for example, assays for detection and localization of antigen-Ab complexes, immunoprecipitation, immunoblotting, and the like) are generally known in the art and described in methodology treatises such as *Current Protocols in Immunology*, Coligan et al., ed., John Wiley & Sons, New York. Techniques of molecular biology are described in detail in treatises such as *Molecular Cloning: A Laboratory Manual*, 2nd ed., vol. 1-3, Sambrook et al., ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 2001; and *Current Protocols in Molecular Biology*, Ausubel et al., ed., Greene Publishing and Wiley-Interscience, New York. Ab methods are described in *Handbook of Therapeutic Abs*, Dubel, S., ed., Wiley-VCH, 2007. Cell culture techniques are generally known in the art and are described in detail in methodology treatises such as *Culture of Animal Cells: A Manual of Basic Technique*, 4th edition, by R. Ian Freshney, Wiley-Liss, Hoboken, N.J., 2000; and *General Techniques of Cell Culture*, by Maureen A. Harrison and Ian F. Rae, Cambridge University Press, Cambridge, UK, 1994. Methods of protein purification are discussed in *Guide to Protein Purification: Methods in Enzymology*, Vol. 182, Deutscher M. P., ed., Academic Press, San Diego, Calif., 1990.

[0024] In one aspect, the invention features a fully human mAb that includes (i) an antigen-binding variable region that exhibits very high binding affinity for human IL-1 α and (ii) a constant region that is effective at both activating the complement system through C1q binding and binding to several different Fc receptors. The human Ab is preferably an IgG1. The K_a of the Ab is preferably at least $1 \times 10^9 \text{ M}^{-1}$ or greater (e.g., greater than $9 \times 10^{10} \text{ M}^{-1}$, $8 \times 10^{10} \text{ M}^{-1}$, $7 \times 10^{10} \text{ M}^{-1}$, $6 \times 10^{10} \text{ M}^{-1}$, $5 \times 10^{10} \text{ M}^{-1}$, $4 \times 10^{10} \text{ M}^{-1}$, $3 \times 10^{10} \text{ M}^{-1}$, $2 \times 10^{10} \text{ M}^{-1}$, or $1 \times 10^{10} \text{ M}^{-1}$).

[0025] Because B lymphocytes which express Ig specific for human IL-1 α occur naturally in human beings, a presently preferred method for raising mAbs is to first isolate such a B lymphocyte from a subject and then immortalize it so that it can be continuously replicated in culture. Subjects lacking large numbers of naturally occurring B lymphocytes which express Ig specific for human IL-1 α may be immunized with one or more human IL-1 α antigens to increase the number of such B lymphocytes. Human mAbs are prepared by immortalizing a human Ab secreting cell (e.g., a human plasma cell). See, e.g., U.S. Pat. No. 4,634,664.

[0026] In an exemplary method, one or more (e.g., 5, 10, 25, 50, 100, 1000, or more) human subjects (e.g., subjects not previously administered a human IL-1 α vaccine) are screened for the presence of such human IL-1 α -specific Ab in their blood. Those subjects that express the desired Ab can then be used as B lymphocyte donors. In one possible method, peripheral blood is obtained from a human donor that possesses B lymphocytes that express human IL-1 α -specific Ab. Such B lymphocytes are then isolated from the blood sample, e.g., by cells sorting (e.g., fluorescence activated cell sorting, “FACS”; or magnetic bead cell sorting) to select B lymphocytes expressing human IL-1 α -specific Ig. These cells can then be immortalized by viral transformation (e.g., using EBV) or by fusion to another immortalized cell such as a human myeloma according to known techniques. The B lymphocytes within this population that express Ig specific for human IL-1 α can then be isolated by limiting dilution methods (e.g., cells in wells of a microtiter plate that are positive for Ig specific for human IL-1 α are selected and subcultured,

and the process repeated until a desired clonal line can be isolated). See, e.g., Goding, *Monoclonal Abs: Principles and Practice*, pp. 59-103, Academic Press, 1986. Those clonal cell lines that express Ig having at least nanomolar or picomolar binding affinities for human IL-1 α are preferred. MAbs secreted by these clonal cell lines can be purified from the culture medium or a bodily fluid (e.g., ascites) by conventional Ig purification procedures such as salt cuts, size exclusion, ion exchange separation, and affinity chromatography.

[0027] Although immortalized B lymphocytes might be used in *in vitro* cultures to directly produce mAbs, in certain cases it might be desirable to use heterologous expression systems to produce mAbs. See, e.g., the methods described in U.S. patent application Ser. No. 11/754,899. For example, the genes encoding an mAb specific for human IL-1 α might be cloned and introduced into an expression vector (e.g., a plasmid-based expression vector) for expression in a heterologous host cell (e.g., CHO cells, COS cells, myeloma cells, and *E. coli* cells). Because Igs include heavy (H) and light (L) chains in an H₂L₂ configuration, the genes encoding each may be separately isolated and expressed in different vectors.

[0028] Although generally less preferred, chimeric mAbs (e.g., "humanized" mAbs), which are antigen-binding molecules having different portions derived from different animal species (e.g., variable region of a mouse Ig fused to the constant region of a human Ig), might be used in the invention. Such chimeric Abs can be prepared by methods known in the art. E. G., Morrison et al., *Proc. Nat'l. Acad. Sci. USA*, 81:6851, 1984; Neuberger et al., *Nature*, 312:604, 1984; Takeda et al., *Nature*, 314:452, 1984. Similarly, Abs can be humanized by methods known in the art. For example, monoclonal Abs with a desired binding specificity can be commercially humanized or as described in U.S. Pat. Nos. 5,693,762; 5,530,101; or 5,585,089.

[0029] The mAbs described herein might be affinity matured to enhance or otherwise alter their binding specificity by known methods such as VH and VL domain shuffling (Marks et al. *Bio/Technology* 10:779-783, 1992), random mutagenesis of the hypervariable regions (HVRs) and/or framework residues (Barbas et al. *Proc Nat. Acad. Sci. USA* 91:3809-3813, 1994; Schier et al. *Gene* 169:147-155, 1995; Yelton et al. *J. Immunol.* 155:1994-2004, 1995; Jackson et al., *J. Immunol.* 154(7):3310-9, 1995; and Hawkins et al., *J. Mol. Biol.* 226:889-896, 1992. Amino acid sequence variants of an Ab may be prepared by introducing appropriate changes into the nucleotide sequence encoding the Ab. In addition, modifications to nucleic acid sequences encoding mAbs might be altered (e.g., without changing the amino acid sequence of the mAb) for enhancing production of the mAb in certain expression systems (e.g., intron elimination and/or codon optimization for a given expression system). The mAbs described herein can also be modified by conjugation to another protein (e.g., another mAb) or non-protein molecule. For example, a mAb might be conjugated to a water soluble polymer such as polyethylene glycol or a carbon nanotube (See, e.g., Kam et al., *Proc. Natl. Acad. Sci. USA* 102: 11600-11605, 2005). See, U.S. patent application Ser. No. 11/754,899.

[0030] Preferably, to ensure that high titers of human IL-1 α -specific mAb can be administered to a subject with minimal adverse effects, the mAb compositions of the invention are at least 0.5, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 95, 96, 97, 98, 99, 99.9 or more percent by weight pure (excluding any excipients). The mAb compositions of the invention might include

only a single type of mAb (i.e., one produced from a single clonal B lymphocyte line) or might include a mixture of two or more (e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) different types of mAbs. In addition to human IL-1 α mAbs, the Ab compositions of the invention might also include other mAbs that specifically bind antigens other than human IL-1 α .

[0031] To modify or enhance their function, the human IL-1 α mAbs might be conjugated another molecule such as a cytotoxin or detectable label. A human IL-1 α specific mAb might be conjugated with one or more cytotoxins to more effectively kill cells expressing IL-1 α . Cytotoxins for use in the invention can be any cytotoxic agent (e.g., molecule that can kill a cell after contacting the cell) that can be conjugated to a human IL-1 α specific mAb. Examples of cytotoxins include, without limitation, radionuclides (e.g., ³⁵S, ¹⁴C, ³²P, ¹²⁵I, ¹³¹I, ⁹⁰Y, ⁸⁹Zr, ²⁰¹Tl, ¹⁸⁶Re, ¹⁸⁷Re, ⁵⁷Cu, ²¹³Bi, and ²¹¹At), conjugated radionuclides, and chemotherapeutic agents. Further examples of cytotoxins include, but are not limited to, antimetabolites (e.g., 5-fluorouracil (5-FU), methotrexate (MTX), fludarabine, etc.), anti-microtubule agents (e.g., vincristine, vinblastine, colchicine, taxanes (such as paclitaxel and docetaxel), etc.), alkylating agents (e.g., cyclophosphamide, melphalan, bischloroethylnitrosourea (BCNU), etc.), platinum agents (e.g., cisplatin (also termed cDDP), carboplatin, oxaliplatin, JM-216, CI-973, etc.), anthracyclines (e.g., doxorubicin, daunorubicin, etc.), antibiotic agents (e.g., mitomycin-C), topoisomerase inhibitors (e.g., etoposide, teniposide, and camptothecin), or other cytotoxic agents such as ricin, diphtheria toxin (DT), *Pseudomonas* exotoxin (PE) A, PE40, abrin, saporin, pokeweed viral protein, ethidium bromide, glucocorticoid, anthrax toxin and others. See, e.g., U.S. Pat. No. 5,932,188.

[0032] The human IL-1 α specific mAb can also be conjugated to a detectable label. Useful detectable labels in the present invention include biotin or streptavidin, magnetic beads, fluorescent dyes (e.g., fluorescein isothiocyanate, texas red, rhodamine, green fluorescent protein, and the like), radiolabels (e.g., ³H, ¹²⁵I, ³⁵S, ¹⁴C, ³²P, ¹¹¹In, ⁹⁷Ru, ⁶⁷Ga, ⁶⁸Ga, or ⁷²As), radioopaque substances such as metals for radioimaging, paramagnetic agents for magnetic resonance imaging, enzymes (e.g., horseradish peroxidase, alkaline phosphatase and others commonly used in an ELISA), and colorimetric labels such as colloidal gold or colored glass or plastic (e.g., polystyrene, polypropylene, latex, etc.) beads. Means of detecting such labels are well known to those of skill in the art. Thus, for example, radiolabels may be detected using photographic film or scintillation counters. Fluorescent markers may also be used and can be detected using a photodetector to detect emitted illumination. Enzymatic labels are typically detected by providing the enzyme with a substrate and detecting the reaction product produced by the action of the enzyme on the substrate, and colorimetric labels are detected by simply visualizing the colored label.

[0033] The present invention also encompasses nucleic acid molecules encoding fully human mAbs specific for human IL-1 α . Although the same nucleic acid molecule might encode both the heavy and light chains of a human IL-1 α -specific mAb, two different nucleic acid molecules, one encoding the heavy chain and the other encoding the light chain might also be used. The amino acid sequences of three IgG1 mAbs specific for human IL-1 α are presented herein. See SEQ ID NOs: 1, 3, 5, 7, 9, and 11. Exemplary nucleic acid molecules encoding these amino acid sequences are also described herein. See SEQ ID NOs: 2, 4, 6, 8, 10, and 12. Any

other suitable nucleic acid that encodes the amino acid sequences of the two described IgG1 mAbs or other mAbs within the invention might also be used.

[0034] For production of mAbs, the nucleic acid molecules of the invention might be incorporated into an expression vector in an orientation wherein such nucleic acid molecules are operatively linked to expression control sequences such as transcriptional and translational control sequences. Examples of expression vectors include vectors derived from plasmids and vectors derived from viruses such as adenoviruses, adeno-associated viruses, and retroviruses. The nucleic acid molecules encoding a light chain and a heavy chain might be incorporated into a single vector or different vectors. The vectors of the invention might also include regulatory sequences such as promoters and/or enhancers (see, U.S. Pat. No. 5,168,062, U.S. Pat. No. 4,510,245 and U.S. Pat. No. 4,968,615), selectable markers, or sequences encoding affinity tags (for facilitating purification) or a detectable label.

[0035] For production of mAbs, the vectors of the invention can be introduced into a suitable host cell, e.g., a prokaryotic cell such as a bacteria or, preferably, a eukaryotic cell such as mammalian, plant, or yeast host cell. Examples of methods for introducing heterologous polynucleotides into host cells include use of viral vectors, electroporation, encapsulation of the polynucleotide(s) in liposomes, dextran-mediated transfection, calcium phosphate precipitation, polybrene-mediated transfection, protoplast fusion, *Agrobacterium*-mediated transformation, biolistic transformation, and direct microinjection of the DNA into nuclei. Mammalian cell lines are presently preferred for expression of mAbs from vectors. Examples of mammalian host cells include Chinese hamster ovary (CHO) cells (e.g., the DG44 CHO cell line), HeLa cells, baby hamster kidney (BHK) cells, African green monkey kidney cells (COS), human hepatocellular carcinoma cells (e.g., Hep G2), NS0 cells, SP2 cells, HEK-293T cells, 293 Freestyle cells, and NIH-3T3 cells. The mAbs of the invention might also be expressed in transgenic animals or plants. See, e.g., U.S. Pat. Nos. 5,827,690; 5,756,687; 5,750,172; 5,741,957; 6,046,037; and 5,959,177.

[0036] The invention provides a method for detecting a human IL-1 α -expressing cell in a sample by contacting the cell with a human IL-1 α -specific mAb and detecting the mAb bound to the cell. The invention also provides a method for killing a human IL-1 α -expressing cell by contacting the cell with a human IL-1 α -specific mAb. Such killing can be accomplished by complement-mediated killing, Ab-dependent cell-mediated cytotoxicity, or Ab-mediated delivery of a cytotoxin. The Abs described herein have also been shown to be useful for other methods. For example, MABp1 has been to reduce IL-1 α induced ICAM1 and E-selectin expression on endothelial cells. MABp1 has also been shown to be used in immunoassays for detecting and quantifying IL-1 α in a biological sample.

EXAMPLES

Example 1

Cloning of Anti-hIL-1 α IgG1 and Kappa Chains

[0037] Variable region heavy chain (V-HC) and variable region light chain (V-LC) sequences were gene synthesized using amino acid sequence information provided in U.S. Pat. No. 5,959,085. V-HC was PCR amplified introducing HindIII/Clal sites upstream of the ATG start codon and a NheI site at the 3' end. The human germline IgG1 constant region (including exons and introns) was PCR amplified modifying the two 5' triplets encoding for the first two amino acids Ala-Ser to an NheI site, and introducing a BamHI site at the 3' end. The

human germline IgG1 constant region amino acid sequence corresponded to Swiss-Prot entry P01857, except for a K171Q and a V261L exchange. The V-HC and constant IgG1-HC sequence were ligated using the NheI site and cloned into pcDNA3 using HindIII and BamHI sites.

>hIL-1 α -IgG1-HC

(SEQ ID NO:1)

```
MEFGLSWVFLVALLRGVQCQVQLVESGGGVVQPGRSRLSCTASGFTFSM
FGVHVRQAPAGKGLWVAASVYDGSNKYYAESVKGRFTISRDNKNI LFL
QMDSLRLLED TAVVYCARGRPKVVIPAPLAHWGQGLVTFSSASTKGPSVF
PLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ
SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKEPKSCDKTHTC
PPCPAPPELLGGPSVFLFPPPKD TLMISRTPEVTVVDSVSHEDPEVKFN
WYVDGVEVHNAQTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTI SKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSD
IALEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFC
VMHEALHNHYTQKSLSLSPGK
```

>hIL-1 α -IgG1-FC

(SEQ ID NO:2)

```
atggagttcgggctgagttgggtgttctgggtggtctgctgctggggcgt
gcagtgccaggtgcagctggtggagagtggtgggtggcgtggtgcagcctg
gcccgtctctgcccgtctcttgcactgctccgggttttacctttctatg
tttgggtgtgcactgggtgcccaggtctcccggaaggagctggaaatgggt
ggccgcccgtgagttacgacgggtccaacaaatattacgctgagagcgtga
aaggcagattcaccatcagcagagataaattccaagaatattctgttctctg
cagatggacagctctgagactggaggacactgctgtgactactgctgctg
tggacgcctcaagtggtcatccccccccctggcacattggggccagg
gaactctggtgacctttctagcgtgacacacagggcccatcggtctctc
ccccggcaccctcctccaagagcactctgggggacagcggccctggg
ctgctgggtcaaggactactccccgaacgggtgacgggtgctgctggaaat
caggcgccctgaccagcggcgtccacaccttcccggctgctctacagctcc
tcaggactctactccctcagcagcgtagtgacgtgcccctccagcagctt
gggacccagacctaactctgcaacgtgaatcacaagcccagcacaaccca
aggtggacaagaaagttagagccaaatcttctgacaaaactcacacatgc
ccacgctgccagcactgaactcctggggggacgctcagctcttctctct
cccccaaaaacccaaggacacccctcatgactctccgggacccctgaggtca
catgctggtggtggacgtgagccacgaagacccctgaggtcaagtccaac
tggtacgtggacggcgtggaggtgcataatgccagacaaagcccgaggga
ggagcagtaaacagcagcgtaccgtgtggtcagcgtcctcaccgtcctgc
accaggaactggctgaatggcaaggagtaacagtgcaaggtctccaacaaa
gccctcccagcccccatcgagaaacacatctccaaagcacaagggcagcc
ccgagaaccacaggtgtacacccctgcccccatcccgggatgagctgacca
agaaccaggtcagcctgacctgacctgctgggtcaaggcttctatccagcgac
atcgccctggagtgaggagcaatgggcagccggagacaaactacaagac
cagcctcccgtgctggactccgacggctccttctcctctacagcagc
tcaccgtggacaagagcaggtggcagcaggggaacgtcttctcagctcc
gtgatgcatgaggtctgacacacccactacacgcagaagagcctcctct
aagtccgggaaaataa
```

[0038] The V-LC was PCR amplified introducing HindIII/Clal sites upstream of the ATG start codon and a BsiWI site at the 3' end. The human constant Kappa-LC sequence was PCR amplified introducing a 5' BsiWI site encoding an additional Arg and the first amino acids Thr, and a BamHI site at the 3' end. The human constant Kappa-LC amino acid sequence corresponded to Swiss-Prot entry P01834. V-HC and constant Kappa-LC sequences were ligated using the BsiWI site and cloned into pcDNA3 using HindIII and BamHI sites.

>hIL-1 α -K-LC

[SEQ ID NO:3]

```
MDMRVPAQLLGLLLWFPGSRCDIQMTQSPSSVSASVGDRTITCRASQ
ISSWLAWYQKPKGKAPKLLIYEASNLETGVPSRFGSGSGSDFTLTISL
QPEDFATYCCQQTSSFLSFGGKTKEHRTVAAPSVFIFPPSDEQLKSGT
ASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSLSTL
TLISKADYEKHIVYACEVTHQGLSSPVTKSFNRGEC
```

>hIL-1 α -K-LC

[SEQ ID NO:4]

```
atggacatgcgcgtgcccggccagctgctggggctgctgctgctggtt
ccctggatctaggtgcgacattcagatgaccagctccccagctcagtg
```

-continued

cagcctccgtggcgacagagtgacaatcacctgcccgcctctcagga
atctctagtgtggctggcctggtaccagcagaagcctggaaaggccccc
gctgctgatctatgaagcctccaaacctggagaccggcgtgcccctc
tcagcggctcaggtcagcagcagtgattttactctgacctcagctcc
cagccagaggatttgcctacttactactgcccagcagacctcttctt
gctgtccttcgggggagggcacaaggtggagcaccgtacgggtggc
catctgtctcattctccgcctcctgctgagcagtgaaatctggaac
gcctctgtgtgtgctgctgaataaactctatcccagagaggccaa
acagtggaaggtggataaacgcccctccaatcgggttaactcccag
tcacagagcaggacagcaaggacagcacctacagcctcagcagcac
acgctgagcaaaagcagactacgagaaacacaaagctcagcctgc
caccatcagggcctgagttcacgggtgacaaagagcttcaacagg
agtgttag

Example 2

Generation of NATHMAB-hIL-1a IgG1 and Kappa Chain

[0039] The complete sequence encoding the NATHMAB-hIL-1a/IgG1 heavy chain was gene synthesized. The V-HC sequence corresponded to the amino acid sequence described in U.S. Pat. No. 5,959,085. The human constant IgG1-HC sequence corresponded to Swiss-Prot entry P01857. The nucleotide sequence was codon optimized for expression in CHO cells. A Kozac sequence (gccacc) was added upstream of the start ATG.

>NATHMAB-hIL-1A-IGG1-HC

[SEQ ID NO:5]

MEFGLSWVFLVALLRGVQCQVQLVESGGGVVQPGSRSLRSLCTAGFTFSM
FGVHWVRQAPGKLEWVAASVYDGSNKYYAESVKGRFTISRDNKNILFL
QMDSLRLLEDVAVYCARGRPKVVIAPLAHWGQGLTVTFSSASTKGPSVF
PLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS
SGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKHTC
PPCPAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFN
WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPI EKKTSKAGGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFPYPSD
IAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS
VMHEALHNHYTQKSLSLSPGK

>NATHMAB-hIL-1A-IGG1-HC

[SEQ ID NO:6]

gccaccatggagtttggtctgtcctgggtgttcttggtggtctgtctgag
gggggtgcagtcgacaggtgcagctggtggagctggtgggggagtggtgc
agcctgggagatctctggcgtgtcttgcaactgcctcgtggttcaacttc
tctatgttggtgtgcatgggtcaggcaagcaccaggccaaggactcga
gtgggtgcagctgtgagctatgacgggtctaaacaaatattacgctgag
ctgtcaagggtgaggttaccatcagccgggataattccaaaatactctg
ttcctgcaaatggactctctgagggtggaagatactgcaatctactatgt
tgcaagggggaggccaaaggtggtgatccccgctccccctcgtcactggg
gacagggaacctgggtgactttcagctctgctagcaccaggccctagc
gtgttcccatggctccttccccaatctacttctggaggcaccgcgc
cctggggtgtctgctgaaagattatttctgagcccgctaccgctgagct
gggaacagcggcgccctgactagcggcgtgcacaccttcccgcagtgctg
caatctagcgggtgtactcctcagctctgtcgtgacctgcccctcag
cagcctcggaactcagacctacatctgcaatgtcaatcaaaacctcta
ataccaaagtcgataaagaaggtcgaaacctaaatcttgcgataaaacct
acctgcccccttgccagcaccgcgaactgctggcggtccctctgtgtt
tctgttcccccccaaaacaaagataacctgatgatctcaggaccccg
aggtcacttgtgtcgtggtggtggtgtgtcccacgaagatccagaagtcaa
ttcaactggtatgtggacgggtgcgaagtgcacacgcgaagacaaagcc
tagggaggaacagataaatagcacatatagggtggtcagcgtcctgaccg
tctgcatcaggactggtgaatggcaagaataaagtgtaaagtgtcc
aacaggccctgcccagcccaatcgaaaagacaatctctaaagccaagg
gcaaccccggaacctcaggtctatacactgccacctctcgggatgaac
tgacaaagatcaggtgagcctgacatgtctgtggaagggttttatccc
tccgacatggcgtggagtgaggagcaatggacaaccagaaaataacta
caaaaccacacccccctgctggactccgatggttctcttctctctact
ctaagctgacagtggaataagtctaggtggcagcagggtggtgtctcc
tgctctgtgatgcagggcagctgcacatcattatcacaaaagtctct
gtctctgtctccaggaaagtaa

[0040] The complete sequence encoding the NATHMAB-hIL-1a/Kappa light chain was gene synthesized. The V-LC sequence corresponded to the amino acid sequence described in U.S. Pat. No. 5,959,085. The human constant Kappa-LC sequence corresponded to Swiss-Prot entry P01834. The nucleotide sequence was codon optimized for expression in CHO cells. A Kozac sequence (gccacc) was added upstream of ATG.

>NATHMAB-hIL-1A-K-LC

[SEQ ID NO:7]

MDMRVPAQLLGLLLWFPGRCDIQMTQSPSSVSASVGRVITICRASQG
ISSWLAWYQQKPGKAPKLLIYEASNLETVPSRFRSGSGSGSDFTLTISL
QPEDFATYYCQQTSSFLSFSGGKVEHTVAAPSVFIFPPSDEQLKSGTA
SVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSLSSTLT
LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

NATHMAB-hIL-1A-K-LC

[SEQ ID NO:8]

gccaccatggacatgcgcgttctgcccagctcctcggaactgctgctgct
ttggttcccaggtcccgggtgtgatattcagatgacacagctcctcctc
cgtatctgcacccgtggcgacagggtcacaatcactgtaggccagc
caggggatctcagttggctcgcaggtaccacaaaagccaggttaaggc
tccgaaactgctcattacgaagctagtaccccgaaacaggcgtgccaa
ggcgggttagcgggtccgggttccgggttctgacttccacctcactattcc
tccctgcaacctgaggattttgccacataattactgtcagcaaaactcttc
tttctgctcctcttgggtgggggaaactaagggtggagcacacagtgccg
ccccagcgtctttatcttcccccaagcgatgaacagctgaaagttaggg
accgccagcgtggtctgctgctcaataattttaccctcgcgaggtctaa
gggtccaatggaaagtggataaacgcccctccagagcggtaactctcagg
ctgtcacagagcaagacagcaaggatagcacctattccctctccagacc
ctgacactgtctaaggccgactacgagaaacacaaagtgtacgcttctga
gggtgactcaccagggtgagtagccctgtgacaaaactcttcaatagg
gagatgctga

Example 3

Expression of NATHMAB-IL1-a (IgG1/k Subtype)

[0041] NATHMAB-IL-1 α was expressed and purified using a transient transfection method. Cell culture supernatant or protein G affinity purified Ab was subjected to further analysis as described below. Human embryonic kidney (HEK) 293T cells were cultured in DMEM containing 10% FCS, and transiently transfected using jetPEI reagent (Polyplus) according to manufacturer's protocol. Cells were seeded on 10 cm dishes (3×10^6 cells per 10 cm dish) 24 h prior to transfection to reach approximately 50% density at the time point of transfection. 5 μ g per dish of pcDNA3-anti-hIL-1 α -IgG1-HC and a 2-fold molar excess of pcDNA3-anti-hIL-1 α -Kappa were used for transfection. After recovery, medium was changed to DMEM containing 2% FCS (10 ml per dish) and Ab was collected for 5 to 6 days. The supernatant was collected, filtered, pH adjusted to 7.5-8, and stored at 4° C. until further use.

[0042] Part of the supernatant (250 ml) was incubated with protein G sepharose (GE Healthcare) for 3 h at 4° C. on a rotation wheel. Then, the protein G sepharose was loaded onto a gravity flow column and washed with PBS. Ab was eluted in 1 ml fractions using 100 mM glycine/150 mM NaCl into 100 μ l Tris (pH 8), followed by dialysis with PBS containing 10% glycerol. The total protein concentration of each fraction was measured using the BCA Protein Detection Kit (Pierce). Correct size of heavy and light chains, and of the assembled native Ab was confirmed by SDS-PAGE.

[0043] Supernatant containing NATHMAB-hIL-1 α purified Ab and Triton X-100 cell lysates of producer HEK 293T cells were tested for antigen binding in a radioimmunoassay (RIA) using ¹²⁵I-hIL-1 α . Binding was assayed by absorption

to protein G. All samples bound ^{125}I -hIL-1 α with highest activity in the eluate. Binding of purified NATHMAB-hIL-1 α in a concentration of 0.012% (half-max activity in RIA) to ^{125}I -hIL-1 α was used for measuring the affinity coefficient. The K_a of NATHMAB-hIL-1 α under these conditions was $3.03 \times 10^{10} \text{ M}^{-1}$. Back calculation revealed an estimated concentration of approximately 30 $\mu\text{g/ml}$ active anti-hIL-1 α -IgG in the purified eluate.

[0044] Neutralizing activity of NATHMAB-hIL1 α was tested in a bioassay using the murine EL4-6.1 subline which produces high levels of IL-2 when treated with murine or human IL-1 α (Zubler et al., J. Immunol. 134:3662-3668, 1985). The indicated concentrations of NATHMAB-hIL-1 α (eluate) were incubated for 30 min at 37° C. with various concentrations of recombinant hIL-1 α (eBioscience) in a final volume of 100 μl /well in a 96-well culture plate (flat bottomed). Each point was carried out in triplicate and in culture medium (DMEM, 5% FCS). To each well were added 100 μl of a suspension of EL4-6.1 cells (5×10^5 cells/ml) in culture medium containing 0.2 $\mu\text{g/ml}$ ionomycin. After incubation for 24 h at 37° C. in a 5% CO_2 incubator, cell free supernatants were harvested and assayed for IL-2 concentrations using a commercially available ELISA (R&D Systems). The results showed that NATHMAB-IL-1 α effectively neutralized hIL-1 α -induced IL-2 secretion by EL-4 cells.

[0045] To test for neutralization of membrane-bound hIL-1 α , the same EL-4 cell-based assay as described above was used with following modifications. Different concentrations of NATHMAB-hIL-1 α (eluate) were incubated with various numbers of human activated monocytes. For monocyte preparation, PBMC were isolated from buffy coat using Ficoll-Paque centrifugation. Monocytes were allowed to adhere for 1.5 h at 37° C. in RPMI on plastic dishes. Non-adherent lymphocytes were washed away to yield a nearly pure monocyte culture. Monocytes were cultured in RPMI containing Gln, Pyr, and 10% FCS for 24 h with LPS (1 $\mu\text{g/ml}$) at 37° C. in a 5% CO_2 incubator. Cells were detached with PBS/2 mM EDTA, carefully scraped from plates, and transferred into Falcon tubes. Cells were washed twice with PBS, resuspended in PBS/1% PFA and fixed for 10 min at 20° C. Cells were washed with glycine buffer (150 mM glycine, 75 mM NaCl, pH 7.4), then with culture medium and counted. The results showed that NATHMAB-hIL-1 α effectively neutralized IL-2 secretion by EL-4 cells induced by membrane-bound hIL-1 α . In an experiment similar to that described above, NATHMAB-hIL-1 α was tested for neutralization of murine IL-1 α . Indicated amounts of NATHMAB-hIL-1 α supernatant were incubated with recombinant human (h) or murine (m) IL-1 α (eBioscience). The supernatant containing the Ab neutralized human, but not murine, IL-1 α .

Example 4

Ab-Mediated Killing of Cancer Cells

[0046] Human peripheral blood mononuclear cells (PBMC) isolated from the buffy coat by standard Ficoll Paque preparation were incubated in either RPMI-1640 CM or RPMI-1640-CM containing rhIL-2 (30 ng/ml, ebioscience) at 37° C. and 5% CO_2 overnight and used as effector cells (E). THP1 cells were used as the targets (T). The assay was carried out in 96-well plates with each point in triplicate. After 1×10^4 targets that were incubated with different concentration of MABp1 for 15 mins, effector cells were added in an ET ratio of 25:1 and 50:1 to 1×10^4 targets and incubated for

another 4 hours. 75 μl of assay volume were transferred to a new 96-well plate and cytotoxicity was assayed using the LDH cytotoxicity detection kit (Roche) according to manufacturer's protocol. % specific lysis = (mean experimental release - mean spontaneous release without antibody) $\times 100$ / (mean maximal release from targets - mean spontaneous release from targets). A. untreated PBMC were used as effector cells. B. rhIL-2-treated PBMC were used as effector cells. In both cases, increasing concentrations (1.25 to 20 $\mu\text{g/ml}$) of MABp1 resulted in increased target cell killing (up to about 90%) at both ET ratios.

Example 5

Human Anti-IL1 α Specific mAb Sequences

[0047] The complete sequence encoding for another human anti-hIL-1 α IgG γ_1 /Kappa light chain specific for human IL1 α (MABp1) was synthesized and expressed as described above. In the nucleic acids encoding the heavy and light chains, a Kozac sequence (gccacc) was added upstream of the start ATG.

Heavy Chain

[0048]

[SEQ ID NO:9]
MEFGLSWFLVALLRGVQCQVQLVESGGGVVQPGSRSLRSLCTASGFTFSM
FGVHWVRQAPGKGLEWVAAYSYDGSNKYYAESVKGRFTISRDNKNI LFL
QMSDLRLLED TAVVYCARGRPKVVIPAPLAHWGQTLVTFSSASTKGPSVF
PLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSVHTFPAVLQS
SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRYEPKSCDKTHTC
PPCPAPELLGGPSVFLFPPPKDITLMISRTEPTCVVVDVSHEDPEVKFN
WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD
TAVIEWESNGQPENNYKTTPVLDSDGSFFFLYSKLTVDKSRWQQGNVFCSC
VMHEALHNHYTQKSLSLSPGK

[SEQ ID NO:10]
gccaccatggagtttggtctgtcctgggtgttcttggtggtctgctgag
gggggtgcagtgccaggtccagctgggtggagctctgggtggggagtggtgc
agcctgggagatctctcggtctgtcttgcaactgcctctggtttcactttc
tctatgtttggtgtgacttggtgcaggaagcaccaggcaaggactcga
gtgggtgcagctgtgagctatgacgggtctaacaaatattacgtgagct
ctgtcaagggtaggtttaccatcagccgggataattccaaaaatctctg
ttcctgcaaatggactctctgaggtctggaagatactgcagctctactattg
tgcaagggggaggccaaagggtggtgatccccgcctccctcgctcactggg
gacagggaaacctgggtgactttcagctctgctagcaccaggccctagc
gtgttcccatggctccttccctccaaatctactctggaggcaccgcgc
cctgggagtgctcgtgaaagattatttctgagcccgctcaccgtgagct
ggaacagcggcgccctgactagcggcgtgcacacctttcccgagtgctg
caatctagcgggtgtactcctgagctctgtcgtgacgtgcccctccag
cagcctcggaactcagacctacatctgcaatgtcaatcataaacctctca
ataccaaagtgcataagagggtcgaaacctaaatcttgcgataaaaacctat
acctgcccccttggccagcaccgaactgctggggcgtccctctgtgtt
tctgttcccccccaaaacaaagataacctgatgatctctaggaccctcg
aggctcacttgtgtcgtggtggatgtgtcccacgaagatccagaagtcaaa
ttcaactggtatgtggacgggtcgaaagtcacacagcaaaagaccagcc
tagggaggaaacagtataatagcacatataagggtggtcagcgtcctgaccg
tccatgcatcaggactggctgaatggcaaaagaataaagtgtaaagtgtcc
aacaaggccctgcccagccccaatcgaaaagacaatctctaaagccaaggg
gcaaccccggaacctcaggtctatacactgccacctctcgggaggaaa
tgaccagaatcagggtgagcctgacatgtctgtgaagggtttttatccc
tccgacatgcccgtggagtgaggagagcaatggacaaccagaaaataacta
caaaaccacacccctgtgctggaactccgatggttctcttctctact
ctaagctgacagtggttaagtctaggtggcagcagggaatgtgttctcc
tgctctgtgatgcacgaggaactgcacaatcattatcacaaaagtctct
gtctctgtctccaggaaagtaa

Light Chain

[0049]

[SEQ ID NO: 11]
 MDMRVPQAQLLGLLLWFPGRCDIQMTQSPSSVSASVGDRTITCRASQG
 ISSWLAWYQQKPKAPKLLIYEASNLETGVPSRFGSGSGSDFTLTISL
 QPEDFATYYCQQTSSFLSFGGKTKVEHKRTVAAPSVFIFPPSDEQLKSG
 TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSST
 LTLISKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

[SEQ ID NO: 12]
 gccaccatggacatgcgcgttctctgccagctcctcggactgctgctgct
 ttggttcccaggtcccggtgtgatattcagatgacacagctcctcctcct
 ccgtatctgcatccgtggcgacaggggcacacacacttctgtagggcagc
 caggggatctctagttggctcgcagtggtaccaacaaaagccaggttaaggc
 tccgaaactgctcatttacgaagctagtaacctcgaacagcgctgccaa
 gccggtttagcggctccggttccggttctgacttcacctcactatttcc
 tccctgcaacctgaggattttgccacataattactgtcagcaaaccttctc
 tttctgctctcctttggtggaggaactaaggtggagcacaagcggacag
 ttgctgctcctagcgtctttatcttccctccaaagcgatgaacagctgaag
 tcagggaccgcgcagcgtggtctgcctgctcaataattttaccctcgcga
 ggctaagggtccaatggaaagtgataaacgccctccagagcggtaactctc
 aggagtctgtccagagcaagacagcaaggatagcacctattccctctcc
 agcaccctgacactgtctaaaggcgcactacgagaaacacaaagtgtacgc
 ttgtgaggtgactcaccagggactgagtagccctgtgacaaaattcttca
 ataggggagaatgctga

Example 6

MABp1 Binding Affinity

[0050] The binding affinity of purified MABp1 was determined using surface plasmon resonance (SPR) on a BIAcore 2000 instrument (GE Health Sciences). A mouse monoclonal anti-human IgG (Fc) Ab was covalently immobilized on the flow cells of a CM5 sensor chip using a human Ab capture kit and amine coupling kit (GE Health Sciences). Immobilization levels of 8000-14000 RU would typically be achieved. After immobilization of the mouse anti-human IgG (Fc) capture Ab, three start-up cycles with HBS-EP running buffer (GE Health Sciences) and two start-up cycles with MABp1 were run to stabilize the CM5 surface and to remove any non-covalently bound Ab. For analysis, MABp1 Ab was diluted into HBS-EP running buffer to a final concentration of 1 µg/mL and immobilized to 700 RU on one flow cell of the CM5 sensor chip. Carrier-free human IL-1A cytokine (eBioscience, #34-8019) was serially diluted in HBS-EP running buffer over a test range from 100 nM to 0.05 nM. Flow rate was 30 µl/min. Dissociation data for each cytokine dilution was recorded for 15 minutes. The CM5 surface was regenerated after each cycle using a single injection of 3 M MgCl₂ for 25 seconds at a flow rate of 30 µl/min. BiaEvaluation software and a Langmuir binding model was used to fit the data. The K_D for MABp1 was determined to be less than 2.0×10¹⁰ M.

Example 7

MABp1 Inhibits Tumor Cell Invasion of a Basement Membrane Matrix

[0051] Matrigel (BD), a basement membrane matrix, was thawed at 4° C. overnight and the dilute (5 mg/ml to 1 mg/ml) in serum free cold cell culture media. 100 µl of the diluted matrigel was placed into the upper chambers of a 24-well transwell (Costar) and the transwell was incubated at 37° C. for at least 4 to 5 h for gelling. Tumor cells (MDA-MB-231 and THP-1) were harvested from tissue culture flasks by Trypsin/EDTA, washed with culture media, and resuspended in medium containing 1% FBS at a density of 1×10⁶ cells/ml. The gelled matrigel was gently washed with warmed serum free-culture media, and 100 µl of the cell suspension was

added in each well. The lower chamber of the transwell was filled with 600 µl of culture media, and the plates was incubated at 37° C. for 12 to 24 h. The cells that did not invade the matrigel were gently scraped off the top of each transwell with a cotton swab. The transwells were then removed from the 24-well plates and stained with crystal violet after fixing the invaded cells with 70% ethanol or methanol. The invaded cells were counted under a light microscope. The percent of cells invading the matrigel was significantly inhibited in the presence of MABp1.

Example 8

MABp1 Blocks Increase in ICAM1 Expression in Endothelial Cells

[0052] Human umbilical vein endothelial cells (HUVEC) (BD Biosciences) were seeded to 24-well plates at 5×10⁵ per well in 1 mL of M-200 medium supplemented with low-serum growth supplement (Invitrogen). Cells were allowed to settle for 3-4 hours. Medium was aspirated and a fresh 1 mL of M-200 was added per well. MABp1 was added directly to cells @ 4.26 µg/mL, co-incubated for 15 minutes at room temperature, and then recombinant human IL-1α (rhIL1A, eBioscience) was added to a final concentration of 40 pg/mL. Positive control wells received the addition of IL-1α only. HUVEC cells in the absence of IL-1α or the absence of MABp1 served as negative controls. After 17-20 hours incubation at 37° C., 5% CO₂, cells were lifted from the plates by a non-enzymatic treatment for 20 minutes using CellStripper reagent (Cellgro Mediatech) and then immediately assayed for CD54 (ICAM-1) expression using standard flow cytometry protocols. Staining buffer comprised Dulbecco's PBS supplemented with 2% heat-inactivated fetal bovine serum. PE-conjugated mouse anti-human CD54 (ICAM-1) mAb (eBioscience, clone HA58) or a PE-conjugated mouse IgG1k isotype control (eBioscience, #12-4714) were used per manufacturer's instructions to stain HUVEC cells in a 100 microliter staining volume for 20 minutes in the dark at room temperature. Two washes in staining buffer were subsequently performed and then samples were acquired on a FAC-SCalibur flow cytometer (BD Biosciences). Among several independent experiments (n=5) the upregulation of ICAM-1 adhesion molecules induced by rhIL1A on the surface of HUVEC cells was neutralized by MABp1 to baseline levels exhibited by the unstimulated HUVEC cells.

Example 9

MABp1 Blocks Increase in E-Selectin Expression in Endothelial Cells

[0053] Similar to its effects on ICAM-1 induction, MABp1-mediated neutralization of induction of CD62E (E-selectin) on HUVEC cells was also observed. This effect was most pronounced when HUVEC cells were stimulated not by soluble rhIL-1α but by membranous IL-1α anchored by glycosyl-phosphatidylinositol to the surface of DG44 CHO cells (GPI-IL1A cells). In this experiment, confluent cultures of HUVEC cells in 6-well plates were co-cultured overnight with 5×10⁶ GPI-IL1A DG44 cells in M-200 medium, either alone, in the presence of 10 µg/mL MABp1, or in the presence of 10 µg/mL D5 isotype control Ab. After 17-20 hours, HUVEC monolayers were washed extensively with Dulbecco's PBS and then lifted by non-enzymatic treatment for 20 minutes with CellStripper reagent (Cellgro Mediatech) and then immediately assayed for CD62E (E-selectin) expression using standard flow-cytometry protocols. Staining buffer comprised Dulbecco's PBS supplemented with 2%

heat-inactivated fetal bovine serum. PE-conjugated mouse anti-human CD62E mAb (eBioscience, clone P2H3) or a PE-conjugated mouse IgG1k isotype control (eBioscience, clone P3) were used per manufacturer's instructions to stain HUVEC cells in a 100 microliter staining volume for 20 minutes in the dark at room temperature. Two washes in staining buffer were subsequently performed and then samples were acquired on a FACSCalibur flow cytometer (BD Biosciences). Upregulated E-selectin expression on the surface of HUVEC cells induced by membranous GPI-IL-1 α was neutralized by MABp1 to baseline levels exhibited by unstimulated HUVEC cells.

Example 10

MRC-5 Bioassay for MABp1 Potency (Neutralization of rhIL1A)

[0054] The MRC-5 cell line, derived from fetal human lung fibroblasts, was obtained from the ATCC collection (CCL-171). The IL-1 neutralizing potency of MABp1 was assayed by measuring IL-1A induced release of IL-6 from MRC-5 cells. MRC-5 cells were seeded at 5×10^3 per well to a 96-well plate in 100 microliters of DMEM complete medium. Cells were cultured overnight at 37° C. in a humidified 5% CO₂ incubator. Confluent MRC-5 cells were subsequently cultured another 24 hours with 20 pg/mL of recombinant human IL-1A (rhIL1A, eBioscience) either alone or in the presence of increasing concentrations of MABp1. Negative control cells were not stimulated with rhIL1A. After the 24 hours, supernatants were collected and assayed for IL-6 release using and IL-6 ELISA kit from eBioscience. The IC₅₀, or concentration of MABp1 required to inhibit 50% of the maximal IL-6 release, was in the range of 0.001-0.01 μ g/mL.

Example 11

MABp 1 Identifies IL-1 α + Cells

[0055] One hundred microliters of sodium heparin anti-coagulated whole blood was aliquoted to polystyrene FACS tubes. Samples were incubated at room temperature for 15 minutes with 1 mg of human IgG (protein-A purified) plus 2 ml of heat-inactivated fetal bovine serum to block Fc receptors. Primary Abs were then added to the sample: Either 1 mg of Alexa-488 labeled MABp1, 1 mg of FITC-labeled monoclonal anti-membrane human IL1A Ab (FAB200F, R&D Systems), or 1 mg of a murine isotype control (IC002F, R&D Systems). Primary Abs were incubated with sample for 30 minutes at room temperature in the dark. Sample erythrocytes were then lysed (BD Biosciences PharmLyse solution) at room temperature for 15 minutes, centrifuged at 300 $\times$ g for 5 minutes, and aspirated. Sample pellets were washed three times with 1 mL Hank's balanced salt solution (HBSS) containing 2% heat-inactivated fetal bovine serum. Sample was resuspended in 0.3 mL HBSS+2% FBS and data was acquired on a FACSCalibur flow cytometer and analyzed using

CellQuest software. Flow cytometric analysis of human PBMC using MABp1 showed that only 0.2% of PBMC were positive for IL-1 α .

Example 12

MABp1 for Detecting and Tracking Infections and Inflammation

[0056] Flow cytometric analysis (as in Example 11) of human PBMC using MABp1 showed a 3.6-fold increase in the percent of PBMC positive for IL-1 α + in a subject with a sub-clinical infection compared to a normal control. Similarly, in a subject with an inflamed wisdom tooth, an increase in the percent of PBMC positive for IL-1 α +. A substantial decrease in the number of IL-1 α + PBMC was observed from 14 to 45 days after removal of the wisdom tooth.

Example 13

Immunoassay for Detecting and/or Quantifying IL-1 α

[0057] In general, very low levels of IL-1 α are present in the plasma of human subjects. Because these levels are often beyond the detection threshold of conventional immunoassays, an ELISA with improved sensitivity was developed. In this ELISA, exogenous anti-IL-1 α Ab (e.g., MABp1) can be added to a biological sample being tested (e.g., human plasma) under conditions that allow the Ab to bind IL-1 α in the sample. Because, it was observed that almost all IL-1 α in human plasma samples exists already bound to endogenous anti-IL-1 α Ab, the latter step can often be omitted. The sample with IL-1 α -Ab complexes is then applied to a filter (Amicon centrifugal device) with a molecular weight cutoff of about 100 kDa to separate the IL-1 α -Ab complexes from molecules in the sample less than the molecular weight cutoff. In one experiment, this resulted in a 50-fold concentration. The processed sample (and dilutions thereof) was then added to wells of a microtiter plate coated with an anti-human IgG capture Ab (2 μ g/ml mouse anti-human IgG, Fc-specific, Southern Biotech product code #9042-01). After allowing time to bind the IL-1 α -Ab complexes in the sample, the wells were washed to remove non-binding material. A labeled anti-human IL-1 α secondary Ab was then added to the wells (0.2 μ g/ml biotin-conjugated monoclonal mouse anti-human IL-1A Ab, clone CRM6, eBioscience catalog #13-7017). After allowing time to bind the IL-1 α in the wells, the plate was washed and the amount of labeled anti-human IL-1 α in each well was quantified as an indication of the concentration of IL-1 α in the sample being tested.

Other Embodiments

[0058] It is to be understood that while the invention has been described in conjunction with the detailed description thereof, the foregoing description is intended to illustrate and not limit the scope of the invention, which is defined by the scope of the appended claims. Other aspects, advantages, and modifications are within the scope of the following claims.

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 12

<210> SEQ ID NO 1

<211> LENGTH: 471

<212> TYPE: PRT

-continued

<213> ORGANISM: homo sapiens

<400> SEQUENCE: 1

```

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Leu Arg Gly
1      5      10      15
Val Gln Cys Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
20      25      30
Pro Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe
35      40      45
Ser Met Phe Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50      55      60
Glu Trp Val Ala Ala Val Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala
65      70      75      80
Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
85      90      95
Ile Leu Phe Leu Gln Met Asp Ser Leu Arg Leu Glu Asp Thr Ala Val
100     105     110
Tyr Tyr Cys Ala Arg Gly Arg Pro Lys Val Val Ile Pro Ala Pro Leu
115     120     125
Ala His Trp Gly Gln Gly Thr Leu Val Thr Phe Ser Ser Ala Ser Thr
130     135     140
Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145     150     155     160
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
165     170     175
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
180     185     190
Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
195     200     205
Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
210     215     220
Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
225     230     235     240
Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
245     250     255
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
260     265     270
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
275     280     285
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
290     295     300
Gly Val Glu Val His Asn Ala Gln Thr Lys Pro Arg Glu Glu Gln Tyr
305     310     315     320
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
325     330     335
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
340     345     350
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
355     360     365
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
370     375     380

```

-continued

Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp
385					390					395					400
Ile	Ala	Leu	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys
			405						410					415	
Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser
			420					425					430		
Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser
	435						440					445			
Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser
	450						455				460				
Leu	Ser	Leu	Ser	Pro	Gly	Lys									
465					470										

<210> SEQ ID NO 2

<211> LENGTH: 1416

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 2

```

atggagttcg ggctgagttg ggtgttcctg gtggctctgc tgcggggcgt gcagtgccag      60
gtgcagctgg tggagagtg gggtggcgtg gtgcagcctg gccggtctct gcgcctgtct      120
tgcactgcct ccggttttac cttttctatg tttggtgtgc actgggtgcg ccaggctccc      180
ggcaaggagc tggaatgggt ggccgcgctg agttacgacg ggtccaacaa atattacgct      240
gagagcgtga aaggcagatt caccatcagc agagataatt ccaagaatat tctgttcctg      300
cagatggaca gtctgagact ggaggacact gctgtgtact actgcgctcg tggacgccct      360
aaggtggtca tccccgcccc cctggcacat tggggccagg gaactctggt gaccttttct      420
agcgctagca ccaaggcccc atcgggtcttc cccctggcac cctcctccaa gagcacctct      480
gggggcacag cgccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg      540
tcgtggaact caggcgccct gaccagcggc gtccacacct tcccggtgt cctacagtcc      600
tcaggactct actccctcag cagcgtagtg accgtgccct ccagcagctt gggcaccag      660
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaagttgag      720
cccaaattct gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg      780
ggaccgtcag tcttctcttt cccccaaaa cccaaggaca ccctcatgat ctcccgacc      840
cctgaggtca catgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac      900
tggtacgtgg acggcgtgga ggtgcataat gccagacaa agccgcggga ggagcagtac      960
aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc     1020
aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc     1080
tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atccccggat     1140
gagctgacca agaaccaggt cagcctgacc tgctgtgtca aaggettcta tcccagcgac     1200
atcgccctgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc     1260
gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg     1320
tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac     1380
acgcagaaga gcctctcctt aagtccggga aaataa                                1416

```

<210> SEQ ID NO 3

-continued

<211> LENGTH: 235

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 3

```

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1             5             10             15

Phe Pro Gly Ser Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
          20             25             30

Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
      35             40             45

Gln Gly Ile Ser Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
 50             55             60

Ala Pro Lys Leu Leu Ile Tyr Glu Ala Ser Asn Leu Glu Thr Gly Val
 65             70             75             80

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp Phe Thr Leu Thr
      85             90             95

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
     100             105             110

Thr Ser Ser Phe Leu Leu Ser Phe Gly Gly Gly Thr Lys Val Glu His
     115             120             125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
     130             135             140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
     145             150             155             160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
     165             170             175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
     180             185             190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
     195             200             205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
     210             215             220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
     225             230             235

```

<210> SEQ ID NO 4

<211> LENGTH: 708

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 4

```

atggacatgc gcgtgccgc ccagctgctg gggctgctgc tgcgtgggtt ccctggatct      60
aggtgcgaca ttcagatgac ccagtcctcc agctcagtg cagcctccgt gggcgacaga      120
gtgacaatca cctgccgcgc ctctcaggga atctctagtt ggctggcctg gtaccagcag      180
aagcctggaa agggccccc aa gctgctgac tatgaagcct ccaacctgga gaccggcgtg      240
ccctctcgct tcagcggtc aggtcaggc agtgatttta ctctgacct cagctccctg      300
cagccagagg atttcgtac ttactactgc cagcagacct cttccttcct gctgtccttc      360
gggggaggca caaagtgga gcaccgtacg gtggctgcac catctgtctt catcttcccg      420
ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc      480
tatccagag agggccaaagt acagtgaag gtggataacg ccctccaatc gggtaactcc      540

```

-continued

```

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcacccctg    600
acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt caccatcag      660
ggcctgagtt caccggtgac aaagagcttc aacaggggag agtggttag                  708

```

```

<210> SEQ ID NO 5
<211> LENGTH: 471
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

```

```

<400> SEQUENCE: 5

```

```

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Leu Arg Gly
1      5      10      15
Val Gln Cys Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
20     25     30
Pro Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe
35     40     45
Ser Met Phe Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50     55     60
Glu Trp Val Ala Ala Val Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala
65     70     75     80
Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
85     90     95
Ile Leu Phe Leu Gln Met Asp Ser Leu Arg Leu Glu Asp Thr Ala Val
100    105    110
Tyr Tyr Cys Ala Arg Gly Arg Pro Lys Val Val Ile Pro Ala Pro Leu
115    120    125
Ala His Trp Gly Gln Gly Thr Leu Val Thr Phe Ser Ser Ala Ser Thr
130    135    140
Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145    150    155    160
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
165    170    175
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
180    185    190
Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
195    200    205
Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
210    215    220
Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
225    230    235    240
Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
245    250    255
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
260    265    270
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
275    280    285
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
290    295    300
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305    310    315    320
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp

```

-continued

325					330					335					
Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu
			340					345					350		
Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg
		355					360					365			
Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys
	370					375					380				
Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp
	385					390					395				400
Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys
			405					410						415	
Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser
			420					425					430		
Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser
		435					440					445			
Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser
		450					455					460			
Leu	Ser	Leu	Ser	Pro	Gly	Lys									
	465					470									

<210> SEQ ID NO 6

<211> LENGTH: 1422

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 6

```

gccaccatgg agtttgggtc gtctgggtg ttcttggtg ctctgctgag gggggtgcag    60
tgccagggtcc agctgggtgga gtctgggtggg ggagtgggtgc agcctgggag atctctgcgg    120
ctgtcttgca ctgcctctgg ttctactttc tctatgtttg gtgtgcattg ggtcaggcaa    180
gcaccaggca aaggactcga gtgggtcgca gctgtgagct atgacgggtc taacaaatat    240
tacgctgagt ctgtcaaggg taggtttacc atcagccggg ataattccaa aaatatactg    300
ttctgcaaaa tggactctct gaggttgaa gatactgcag tctactattg tgcaaggggg    360
aggccaaagg tggatgaccc cgctccctc gctcactggg gacagggaac cctggtgact    420
ttcagctctg ctagaccaa gggccctagc gtgttcccat tggctccttc ctccaaatct    480
acttctggag gcaccgccgc cctgggatgt ctctgtaaag attatcttcc tgagcccgtc    540
accgtgagct ggaacagcgg cgccctgact agcggcgtgc acacotttcc cgcagtgtcg    600
caatctagcg ggctgtactc cctgagctct gtcgtgaccg tgccctccag cagcctcgga    660
actcagacct acatctgcaa tgtcaatcat aaaccctcta ataccaaagt cgataagaag    720
gtcgaacctc aatcttgcca taaaacccat acctgcccc cttgccagc acccgaaactg    780
ctgggcggtc cctctgtgtt tctgttcccc cccaaacca aagataccct gatgatctct    840
aggacccccg aggtcacttg tgctgtggtg gatgtgtccc acgaagatcc agaagtcaaa    900
ttcaactggt atgtggacgg ggtcgaagtg cacaacgcaa agaccaagcc tagggaggaa    960
cagtataata gcacatatag ggtggtcagc gtctgaccg tcctgcatca ggactggctg   1020
aatggcaaag aatataagtg taaagtgtcc aacaaggccc tgccagcccc aatcgaaaag   1080
acaatctcta aagccaaggg gcaaccccg gaaacctcagg tctatacact gccaccctct   1140
cgggatgaac tgaccaagaa tcagggtgagc ctgacatgtc ttgtgaaggg tttttatccc   1200

```

-continued

```
tccgacattg ccgtaggagtg ggagagcaat ggacaaccag aaaataacta caaaaccaca 1260
ccccctgtgc tggactccga tggttccttc ttcctctact ctaagctgac agtggataag 1320
tctaggtggc agcaggggaa tgtgttctcc tgctctgtga tgcacgaggc actgcacaat 1380
cattatacac aaaagtctct gtctctgtct ccaggaaagt aa 1422
```

```
<210> SEQ ID NO 7
<211> LENGTH: 234
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
```

```
<400> SEQUENCE: 7
```

```
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp
1      5      10      15
Phe Pro Gly Ser Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
      20      25      30
Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
      35      40      45
Gln Gly Ile Ser Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
      50      55      60
Ala Pro Lys Leu Leu Ile Tyr Glu Ala Ser Asn Leu Glu Thr Gly Val
65      70      75      80
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp Phe Thr Leu Thr
      85      90      95
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
      100     105     110
Thr Ser Ser Phe Leu Leu Ser Phe Gly Gly Gly Thr Lys Val Glu His
      115     120     125
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
      130     135     140
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145     150     155     160
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
      165     170     175
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
      180     185     190
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
      195     200     205
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
      210     215     220
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225      230
```

```
<210> SEQ ID NO 8
<211> LENGTH: 711
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
```

```
<400> SEQUENCE: 8
```

```
gccaccatgg acatgcgcgt tcctgccag ctctcggac tgctgctgct ttggttccca 60
ggctcccggg gtgatattca gatgacacag tctccctcct ccgtatctgc atccgtgggc 120
gacagggtca caatcacttg tagggccagc caggggatct ctagtggct cgcattgtac 180
```

-continued

```

caacaaaagc caggttaaggc tccgaaactg ctcatttacg aagctagtaa cctcgaaaca    240
ggcgtgccaa gcgcgttttag cggctccggt tccggttctg acttcaccct cactatttcc    300
tccttgcaac ctgaggattt tgccacatat tactgtcagc aaacttcttc ttttctgctc    360
tcctttggtg ggggaactaa ggtggagcac acagtggcgc cccccagcgt ctttatcttc    420
cccccaagcg atgaacagct gaagtcaggg accgccagcg tggctcgcct gctcaataat    480
ttttaccctc gcgaggctaa ggtccaatgg aaagtggata acgcctcca gagcggtaac    540
tctcaggagt ctgtcacaga gcaagacagc aaggatagca cctattccct ctccagcacc    600
ctgacactgt ctaaggccga ctacagagaaa cacaaagtgt acgcttgtga ggtgactcac    660
cagggactga gtgacctgt gacaaaatct ttcaataggg gagaatgctg a              711

```

<210> SEQ ID NO 9

<211> LENGTH: 471

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 9

```

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Leu Arg Gly
1           5           10          15
Val Gln Cys Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
          20          25          30
Pro Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe
          35          40          45
Ser Met Phe Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
          50          55          60
Glu Trp Val Ala Ala Val Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala
65          70          75          80
Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
          85          90          95
Ile Leu Phe Leu Gln Met Asp Ser Leu Arg Leu Glu Asp Thr Ala Val
          100         105         110
Tyr Tyr Cys Ala Arg Gly Arg Pro Lys Val Val Ile Pro Ala Pro Leu
          115         120         125
Ala His Trp Gly Gln Gly Thr Leu Val Thr Phe Ser Ser Ala Ser Thr
          130         135         140
Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145         150         155         160
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
          165         170         175
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
          180         185         190
Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
          195         200         205
Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
          210         215         220
Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225         230         235         240
Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
          245         250         255
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
          260         265         270

```

-continued

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 275 280 285
 Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 290 295 300
 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
 305 310 315 320
 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 325 330 335
 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
 340 345 350
 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 355 360 365
 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
 370 375 380
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 385 390 395 400
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 405 410 415
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 420 425 430
 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
 435 440 445
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 450 455 460
 Leu Ser Leu Ser Pro Gly Lys
 465 470

<210> SEQ ID NO 10

<211> LENGTH: 1422

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 10

```

gccaccatgg agtttgggtct gtectgggtg ttcttgggtg ctctgctgag ggggggtgcag    60
tgccaggtcc agctgggtgga gtctgggtgg ggagtgggtc agcctgggag atctctgcgg    120
ctgtcttgca ctgcctctgg ttctactttc tctatgtttg gtgtgcattg ggtcaggcaa    180
gcaccaggca aaggactcga gtgggtcgca gctgtgagct atgacgggtc taacaaatat    240
tacgtgagat ctgtcaaggg taggtttacc atcagccggg ataattccaa aaatatcctg    300
ttcttgcaaa tggactctct gaggctggaa gatactgcag tctactattg tgcaaggggg    360
aggccaaagg tggatgaccc cgctcccttc gctcactggg gacaggaac cctgggtgact    420
ttcagctctg ctagaccaa gggccctagc gtgttcccat tggctccttc ctccaaatct    480
acttctggag gcaccgccg cctgggatgt ctctgaaag attattttcc tgagcccgctc    540
accgtgagct ggaacacgg cgccctgact agcggcgtgc acacctttcc cgcagtgtctg    600
caatctagcg ggctgtactc cctgagctct gtcgtgaccg tgccctccag cagcctcgga    660
actcagacct acatctgcaa tgtcaatcat aaacctcta ataccaaagt cgataagagg    720
gtcgaaacct aatcttgca taaaacctat acctgcccc cttgccagc acccgaaactg    780
ctggggcggtc cctctgtgtt tctgttcccc cccaaacca aagataccct gatgatctct    840

```

-continued

```

aggacccccg aggtcacttg tgctcgtggtg gatgtgtccc acgaagatcc agaagtcaaa    900
ttcaactggt atgtggacgg ggtcgaagtg cacaacgcaa agaccaagcc tagggaggaa    960
cagtataata gcacatatag ggtgggtcagc gtcctgaccg tctgcatca ggactggctg    1020
aatggcaaag aatataagtg taaagtgtcc aacaaggccc tgccagcccc aatcgaaaag    1080
acaatctcta aagccaaggg gcaacccccg gaacctcagg tctatacact gccaccctct    1140
cgggaggaaa tgaccaagaa tcaggtgagc ctgacatgtc ttgtgaaggg tttttatccc    1200
tccgacattg ccgtggagtg ggagagcaat ggacaaccag aaaataacta caaaaccaca    1260
ccccctgtgc tggactccga tggttccttc ttcctctact ctaagctgac agtggataag    1320
tctaggtggc agcaggggaa tgtgttctcc tgctctgtga tgcacgaggc actgcacaat    1380
cattatacac aaaagtctct gtctctgtct ccaggaaagt aa                        1422

```

<210> SEQ ID NO 11

<211> LENGTH: 236

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 11

```

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp
1          5          10          15
Phe Pro Gly Ser Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
20        25        30
Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
35        40        45
Gln Gly Ile Ser Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
50        55        60
Ala Pro Lys Leu Leu Ile Tyr Glu Ala Ser Asn Leu Glu Thr Gly Val
65        70        75        80
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp Phe Thr Leu Thr
85        90        95
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
100       105       110
Thr Ser Ser Phe Leu Leu Ser Phe Gly Gly Gly Thr Lys Val Glu His
115       120       125
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
130       135       140
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
145       150       155       160
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
165       170       175
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
180       185       190
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
195       200       205
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
210       215       220
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225       230       235

```

<210> SEQ ID NO 12

<211> LENGTH: 717

-continued

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 12

```

gccaccatgg acatgcgcgt tctgcccag ctctcggac tgetgctget ttggttccca    60
ggctcccggt gtgatattca gatgacacag tctccctcct cegtatctgc atccgtgggc    120
gacaggggtca caatcacttg tagggccagc caggggatct ctagtggct cgcattggta    180
caacaaaagc caggaagcg tccgaaactg ctcatattacg aagctagtaa cctcgaaaca    240
ggcgtgccaa gccggtttag cggtccgggt tccggttctg acttcacct cactatttcc    300
tccctgcaac ctgaggattt tgccacatat tactgtcagc aaactttctt tttctgtctc    360
tcctttgggtg gaggaactaa ggtggagcac aagcggacag ttgetgctcc tagcgtcttt    420
atcttccctc caagcgatga acagctgaag tcagggaccg ccagcgtggt ctgcctgctc    480
aataattttt accctcgcca ggctaaggtc caatggaaag tggataacgc cctccagagc    540
ggtaactctc aggagtctgt cacagagcaa gacagcaagg atagcaccta tccctctctc    600
agcaccctga cactgtctaa ggccgactac gagaaacaca aagtgtacgc ttgtgagggtg    660
actcaccagg gactgagtag ccctgtgaca aaatctttca ataggggaga atgctga      717

```

What is claimed is:

1-22. (canceled)

23. A purified human IgG1 mAb that specifically binds to human IL-1 α , the mAb comprising a heavy chain covalently joined to a light chain.

24. The purified human IgG1 monoclonal Ab of claim **23**, wherein the heavy chain comprises the amino acid sequence of SEQ ID NO: 9 and the light chain comprises the amino acid sequence of SEQ ID NO:11.

25. A set of isolated nucleic acids comprising a first nucleic acid encoding the heavy chain of a human IgG1 mAb that specifically binds to IL-1 α , and a second nucleic acid encoding the light chain of the human IgG1 mAb that specifically binds to human IL-1 α .

26. The set of isolated nucleic acids of claim **25**, wherein the first nucleic acid encodes the amino acid sequence of SEQ ID NO: 9 and the second nucleic acid encodes the amino acid sequence of SEQ ID NO:11.

27. The set of nucleic acids of claim **26**, wherein the first nucleic acid comprises the nucleotide sequence of SEQ ID NO: 10 and the second nucleic acid comprises the nucleotide sequence of SEQ ID NO:12.

28. The set of isolated nucleic acids of claim **25**, wherein the set of isolated nucleic acids is comprised within at least one expression vector.

29. The set of isolated nucleic acids of claim **26**, wherein the set of isolated nucleic acids is comprised within at least one expression vector.

30. The set of isolated nucleic acids of claim **27**, wherein the set of isolated nucleic acids is comprised within at least one expression vector.

31. The set of isolated nucleic acids of claim **25**, wherein the set of isolated nucleic acids is comprised within an isolated host cell.

32. The set of isolated nucleic acids of claim **26**, wherein the set of isolated nucleic acids is comprised within an isolated host cell.

33. The set of isolated nucleic acids of claim **32**, wherein the host cell is a mammalian cell.

34. A method of killing a cell expressing human IL-1 α , the method comprising the step of contacting the cell with a purified human IgG1 mAb that specifically binds to human IL-1 α .

35. The method of claim **34**, wherein the human IgG1 mAb comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 9 and a light chain comprising the amino acid sequence of SEQ ID NO:11.

36. A method of inhibiting migration of a cell through a basement membrane matrix, the method comprising the step of adding a purified mAb that specifically binds to human IL-1 α to a mixture comprising the basement membrane matrix and the cell.

37. The method of claim **36**, wherein the purified mAb is a human IgG1 mAb comprising a heavy chain covalently joined to a light chain.

38. The method of claim **37**, wherein the heavy chain comprises the amino acid sequence of SEQ ID NO: 9 and a light chain comprises the amino acid sequence of SEQ ID NO:11.

39. A method of inhibiting an IL-1 α -induced increase in expression of ICAM-1 or E-selectin on the surface of a human endothelial cell, the method comprising the step of adding a purified mAb that specifically binds to human IL-1 α to a mixture comprising the endothelial cell and IL-1 α .

40. The method of claim **39**, wherein the purified mAb is a human IgG1 mAb comprising a heavy chain covalently joined to a light chain.

41. The method of claim **40**, wherein the heavy chain comprises the amino acid sequence of SEQ ID NO: 9 and a light chain comprises the amino acid sequence of SEQ ID NO:11.

42. A method of tracking inflammation in a human subject previously subjected to the steps of: obtaining from the subject a first sample of peripheral blood mononuclear cells at a first time; contacting the first sample with a purified mAb that specifically binds to human IL-1 α ; and determining the per-

cent of cells in the first sample that bind the monoclonal Ab, the method comprising the steps of:

- (a) obtaining from the subject a second sample of peripheral blood mononuclear cells at a second time;
- (b) contacting the second sample with the purified mAb that specifically binds to human IL-1 α ;
- (c) determining the percent of cells in the second sample that bind the monoclonal Ab; and
- (d) comparing the percent of cells in the first sample that bind the mAb to the percent of cells in the second sample that bind the monoclonal Ab.

43. The method of claim **42**, wherein the purified mAb is a human IgG1 mAb comprising a heavy chain covalently joined to a light chain.

44. The method of claim **43**, wherein the heavy chain comprises the amino acid sequence of SEQ ID NO: 9 and a light chain comprises the amino acid sequence of SEQ ID NO: 1.

45. A method comprising the steps of:

- (a) enriching a biological sample obtained from a human subject using a filter that separates molecules according to molecular weight into a first fraction comprising intact IgG complexed with IL-1 α and second fraction comprising molecule less than 100 Kda; and
- (b) quantifying the amount of IL-1 α in the first fraction.

46. The method of claim **45**, comprising the steps of:

- (a) enriching a sample of plasma obtained from a human subject using a filter that separates molecules according to molecular weight into a first fraction comprising intact IgG complexed with IL-1 α and second fraction comprising molecules less than 100 Kda;
- (b) adding the first fraction to a substrate comprising immobilized anti-human IgG Abs under conditions that allow IgG in the first fraction to specifically bind the anti-human IgG Abs immobilized on the substrate;
- (c) washing the substrate to remove material in the first fraction that does not specifically bind the immobilized anti-human IgG Abs;
- (d) contacting the substrate washed in step (c) with an Ab that specifically binds human IL-1 α under conditions that allows the Ab that specifically binds human IL-1 α to specifically bind any human IL-1 α bound to the substrate;
- (e) washing the substrate to remove any of the Ab that specifically binds human IL-1 α that is not bound to the substrate; and
- (f) quantifying the amount of Ab that specifically binds human IL-1 α remaining bound to the substrate after step (e).

* * * * *

专利名称(译)	白细胞介素-1αABS和使用方法		
公开(公告)号	US20090298096A1	公开(公告)日	2009-12-03
申请号	US12/455458	申请日	2009-06-01
[标]申请(专利权)人(译)	埃克斯生物科技公司		
申请(专利权)人(译)	XBIOTECH INC.		
当前申请(专利权)人(译)	XBIOTECH INC.		
[标]发明人	SIMARD JOHN		
发明人	SIMARD, JOHN		
IPC分类号	G01N33/53 C07K16/00 C07H21/00 C12N5/00 C12N5/08 G01N33/68 G01N33/543 C12N5/071 C12N5/09		
CPC分类号	A61K2039/55527 C07K16/245 C07K2317/21 C07K2317/76 G01N2333/545 C12N5/069 C12N5/0693 G01N33/6869 C07K2317/92 A61P29/00 A61K39/3955 C07K14/545 G01N33/6863 A61K39/395 A61K2039/505 C07K16/24 C12N5/10 C07K14/5412 C07K2317/14 C07K2317/24 C12N2330/50		
优先权	61/057586 2008-05-30 US 61/121391 2008-12-10 US 61/178350 2009-05-14 US		
其他公开文献	US8034337		
外部链接	Espacenet USPTO		

摘要(译)

完全人单克隆抗体包括 (i) 对IL-1α表现出非常高的结合亲和力的抗原结合可变区和 (ii) 通过C1q结合和与几种不同Fc受体结合而有效激活补体系统的恒定区。。