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(54) Title: METALLOPROTEINASE 12 BINDING PROTEINS

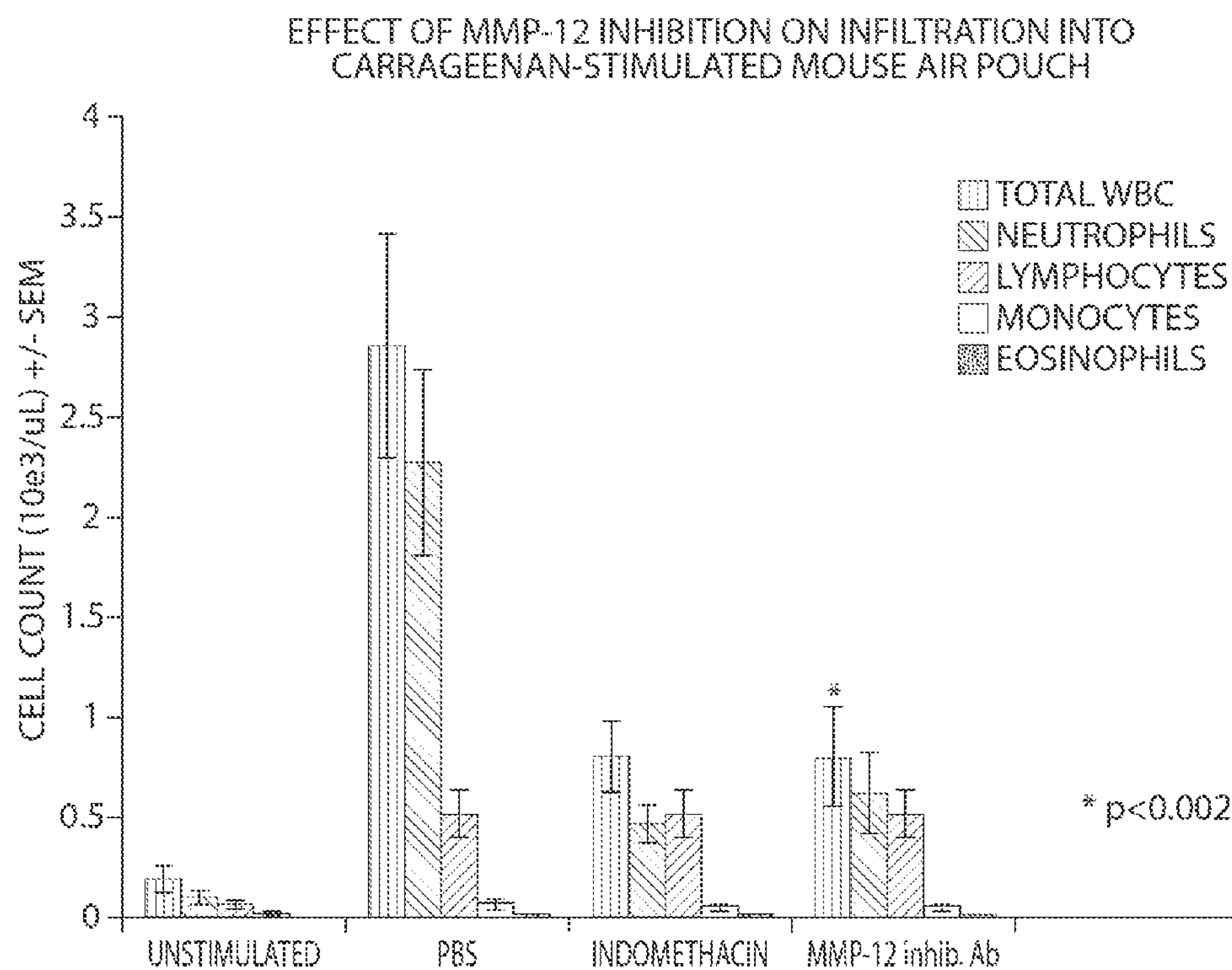


Figure 8

(57) Abrégé/Abstract:

Proteins that bind to matrix metalloproteinase 12 and methods of using such proteins are described.

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(57) Abstract: Proteins that bind to matrix metalloproteinase 12 and methods of using such proteins are described.

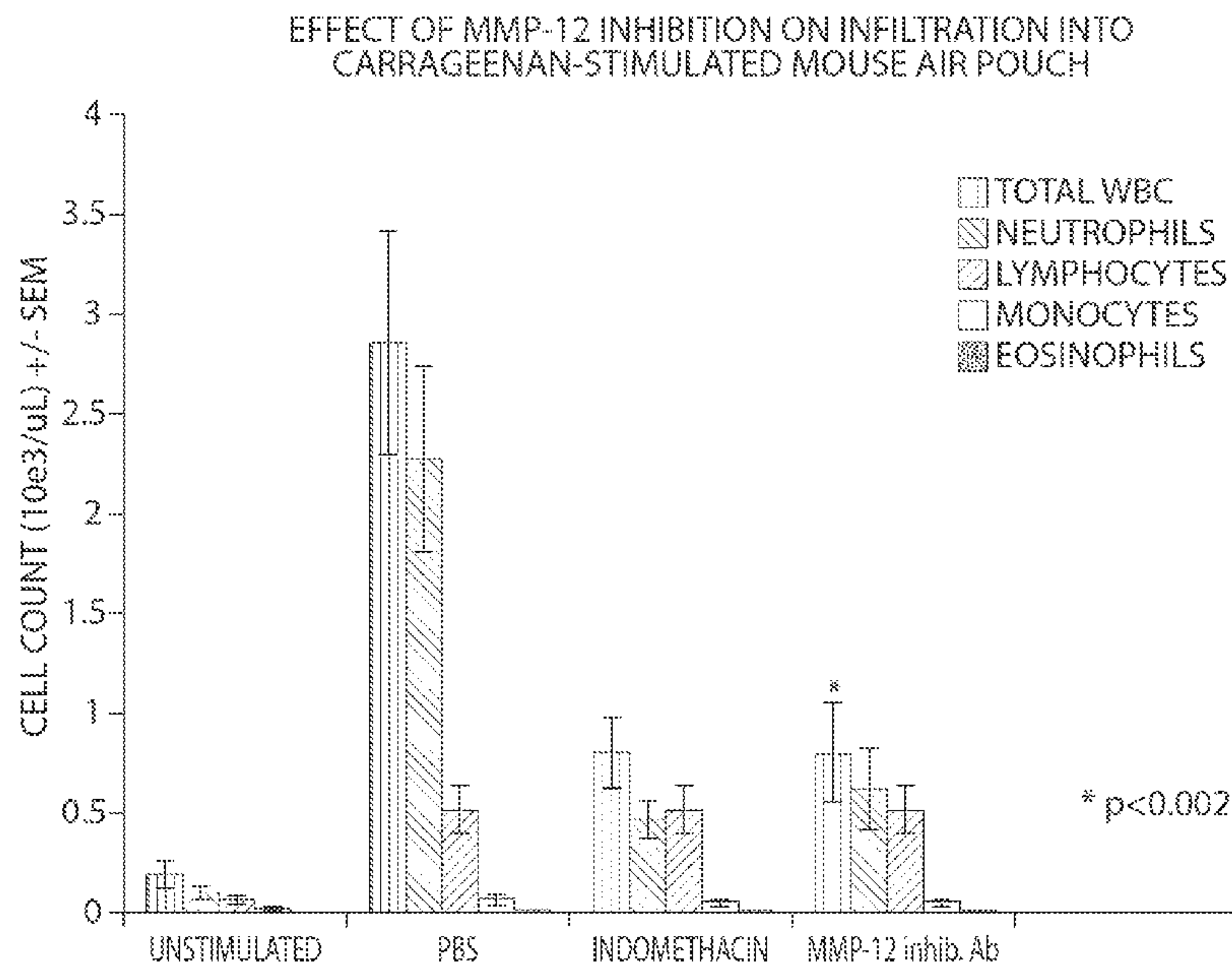


Figure 8

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METALLOPROTEINASE 12 BINDING PROTEINS

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims priority to U.S. Application Serial No. 61/033,348, filed on March 3, 2008 and U.S. Application Serial No. 61/127,830, filed on May 14, 2008. The disclosures of the prior applications are considered part of (and are incorporated by reference in) the disclosure of this application.

BACKGROUND

Matrix Metalloproteinases (MMPs) are a family of zinc metalloendopeptidases secreted by cells, and are responsible for much of the turnover of matrix components. The MMP family consists of at least 26 members, all of which share a common catalytic core with a zinc molecule in the active site.

SUMMARY

This disclosure relates, *inter alia*, to proteins that bind MMP-12, herein referred to as “MMP-12 binding proteins,” and methods of identifying and using such proteins. These proteins include antibodies and antibody fragments (e.g., primate antibodies and Fabs, especially human antibodies and Fabs) that bind to MMP-12 (e.g., human MMP-12). In some embodiments, these proteins include antibodies and antibody fragments (e.g., primate antibodies and Fabs, especially human antibodies and Fabs) that inhibit MMP-12 (e.g., human MMP-12) (e.g., inhibit the catalytic activity of MMP-12). The MMP-12 binding proteins can be used in the treatment of diseases, particularly human disease, such as cancer, inflammation, cardiovascular disease, aneurysm, wound healing, aging, and nerve damage in which excess or inappropriate activity of MMP-12 features. In many cases, the proteins have tolerable low or no toxicity.

In some aspects, the disclosure relates to proteins (e.g., antibodies, peptides and Kunitz domain proteins) that bind MMP-12, in particular, proteins (e.g., antibodies (e.g., human antibodies), peptides and Kunitz domain proteins) that bind and inhibit MMP-12.

In one embodiment, the disclosure provides a human antibody that binds to human MMP-12. In one embodiment, the human antibody is an inhibitor of the catalytic activity of MMP-12.

The antibody can be, e.g., an IgG1, IgG2, IgG3, IgG4, Fab, Fab2', scFv, minibody, scFv::Fc fusion, Fab::HSA fusion, HSA::Fab fusion, Fab::HSA::Fab fusion, or other molecule that comprises the antigen combining site of one of the antibodies herein listed. In one embodiment, the antibody is used to guide a nano-particle or toxin to a cell expressing MMP-12 on the cell surface. In one embodiment, the antibody causes effector functions (CDC or ADCC) to kill the cell which expresses MMP-12.

In some embodiments, the VH and VL regions of the binding proteins (e.g., Fabs) can be provided as IgG, Fab, Fab2, Fab2', scFv, PEGylated Fab, PEGylated scFv, PEGylated Fab2, VH::CH1::HSA+LC, HSA::VH::CH1+LC, LC::HSA + VH::CH1, HSA::LC + VH::CH1, or other appropriate construct.

In another embodiment, the binding protein comprises a Kunitz domain protein or modified version (e.g., HSA fusion) or peptide-based MMP-12 binding protein that can inhibit MMP-12 activity.

In one aspect, the disclosure features a protein (e.g., an isolated protein) that binds to MMP-12 (e.g., human MMP-12) and includes at least one immunoglobulin variable region. For example, the protein includes a heavy chain (HC) immunoglobulin variable domain sequence and a light chain (LC) immunoglobulin variable domain sequence. In one embodiment, the protein binds to and inhibits MMP-12 (e.g., inhibits MMP-12 catalytic activity), e.g., human MMP-12.

In some embodiments, the protein binds to human MMP-12 specifically, and not to MMP-12 from another species (e.g., the protein does not bind to MMP-12 from another species with greater than background levels of binding).

In some embodiments, the protein binds MMP-12 specifically, and not to another matrix metalloproteinase (e.g., the protein does not bind to any other matrix metalloproteinase with greater than background levels of binding).

Such binding proteins can be conjugated to a drug (e.g., to form a MMP-12 binding protein-drug conjugate) and used therapeutically. This disclosure relates, in part, to MMP-12 binding protein-drug conjugates, the preparation of these conjugates, and uses thereof. The conjugates can be used, e.g., in the treatment of disorders, e.g., for the treatment of cancer, inflammation, cardiovascular disease, aneurysm, wound healing, aging, or nerve damage.

Targeting (e.g., a killing) of the MMP-12 expressing cells and/or tumors, e.g., with high affinity binding protein-drug conjugates can be a potent therapy in the treatment of diseases, e.g., cancer, inflammation, cardiovascular disease, aneurysm, wound healing, aging, and nerve damage.

The protein can include one or more of the following characteristics: (a) a human CDR or human framework region; (b) the HC immunoglobulin variable domain sequence comprises one or more (e.g., 1, 2, or 3) CDRs that are at least 85, 88, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100% identical to a CDR of a HC variable domain described herein; (c) the LC immunoglobulin variable domain sequence comprises one or more (e.g., 1, 2, or 3) CDRs that are at least 85, 88, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100% identical to a CDR of a LC variable domain described herein; (d) the LC immunoglobulin variable domain sequence is at least 85, 88, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100% identical to a LC variable domain described herein; (e) the HC immunoglobulin variable domain sequence is at least 85, 88, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100% identical to a HC variable domain described herein; (f) the protein binds an epitope bound by a protein described herein, or an epitope that overlaps with such epitope; and (g) a primate CDR or primate framework region.

The protein can bind to MMP-12, e.g., human MMP-12, with a binding affinity of at least 10^5 , 10^6 , 10^7 , 10^8 , 10^9 , 10^{10} and 10^{11} M^{-1} . In one embodiment, the protein binds to MMP-12 with a K_{off} slower than 1×10^{-3} , 5×10^{-4} s^{-1} , or 1×10^{-4} s^{-1} . In one embodiment, the protein binds to MMP-12 with a K_{on} faster than 1×10^2 , 1×10^3 , or 5×10^3 $M^{-1}s^{-1}$. In one embodiment, the protein inhibits human MMP-12 activity, e.g., with a K_i of less than 10^{-5} , 10^{-6} , 10^{-7} , 10^{-8} , 10^{-9} , and 10^{-10} M. The protein can have, for example, an IC_{50} of less than 100 nM, 10 nM or 1 nM. In some embodiments, the protein has an IC_{50} of about 1.8 nM. The affinity of the protein for MMP-12 can be characterized by a K_D of less than 100 nM, less than 10 nM, or about 3 nM (e.g., 3.1 nM), about 5 nM (e.g., 5 nM), about 6 nM (e.g., 5.9 nM), about 7 nM (e.g., 7.1 nM), or about 10 nM (e.g., 9.6 nM).

In some embodiments, the protein has a $K_D < 200$ nM.

In some embodiments, the protein has a $t_{1/2}$ of at least about 10 minutes (e.g., 11 minutes), at least about 20 minutes (e.g., 18 minutes), at least about 25 minutes (e.g., 25 minutes), at least about 35 minutes (e.g., 33 minutes), or at least about 60 minutes (e.g., 57 minutes).

In one embodiment, the protein binds the catalytic domain of human MMP-12, e.g., the protein contacts residues in or near the active site of MMP-12.

In some embodiments, the protein does not contact residues in or near the active site of MMP-12 but instead binds elsewhere on MMP-12 and causes a steric change in MMP-12 that affects (e.g., inhibits) its activity.

In a preferred embodiment, the protein is a human antibody having the light and heavy chains of antibodies picked from the list comprising M0134-A02, M134-A05, M134-A07, M134-A09, M134-A10, M134-A11, M0134-B01, M134-B04, M0134-B08, M0134-B11, M0134-C01, M0134-C02, M0134-C06, M0134-C09, M0134-C10, M0134-C11, M0134-C12, M0134-D02, M0134-D03, M0134-E04, M0134-E07, M0134-E08, M134-E11, M0134-F01, M0134-F05, M0134-G02, M0134-G04, M0134-G07, M0135-A03, M0135-A05, M0135-A06, M0135-A07, M0135-B02, M0135-B08, M0135-C01, M0135-C11, M0135-E03, M0135-F03, M0135-F11, M0135-G02, M0135-G03, M0135-G07, M0135-G11, M0135-H03, M0135-H10, M0105-C05, M0105-E11, M0105-F08, M0107-A12, M0108-A02, M0109-G11, M0110-G05, M0129-B11, M0130-A01, M0130-C12, M0130-F06, M0130-H04, M0131-A06, M0131-D03, M0132-A04, M0133-B08, M0133-E05, M0121-E07, M0118-F11, M0125-G07, M0124-E07, M0119-D01, M0119-A02, M0122-C06, M0123-G07, M0063-A02, M0063-A04, M0063-B01, M0063-B11, M0063-C07, M0063-G01, M0065-E12, M0065-G03, M0065-H05, M0067-A02, M0067-B06, M0067-B09, M0067-C10, M0067-F02, M0067-F06, M0069-A04, M0069-A11, M0069-C02, M0069-D10, M0069-G07, M0071-A01, M0071-B07, M0071-D05, M0071-D09, M0071-H03, M0071-H06, M0087-F09, M0088-F07, M0088-G10, M0088-H10, M0089-C01, M0089-F05, M0089-B07, M0089-H11, M0034-C04, M0039-F01, M0041-B05, M0041-G01, M0042-B06, M0006-B10, M0007-H06, M0008-H09, M0009-H08, M0011-H11, M0015-F02, M0016-D01, M0013-D11, M0013-G12, M0013-H06, M0014-C09, M0014-G11, M0016-A11, M0016-H05, M0019-C05, M0020-B01, M0022-C07, M0025-D04 and M0027-E11. In a preferred embodiment, the protein is a human antibody having its heavy chain picked from the list comprising M0134-A02, M134-A05, M134-A07, M134-A09, M134-A10, M134-A11, M0134-B01, M134-B04, M0134-B08, M0134-B11, M0134-C01, M0134-C02, M0134-C06, M0134-C09, M0134-C10, M0134-C11, M0134-C12, M0134-D02, M0134-D03, M0134-E04, M0134-E07, M0134-E08, M134-E11, M0134-F01, M0134-F05, M0134-G02, M0134-G04, M0134-G07, M0135-A03, M0135-A05, M0135-A06, M0135-A07, M0135-B02, M0135-B08, M0135-C01, M0135-C11, M0135-E03, M0135-F03, M0135-F11, M0135-G02, M0135-G03, M0135-G07, M0135-G11, M0135-H03, M0135-H10, M0105-C05, M0105-E11, M0105-F08,

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preferred embodiment, the protein is a human antibody having one or more (e.g., 1, 2, or 3) heavy chain CDRs picked from the corresponding CDRs of the list of heavy chains comprising M0134-A02, M134-A05, M134-A07, M134-A09, M134-A10, M134-A11, M0134-B01, M134-B04, M0134-B08, M0134-B11, M0134-C01, M0134-C02, M0134-C06, M0134-C09, M0134-C10, M0134-C11, M0134-C12, M0134-D02, M0134-DO3, M0134-E04, M0134-E07, M0134-E08, M134-E11, M0134-F01, M0134-F05, M0134-G02, M0134-G04, M0134-G07, M0135-A03, M0135-A05, M0135-A06, M0135-A07, M0135-B02, M0135-B08, M0135-C01, M0135-C11, M0135-E03, M0135-F03, M0135-F11, M0135-G02, M0135-G03, M0135-G07, M0135-G11, M0135-H03, M0135-H10, M0105-C05, M0105-E11, M0105-F08, M0107-A12, M0108-A02, M0109-G11, M0110-G05, M0129-B11, M0130-A01, M0130-C12, M0130-F06, M0130-H04, M0131-A06, M0131-D03, M0132-A04, M0133-B08, M0133-E05, M0121-E07, M0118-F11, M0125-G07, M0124-E07, M0119-D01, M0119-A02, M0122-C06, M0123-G07, M0063-A02, M0063-A04, M0063-B01, M0063-B11, M0063-C07, M0063-G01, M0065-E12, M0065-G03, M0065-H05, M0067-A02, M0067-B06, M0067-B09, M0067-C10, M0067-F02, M0067-F06, M0069-A04, M0069-A11, M0069-C02, M0069-D10, M0069-G07, M0071-A01, M0071-B07, M0071-D05, M0071-D09, M0071-H03, M0071-H06, M0087-F09, M0088-F07, M0088-G10, M0088-H10, M0089-C01, M0089-F05, M0089-B07, M0089-H11, M0034-C04, M0039-F01, M0041-B05, M0041-G01, M0042-B06, M0006-B10, M0007-H06, M0008-H09, M0009-H08, M0011-H11, M0015-F02, M0016-D01, M0013-D11, M0013-G12, M0013-H06, M0014-C09, M0014-G11, M0016-A11, M0016-H05, M0019-C05, M0020-B01, M0022-C07, M0025-D04 and M0027-E11. In a preferred embodiment, the protein is a human antibody having one or more (e.g., 1, 2, or 3) light chain CDRs picked from the corresponding CDRs of the list of light chains comprising M0134-A02, M134-A05, M134-A07, M134-A09, M134-A10, M134-A11, M0134-B01, M134-B04, M0134-B08, M0134-B11, M0134-C01, M0134-C02, M0134-C06, M0134-C09, M0134-C10, M0134-C11, M0134-C12, M0134-D02, M0134-DO3, M0134-E04, M0134-E07, M0134-E08, M134-E11, M0134-F01, M0134-F05, M0134-G02, M0134-G04, M0134-G07, M0135-A03, M0135-A05, M0135-A06, M0135-A07, M0135-B02, M0135-B08, M0135-C01, M0135-C11, M0135-E03, M0135-F03, M0135-F11, M0135-G02, M0135-G03, M0135-G07, M0135-G11, M0135-H03, M0135-H10, M0105-C05, M0105-E11, M0105-F08, M0107-A12, M0108-A02, M0109-G11, M0110-G05, M0129-B11, M0130-A01, M0130-C12, M0130-F06, M0130-H04, M0131-A06, M0131-D03, M0132-A04, M0133-B08, M0133-E05,

M0121-E07, M0118-F11, M0125-G07, M0124-E07, M0119-D01, M0119-A02, M0122-C06, M0123-G07, M0063-A02, M0063-A04, M0063-B01, M0063-B11, M0063-C07, M0063-G01, M0065-E12, M0065-G03, M0065-H05, M0067-A02, M0067-B06, M0067-B09, M0067-C10, M0067-F02, M0067-F06, M0069-A04, M0069-A11, M0069-C02, M0069-D10, M0069-G07, M0071-A01, M0071-B07, M0071-D05, M0071-D09, M0071-H03, M0071-H06, M0087-F09, M0088-F07, M0088-G10, M0088-H10, M0089-C01, M0089-F05, M0089-B07, M0089-H11, M0034-C04, M0039-F01, M0041-B05, M0041-G01, M0042-B06, M0006-B10, M0007-H06, M0008-H09, M0009-H08, M0011-H11, M0015-F02, M0016-D01, M0013-D11, M0013-G12, M0013-H06, M0014-C09, M0014-G11, M0016-A11, M0016-H05, M0019-C05, M0020-B01, M0022-C07, M0025-D04 and M0027-E11.

In a more preferred embodiment, the protein is a human antibody having the light and heavy chains of antibodies from M0008-H09, M0131-A06 or M0121-E07. In another preferred embodiment, the protein is a human antibody having its heavy chain from M0008-H09, M0131-A06 or M0121-E07. In yet another preferred embodiment, the protein is a human antibody having its light chain from M0008-H09, M0131-A06 or M0121-E07. In an even more preferred embodiment, the protein is a human antibody having one or more (e.g., 1, 2, or 3) heavy chain CDRs from the corresponding CDRs of the heavy chain comprising M0008-H09, M0131-A06 or M0121-E07. In another even more preferred embodiment, the protein is a human antibody having one or more (e.g., 1, 2, or 3) light chain CDRs from the corresponding CDRs of the light chains comprising M0008-H09, M0131-A06 or M0121-E07.

In a more preferred embodiment, the protein is a human antibody having the light and heavy chains of antibody DX-2712 (also referred to as M0131-A06-GA-S). In another preferred embodiment, the protein is a human antibody having its heavy chain from antibody DX-2712. In yet another preferred embodiment, the protein is a human antibody having its light chain from antibody DX-2712. In an even more preferred embodiment, the protein is a human antibody having one or more (e.g., 1, 2, or 3) heavy chain CDRs from the corresponding CDRs of the heavy chain from antibody DX-2712. In another even more preferred embodiment, the protein is a human antibody having one or more (e.g., 1, 2, or 3) light chain CDRs from the corresponding CDRs of the light chains from antibody DX-2712.

In another embodiment, the protein is a human antibody having the light and heavy chains of a mutant or variant of DX-2712, e.g., a mutant or variant described herein. In another

preferred embodiment, the protein is a human antibody having its heavy chain from a mutant or variant of DX-2712, e.g., a mutant or variant described herein. In yet another preferred embodiment, the protein is a human antibody having its light chain from a variant of DX-2712, e.g., a mutant or variant described herein. In an even more preferred embodiment, the protein is a human antibody having one or more (e.g., 1, 2, or 3) heavy chain CDRs from the corresponding CDRs of the heavy chain from a mutant or variant of DX-2712, e.g., a mutant or variant described herein. In another even more preferred embodiment, the protein is a human antibody having one or more (e.g., 1, 2, or 3) light chain CDRs from the corresponding CDRs of the light chains from a mutant or variant of DX-2712, e.g., a mutant or variant described herein.

In a more preferred embodiment, the protein is a human antibody having the light and heavy chains of antibody 539B-X0041-D02. In another preferred embodiment, the protein is a human antibody having its heavy chain from antibody 539B-X0041-D02. In yet another preferred embodiment, the protein is a human antibody having its light chain from antibody 539B-X0041-D02. In an even more preferred embodiment, the protein is a human antibody having one or more (e.g., 1, 2, or 3) heavy chain CDRs from the corresponding CDRs of the heavy chain from antibody 539B-X0041-D02. In another even more preferred embodiment, the protein is a human antibody having one or more (e.g., 1, 2, or 3) light chain CDRs from the corresponding CDRs of the light chains from antibody 539B-X0041-D02.

In another embodiment, the protein is a human antibody having the light and heavy chains of a variant of 539B-X0041-D02, e.g., a variant described herein. In another preferred embodiment, the protein is a human antibody having its heavy chain from a variant of 539B-X0041-D02, e.g., a variant described herein. In yet another preferred embodiment, the protein is a human antibody having its light chain from a variant of 539B-X0041-D02, e.g., a variant described herein. In an even more preferred embodiment, the protein is a human antibody having one or more (e.g., 1, 2, or 3) heavy chain CDRs from the corresponding CDRs of the heavy chain from a variant of 539B-X0041-D02, e.g., a variant described herein. In another even more preferred embodiment, the protein is a human antibody having one or more (e.g., 1, 2, or 3) light chain CDRs from the corresponding CDRs of the light chains from a variant of 539B-X0041-D02, e.g., a variant described herein.

In one embodiment, the HC and LC variable domain sequences are components of the same polypeptide chain. In another, the HC and LC variable domain sequences are components

of different polypeptide chains. For example, the protein is an IgG, e.g., IgG1, IgG2, IgG3, or IgG4. The protein can be a soluble Fab (sFab). In other implementations the protein includes a Fab2', scFv, minibody, scFv::Fc fusion, Fab::HSA fusion, HSA::Fab fusion, Fab::HSA::Fab fusion, or other molecule that comprises the antigen combining site of one of the binding proteins herein. The VH and VL regions of these Fabs can be provided as IgG, Fab, Fab2, Fab2', scFv, PEGylated Fab, PEGylated scFv, PEGylated Fab2, VH::CH1::HSA+LC, HSA::VH::CH1+LC, LC::HSA + VH::CH1, HSA::LC + VH::CH1, or other appropriate construction.

In one embodiment, the protein is a human or humanized antibody or is non-immunogenic in a human. For example, the protein includes one or more human antibody framework regions, e.g., all human framework regions. In one embodiment, the protein includes a human Fc domain, or an Fc domain that is at least 95, 96, 97, 98, or 99% identical to a human Fc domain.

In one embodiment, the protein is a primate or primatized antibody or is non-immunogenic in a human. For example, the protein includes one or more primate antibody framework regions, e.g., all primate framework regions. In one embodiment, the protein includes a primate Fc domain, or an Fc domain that is at least 95, 96, 97, 98, or 99% identical to a primate Fc domain. "Primate" includes humans (*Homo sapiens*), chimpanzees (*Pan troglodytes* and *Pan paniscus* (bonobos)), gorillas (*Gorilla gorilla*), gibbons, monkeys, lemurs, aye-ayes (*Daubentonia madagascariensis*), and tarsiers.

In certain embodiments, the protein includes no sequences from mice or rabbits (e.g., is not a murine or rabbit antibody).

In one embodiment, protein is physically associated with a nanoparticle, and can be used to guide a nanoparticle to a cell expressing MMP-12 on the cell surface. In one embodiment, the protein causes effector cells (CDC or ADCC) to kill a cell which expresses MMP-12.

In another aspect, the disclosure features a MMP-12 binding protein that is a competitive inhibitor of MMP-12. In some embodiments, the binding protein competes with an MMP-12 substrate (e.g., lung extracellular matrix, elastin, gelatin, fibronectin, apo[a], apoB-100, collagen, osteonectin, TFPI, alpha 1-protease inhibitor, uPAR and CD14), e.g., binds to the same epitope as the substrate, e.g., and prevents substrate binding.

In some aspects, the disclosure features a method of inhibiting an interaction between MMP-12 and an MMP-12 substrate (e.g., lung extracellular matrix, elastin, gelatin, fibronectin, apo[a], apoB-100, collagen, osteonectin, TFPI, alpha 1-protease inhibitor, uPAR and CD14). The method includes contacting an MMP-12 binding protein described herein with MMP-12 (e.g., *in vitro* or *in vivo*), wherein the binding protein binds to MMP-12 and thereby prevents the binding of an MMP-12 substrate to MMP-12. In some embodiments, the binding protein binds to the same epitope on MMP-12 as the substrate, e.g., the binding protein is a competitive inhibitor. In some embodiments, the binding protein does not bind the same epitope as the substrate but causes a steric change in MMP-12 that decreases or inhibits the ability of the substrate to bind.

In one aspect, the disclosure features a MMP-12 binding protein-drug conjugate that includes a MMP-12 binding protein and a drug.

In one embodiment, the binding protein comprises at least one immunoglobulin variable region, and/or the protein binds to and/or inhibits MMP-12, e.g., inhibits MMP-12 catalytic activity.

In one embodiment, the drug is a cytotoxic or cytostatic agent. The cytotoxic agent can be, e.g., selected from the group consisting of an auristatin, a DNA minor groove binding agent, a DNA minor groove alkylating agent, an enediyne, a lexitropsin, a duocarmycin, a taxane, a puromycin, a dolastatin, a podophyllotoxin, a baccatin derivative, a cryptophysin, a combretastatin, a maytansinoid, and a vinca alkaloid. In one embodiment, the cytotoxic agent is an auristatin and, e.g., the auristatin is selected from AFP, MMAF, MMAE, AEB, AEVB and auristatin E. In one embodiment, the auristatin is AFP or MMAF. In another embodiment, the cytotoxic agent is a maytansinoid and, e.g., the maytansinoid is selected from a maytansinol, maytansine, DM1, DM2, DM3 and DM4. In one embodiment, the maytansinoid is DM1. In another embodiment, the cytotoxic agent is selected from paclitaxel, docetaxel, CC-1065, SN-38, topotecan, morpholino-doxorubicin, rhizoxin, cyanomorpholino-doxorubicin, dolastatin-10, echinomycin, combretastatin, calicheamicin, and netropsin. In one embodiment, the cytotoxin is an auristatin, a maytansinoid, or calicheamicin.

In one embodiment, the cytotoxic agent is an antitubulin agent and, e.g., the antitubulin agent is selected from AFP, MMAP, MMAE, AEB, AEVB, auristatin E, vincristine, vinblastine, vindesine, vinorelbine, VP-16, camptothecin, paclitaxel, docetaxel, epothilone A, epothilone B, nocodazole, colchicines, colcimid, estramustine, cemadotin, discodermolide, maytansinol, maytansine, DM1, DM2, DM3, DM4 and eleutherobin.

In one embodiment, the MMP-12 binding protein (e.g., antibody) is conjugated to the drug (e.g., cytotoxic agent) via a linker. In one embodiment, the linker is cleavable under intracellular conditions, e.g., the cleavable linker is a peptide linker cleavable by an intracellular protease. In one embodiment, the linker is a peptide linker, e.g., a dipeptide linker, e.g., a val-cit linker or a phe-lys linker. In one embodiment, the cleavable linker is hydrolyzable at a pH of less than 5.5, e.g., the hydrolyzable linker is a hydrazone linker. In another embodiment, the cleavable linker is a disulfide linker.

A binding protein described herein can be provided as a pharmaceutical composition, e.g., including a pharmaceutically acceptable carrier. The composition can be at least 10, 20, 30, 50, 75, 85, 90, 95, 98, 99, or 99.9% free of other protein species. In some embodiments, the binding protein can be produced under GMP (good manufacturing practices). In some embodiments, the binding protein is provided in pharmaceutically acceptable carriers, e.g., suitable buffers or excipients.

The dose of a binding protein (e.g., a pharmaceutical composition containing a binding protein described herein) is sufficient to block about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 85%, about 90%, about 95%, about 99%, or about 100% of the activity of MMP-12 in the patient, e.g., at the site of disease. Depending on the disease, this may require a dose, e.g., of between about 0.01 mg/Kg to about 100 mg/Kg, e.g., between about 0.1 and about 10 mg/Kg. For example, the dose can be a dose of about 0.1, about 1, about 3, about 6, or about 10 mg/Kg. For example, for an IgG having a molecular mass of 150,000 g/mole (2 binding sites), these doses correspond to approximately 18 nM, 180 nM, 540 nM, 1.08 microM, and 1.8 microM, respectively, of binding sites for a 5 L blood volume. Medicine being partly an art, the optimal dose will be established by clinical trials, but will most likely lie in this range.

In another aspect, the disclosure features a method of detecting an MMP-12 in a sample, e.g., a sample from a patient (e.g., tissue biopsy or blood sample). The method includes: contacting the sample with an MMP-12 binding protein; and detecting an interaction between the protein and the MMP-12, if present. In some embodiments, the protein includes a detectable label. An MMP-12 binding protein can be used to detect MMP-12 in a subject. The method includes: administering an MMP-12 binding protein to a subject; and detecting the protein in the subject. In some embodiments, the protein further includes a detectable label. For example, the detecting comprises imaging the subject. For example, MMP-12 activity can be a marker of inflammation and/or disease progression in subjects with, or suspected of having, an inflammatory disorder of the lung such as, e.g., emphysema and chronic obstructive pulmonary disease (COPD).

In another aspect, the disclosure features a method of modulating MMP-12 activity. The method includes: contacting an MMP-12 with an MMP-12 binding protein (e.g., in a human subject), thereby modulating MMP-12 activity. In some embodiments, the binding protein inhibits MMP-12 activity (e.g., inhibits MMP-12 catalytic activity).

In another aspect, the disclosure features a method of treating cancer (e.g., metastatic cancer) (e.g., in a subject that has cancer or is suspected of having cancer). The method includes: administering, to a subject, an MMP-12 binding protein in an amount sufficient to treat a cancer in the subject. For example, the cancer is head and neck cancer, oral cavity cancer, laryngeal cancer, chondrosarcoma, breast cancer (which may be estrogen receptor positive (ER+), estrogen receptor negative (ER-), Her2 positive (Her2+), Her2 negative (Her2-), or a combination thereof, e.g., ER+/Her2+, ER+/Her2-, ER-/Her2+, or ER-/Her2-), laryngeal cancer, ovarian cancer, lung cancer (e.g., non-small cell lung cancer), prostate cancer, colon cancer, colorectal cancer, hepatocellular cancer, testicular carcinoma, melanoma, or a brain tumor (e.g., astrocytomas, glioblastomas, gliomas).

MMP-12 binding proteins can be useful for modulating metastatic activity in a subject (e.g., in a subject that has a metastatic cancer or is suspected of having a metastatic cancer). The protein can be administered, to the subject, in an amount effective to modulate metastatic

activity. For example, the protein inhibits one or more of: tumor growth, tumor embolism, tumor mobility, tumor invasiveness, and cancer cell proliferation.

The methods disclosed herein relating to the treatment cancer (e.g., treating cancer and/or modulation of metastatic activity) can further include providing (e.g., administering) to the subject a second therapy that is an anti-cancer therapy, e.g., administration of a chemotherapeutic, e.g., an agent that antagonizes signaling through a VEGF pathway, e.g., bevacizumab (AVASTIN®). In one embodiment, the second therapy includes administering 5-FU, leucovorin, and/or irinotecan. In one embodiment, the second therapy includes administering a Tie1 inhibitor (e.g., an anti-Tie1 antibody). In one embodiment, the second therapy is an inhibitor of plasmin (e.g., a kunitz domain disclosed in U.S. Patent No. 6,010,880, such as a protein or polypeptide comprising the amino acid sequence MHSFCAFKAE TGPCRARFDRWFFNIFTRQCEEFIYGGCEGNQNR FESLEECKKMCTRD (SEQ ID NO:1).

In another aspect, the disclosure features a method of treating inflammation (e.g., in a subject that has inflammation or is suspected of having inflammation, e.g., inflammation associated with an inflammatory disease) or an inflammatory disease (e.g., in a subject that has an inflammatory disease or is suspected of having an inflammatory disease). Inflammatory diseases that can be treated include, e.g., atherosclerosis, multiple sclerosis, systemic sclerosis, nephritis, encephalomyelitis (e.g., experimental autoimmune encephalomyelitis), rheumatoid arthritis, encephalitis (e.g., viral encephalitis), colitis (e.g., enterocolitis) and neuroinflammatory disease. The method includes: administering, to a subject, an MMP-12 binding protein in an amount sufficient to treat inflammation in the subject. The method can further include providing to the subject a second therapy that is an inflammation therapy. For example, particularly for rheumatoid arthritis, the second therapy comprises administering one or more of the following agents: aspirin, naproxen, ibuprofen, etodolac, cortisone (corticosteroids), antacids, sucralfate, proton-pump inhibitors, misoprostol, gold (e.g., gold salts, gold thioglucose, gold thiomalate, oral gold), methotrexate, sulfasalazine, D-penicillamine, azathioprine, cyclophosphamide, chlorambucil, cyclosporine, leflunomide, etanercept, infliximab, anakinra, adalimumab, and/or hydroxychloroquine.

In another aspect, the disclosure features a method of treating a disease associated with inflammation of the lung (e.g., in a subject that has inflammation of the lung or is suspected of having inflammation of the lung) or a disease associated with inflammation of the lung (e.g., in a subject that has a disease associated with inflammation of the lung or is suspected of having a disease associated with inflammation of the lung). Diseases associated with inflammation of the lung include, e.g., emphysema, chronic obstructive pulmonary disease (COPD), asthma, and lung injury in hyperoxia. The method includes: administering, to a subject, an MMP-12 binding protein in an amount sufficient to treat inflammation of the lung in the subject. The method can further include providing to the subject a second therapy that is an inflammation therapy.

In another aspect, the disclosure features a method of treating cardiovascular disease (e.g., in a subject that has cardiovascular disease or is suspected of having cardiovascular disease). The method includes: administering, to a subject, an MMP-12 binding protein in an amount sufficient to treat cardiovascular disease in the subject. The method can further include providing to the subject a second therapy that is a therapy for cardiovascular disease.

In another aspect, the disclosure features a method of treating a stroke or aneurysm (e.g., in a subject that has a stroke or aneurysm or is suspected of having a stroke or aneurysm). The method includes: administering, to a subject, an MMP-12 binding protein in an amount sufficient to treat the stroke or aneurysm in the subject. The method can further include providing to the subject a second therapy that is a therapy for stroke or aneurysm.

In another aspect, the disclosure features a method of treating nerve damage associated with excess or inappropriate activity of MMP-12 (e.g., spinal cord injury). The method includes: administering, to a subject, an MMP-12 binding protein in an amount sufficient to treat the nerve damage in the subject. In one embodiment, the method further includes administering a second therapy that is a therapy for nerve damage.

Other exemplary therapeutic methods that include administering an MMP-12 binding protein are described below. An MMP-12 binding protein described herein can be administered in combination with one or more other MMP inhibitors, e.g., small molecule inhibitors, e.g.,

broad specificity inhibitors. In one embodiment, the small molecule inhibitors are one or more of the small molecule inhibitors described herein. In another embodiment, the one or more MMP inhibitors include another MMP-12 binding protein, e.g., another MMP-12 binding protein described herein.

MMP-12 binding proteins are useful for targeted delivery of an agent to a subject (e.g., a subject who has or is suspected of having a tumor), e.g., to direct the agent to a tumor in the subject. For example, an MMP-12 binding protein that is coupled to an anti-tumor agent (such as a chemotherapeutic, toxin, drug, or a radionuclide (e.g., ^{131}I , ^{90}Y , ^{177}Lu)) can be administered to a subject who has or is suspected of having a tumor.

In another aspect, the disclosure features a method of imaging a subject. The method includes administering an MMP-12 binding protein to the subject. In some embodiments, the protein is one that does not substantially inhibit MMP-12 catalytic activity. Exemplary MMP-12 binding proteins are described herein such as, e.g., M0013-A02, M0013-A03, M0013-A11, M0013-B07, M0013-B08, M0013-B10, M0013-D02, M0013-D04, M0013-D06, M0013-D10, M0013-E05, M0013-F07, M0013-G04, M0013-H04, M0014-A09, M0014-B09, M0014-D11, M0015-G04, M0016-A02, M0016-A04, M0016-C03, M0016-C10, M0016-D07, M0016-F03, M0016-H09, M0018-A05, M0018-D01, M0019-A10, M0019-C07, M0019-G07, M0019-G10, M0020-C08, M0020-H02, M0021-B03, M0021-D06, M0021-E12, M0021-G07, M0022-A02, M0023-B11, M0023-D03, M0023-D05, M0023-E09, M0023-H01, M0024-C02, M0025-F02, M0025-G01, M0025-H03, M0025-H11, M0026-A01, M0026-A05, M0026-A09, M0026-A10, M0026-B11, M0026-C03, M0026-C07, M0026-E01, M0026-E11, M0026-F03, M0026-F04, M0026-G12, M0026-H05, M0027-A08, M0027-B03, M0027-B08, M0027-C07, M0027-G02, M0027-H04, M0028-E09, M0028-F04, M0035-C05, M0040-A02, M0041-G04, M0007-A10, M0052-F03, M0041-A05, M0034-C04, M0038-D06, M0007-H06, M0038-A03, M0039-B02, M0035-D06, M0042-H01, M0040-C08, M0038-F09, M0040-E08, M0034-E11, M0008-E08, M0039-F01, M0030-A10, M0052-E10, M0040-A03, M0040-B05, M0041-G01, M0038-H04 and M0032-H09. Preferably, the MMP-12 binding protein is M0030-A10, M0032-H09, M0038-A03, M0038-H04, M0039-B02, M0040-B05, M0041-A05, R011-B11, M0007-A10 (also referred to as M7A10) or M0008-E08 (also referred to as M8E8). The MMP-12 binding protein may include a detectable label (e.g., a radionuclide or an MRI-detectable label). In one

embodiment, the subject has or is suspected of having a tumor. The method is useful for cancer diagnosis, intraoperative tumor detection, post-operative tumor detection, or monitoring tumor invasive activity.

In one aspect, the disclosure features the use of an MMP-12 binding protein described herein for the manufacture of a medicament for the treatment of a disorder described herein, e.g., cancer, inflammation, cardiovascular disease, aneurysm, wound healing, aging, and nerve damage cancer, inflammation, cardiovascular disease, aneurysm, wound healing, aging, and nerve damage.

The details of one or more embodiments of the invention are set forth in the accompanying drawings and the description below. Other features, objects, and advantages of the invention will be apparent from the description and drawings, and from the claims.

The contents of all cited references including literature references, issued patents, published or non-published patent applications cited throughout this application as well as those listed below are hereby expressly incorporated by reference in their entireties. In case of conflict, the present application, including any definitions herein, will control.

DESCRIPTION OF DRAWINGS

FIGURE 1 is a graph depicting inhibition assays of MMP-12 using non-inhibitor binding proteins.

FIGURES 2A, 2B and 2C: FIGURE 2A is a line graph showing human MMP-12 activity (Fluo/min) in the presence of increasing concentrations (nM) of an MMP-12 binding protein (539B-M08H09). FIGURE 2B is a line graph showing the binding rate of elastin (dF/min) in the presence of increasing concentrations (nM) of an MMP-12 binding protein (539B-M08H09). FIGURE 2C is a line graph showing murine MMP-12 activity (Fluo/sec) in the presence of increasing concentrations (nM) of an MMP-12 binding protein (539B-M08H09).

FIGURES 3A and 3B: FIGURE 3A is a line graph showing measured IC_{50} (nM) of an MMP-12 binding protein (M08H09) versus substrate concentration (μ M) of human MMP-12.

FIGURE 3B is a line graph showing measured IC_{50} (nM) of an MMP-12 binding protein (M08H09) versus substrate concentration (μ M) of murine MMP-12.

FIGURES 4A and 4B are line graphs showing murine MMP-12 activity (Fluo/sec) in the presence of increasing concentrations (nM) of an MMP-12 binding protein (539B-M11H11 Fab (FIGURE 4A) and IgG (FIGURE 4B)).

FIGURE 5 is a bar graph showing ELISA competition assays with four different MMP-12 binding proteins, M08H09, M0013-G12, M0016-A11 and R0062-E11.

FIGURE 6 is a bar graph showing the effect of various doses of MMP-12 binding proteins M08-H09 and M11-H11 on peribronchial inflammation score in OVA-challenged mouse model of airway inflammation.

FIGURES 7A and 7B are bar graphs showing eosinophil percentages (FIGURE 7A) and counts (FIGURE 7B) in OVA-challenged mouse model of airway inflammation administered various doses of MMP-12 binding proteins M08-H09 and M11-H11.

FIGURE 8 is a bar graph showing the effect of an MMP-12 binding protein (M08-H09) on inflammatory cell infiltration into a carrageenan-stimulated mouse air pouch.

FIGURE 9 is a line graph showing human MMP-12 activity (Fluo/sec) in the presence of increasing concentrations (nM) of an MMP-12 binding protein (539B-M131A06) and an MMP-12 binding protein (539B-M131A06-GA-S) which is a version of 539B-M131A06 that has been modified to remove a glycosylation site.

FIGURES 10A and 10B summarize the identification of amino acid changes in affinity matured variant HV-CDRs (cycles 1 and 2) that contribute to improvement in affinity and inhibition properties. The rows in FIGURE 10B correspond to the rows in FIGURE 10A.

DETAILED DESCRIPTION

Matrix metalloproteinase-12 (MMP-12) is a type IV collagenase that is members of a group of secreted zinc metalloproteases which, in mammals, degrade various proteins of the extracellular matrix. Other members of this group include interstitial collagenase (MMP-1) and stromelysin (MMP-3). MMP-12 (a.k.a. macrophage elastase, macrophage metalloelastase, or matrix metalloproteinase 12) is thought to be involved in many disease states. Many small molecule inhibitors of MMP-12 have been tested for safety and efficacy in cancer and other

diseases. So far, all have lacked either sufficient potency or sufficient specificity or both. The present disclosure provides proteins that bind MMP-12, and in some instances, inhibit MMP-12 activity. In many instances, the disclosed MMP-12 binding proteins bind and inhibit human and mouse MMP12 enzyme activity. In other instances, MMP-12 binding proteins are disclosed that bind MMP-12 but do not inhibit MMP-12 activity. Such MMP-12 binding proteins are useful, e.g., to determine the presence of MMP-12.

The term “binding protein” refers to a protein that can interact with a target molecule. This term is used interchangeably with “ligand.” An “MMP-12 binding protein” refers to a protein that can interact with MMP-12, and includes, in particular, proteins that preferentially interact with and/or inhibit MMP-12. For example, the MMP-12 binding protein is an antibody.

The term “antibody” refers to a protein that includes at least one immunoglobulin variable domain or immunoglobulin variable domain sequence. For example, an antibody can include a heavy (H) chain variable region (abbreviated herein as VH), and a light (L) chain variable region (abbreviated herein as VL). In another example, an antibody includes two heavy (H) chain variable regions and two light (L) chain variable regions. The term “antibody” encompasses antigen-binding fragments of antibodies (e.g., single chain antibodies, Fab and sFab fragments, F(ab')₂, Fd fragments, Fv fragments, scFv, and domain antibodies (dAb) fragments (de Wildt et al., Eur J Immunol. 1996; 26(3):629-39.)) as well as complete antibodies. An antibody can have the structural features of IgA, IgG, IgE, IgD, IgM (as well as subtypes thereof). Antibodies may be from any source, but primate (human and non-human primate) and primatized are preferred.

The VH and VL regions can be further subdivided into regions of hypervariability, termed “complementarity determining regions” (“CDR”), interspersed with regions that are more conserved, termed “framework regions” (“FR”). The extent of the framework region and CDRs has been precisely defined (see, Kabat, E.A., et al. (1991) *Sequences of Proteins of Immunological Interest, Fifth Edition*, U.S. Department of Health and Human Services, NIH Publication No. 91-3242, and Chothia, C. et al. (1987) J. Mol. Biol. 196:901-917, see also www.hgmp.mrc.ac.uk). Kabat definitions are used herein. Each VH and VL is typically composed of three CDRs and four FRs, arranged from amino-terminus to carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4.

As used herein, an “immunoglobulin variable domain sequence” refers to an amino acid sequence which can form the structure of an immunoglobulin variable domain such that one or more CDR regions are positioned in a conformation suitable for an antigen binding site. For example, the sequence may include all or part of the amino acid sequence of a naturally-occurring variable domain. For example, the sequence may omit one, two or more N- or C-terminal amino acids, internal amino acids, may include one or more insertions or additional terminal amino acids, or may include other alterations. In one embodiment, a polypeptide that includes immunoglobulin variable domain sequence can associate with another immunoglobulin variable domain sequence to form an antigen binding site, e.g., a structure that preferentially interacts with an MMP-12 protein, e.g., the MMP-12 catalytic domain.

The VH or VL chain of the antibody can further include all or part of a heavy or light chain constant region, to thereby form a heavy or light immunoglobulin chain, respectively. In one embodiment, the antibody is a tetramer of two heavy immunoglobulin chains and two light immunoglobulin chains, wherein the heavy and light immunoglobulin chains are inter-connected by, e.g., disulfide bonds. In IgGs, the heavy chain constant region includes three immunoglobulin domains, CH1, CH2 and CH3. The light chain constant region includes a CL domain. The variable region of the heavy and light chains contains a binding domain that interacts with an antigen. The constant regions of the antibodies typically mediate the binding of the antibody to host tissues or factors, including various cells of the immune system (e.g., effector cells) and the first component (C1q) of the classical complement system. The light chains of the immunoglobulin may be of type kappa or lambda. In one embodiment, the antibody is glycosylated. An antibody can be functional for antibody-dependent cytotoxicity and/or complement-mediated cytotoxicity.

One or more regions of an antibody can be human or effectively human. For example, one or more of the variable regions can be human or effectively human. For example, one or more of the CDRs can be human, e.g., HC CDR1, HC CDR2, HC CDR3, LC CDR1, LC CDR2, and LC CDR3. Each of the light chain CDRs can be human. HC CDR3 can be human. One or more of the framework regions can be human, e.g., FR1, FR2, FR3, and FR4 of the HC or LC. For example, the Fc region can be human. In one embodiment, all the framework regions are human, e.g., derived from a human somatic cell, e.g., a hematopoietic cell that produces immunoglobulins or a non-hematopoietic cell. In one embodiment, the human sequences are

germline sequences, e.g., encoded by a germline nucleic acid. In one embodiment, the framework (FR) residues of a selected Fab can be converted to the amino-acid type of the corresponding residue in the most similar primate germline gene, especially the human germline gene. One or more of the constant regions can be human or effectively human. For example, at least 70, 75, 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100% of an immunoglobulin variable domain, the constant region, the constant domains (CH1, CH2, CH3, CL1), or the entire antibody can be human or effectively human.

All or part of an antibody can be encoded by an immunoglobulin gene or a segment thereof. Exemplary human immunoglobulin genes include the kappa, lambda, alpha (IgA1 and IgA2), gamma (IgG1, IgG2, IgG3, IgG4), delta, epsilon and mu constant region genes, as well as the many immunoglobulin variable region genes. Full-length immunoglobulin “light chains” (about 25 KDa or about 214 amino acids) are encoded by a variable region gene at the NH₂-terminus (about 110 amino acids) and a kappa or lambda constant region gene at the COOH--terminus. Full-length immunoglobulin “heavy chains” (about 50 KDa or about 446 amino acids), are similarly encoded by a variable region gene (about 116 amino acids) and one of the other aforementioned constant region genes, e.g., gamma (encoding about 330 amino acids). The length of human HC varies considerably because HC CDR3 varies from about 3 amino-acid residues to over 35 amino-acid residues.

The term “antigen-binding fragment” of a full length antibody refers to one or more fragments of a full-length antibody that retain the ability to specifically bind to a target of interest. Examples of binding fragments encompassed within the term “antigen-binding fragment” of a full length antibody include (i) a Fab fragment, a monovalent fragment consisting of the VL, VH, CL and CH1 domains; (ii) a F(ab')₂ fragment, a bivalent fragment including two Fab fragments linked by a disulfide bridge at the hinge region; (iii) a Fd fragment consisting of the VH and CH1 domains; (iv) a Fv fragment consisting of the VL and VH domains of a single arm of an antibody, (v) a dAb fragment (Ward *et al.*, (1989) *Nature* 341:544-546), which consists of a VH domain; and (vi) an isolated complementarity determining region (CDR) that retains functionality. Furthermore, although the two domains of the Fv fragment, VL and VH, are coded for by separate genes, they can be joined, using recombinant methods, by a synthetic linker that enables them to be made as a single protein chain in which the VL and VH regions pair to form monovalent molecules known as single chain Fv (scFv). See *e.g.*, US patents

5,260,203, 4,946,778, and 4,881,175; Bird *et al.* (1988) *Science* 242:423-426; and Huston *et al.* (1988) *Proc. Natl. Acad. Sci. USA* 85:5879-5883.

Antibody fragments can be obtained using any appropriate technique including conventional techniques known to those with skill in the art. The term “monospecific antibody” refers to an antibody that displays a single binding specificity and affinity for a particular target, e.g., epitope. This term includes a “monoclonal antibody” or “monoclonal antibody composition,” which as used herein refer to a preparation of antibodies or fragments thereof of single molecular composition, irrespective of how the antibody was generated.

An “effectively human” immunoglobulin variable region is an immunoglobulin variable region that includes a sufficient number of human framework amino acid positions such that the immunoglobulin variable region does not elicit an immunogenic response in a normal human. An “effectively human” antibody is an antibody that includes a sufficient number of human amino acid positions such that the antibody does not elicit an immunogenic response in a normal human.

A “humanized” immunoglobulin variable region is an immunoglobulin variable region that is modified to include a sufficient number of human framework amino acid positions such that the immunoglobulin variable region does not elicit an immunogenic response in a normal human. Descriptions of “humanized” immunoglobulins include, for example, US 6,407,213 and US 5,693,762.

As used herein, “binding affinity” refers to the apparent association constant or K_a . The K_a is the reciprocal of the dissociation constant (K_d). A binding protein may, for example, have a binding affinity of at least 10^5 , 10^6 , 10^7 , 10^8 , 10^9 , 10^{10} and 10^{11} M^{-1} for a particular target molecule, e.g., MMP-9, MMP-16, or MMP-24. Higher affinity binding of a binding protein to a first target relative to a second target can be indicated by a higher K_a (or a smaller numerical value K_d) for binding the first target than the K_a (or numerical value K_d) for binding the second target. In such cases, the binding protein has specificity for the first target (e.g., a protein in a first conformation or mimic thereof) relative to the second target (e.g., the same protein in a second conformation or mimic thereof; or a second protein). Differences in binding affinity (e.g., for specificity or other comparisons) can be at least 1.5, 2, 3, 4, 5, 10, 15, 20, 37.5, 50, 70, 80, 91, 100, 500, 1000, or 10^5 fold.

Binding affinity can be determined by a variety of methods including equilibrium dialysis, equilibrium binding, gel filtration, ELISA, surface plasmon resonance, or spectroscopy (e.g., using a fluorescence assay). Exemplary conditions for evaluating binding affinity are in TRIS-buffer (50mM TRIS, 150mM NaCl, 5mM CaCl₂ at pH7.5). These techniques can be used to measure the concentration of bound and free binding protein as a function of binding protein (or target) concentration. The concentration of bound binding protein ([Bound]) is related to the concentration of free binding protein ([Free]) and the concentration of binding sites for the binding protein on the target where (N) is the number of binding sites per target molecule by the following equation:

$$[\text{Bound}] = N \cdot [\text{Free}] / ((1/K_a) + [\text{Free}]).$$

It is not always necessary to make an exact determination of K_a, though, since sometimes it is sufficient to obtain a quantitative measurement of affinity, e.g., determined using a method such as ELISA or FACS analysis, is proportional to K_a, and thus can be used for comparisons, such as determining whether a higher affinity is, e.g., 2-fold higher, to obtain a qualitative measurement of affinity, or to obtain an inference of affinity, e.g., by activity in a functional assay, e.g., an *in vitro* or *in vivo* assay.

An “isolated composition” refers to a composition (e.g., protein) that is removed from at least 90% of at least one component of a natural sample from which the isolated composition can be obtained. Compositions produced artificially or naturally can be “compositions of at least” a certain degree of purity if the species or population of species of interests is at least 5, 10, 25, 50, 75, 80, 90, 92, 95, 98, or 99% pure on a weight-weight basis.

An “epitope” refers to the site on a target compound that is bound by a binding protein (e.g., an antibody such as a Fab or full length antibody). In the case where the target compound is a protein, the site can be entirely composed of amino acid components, entirely composed of chemical modifications of amino acids of the protein (e.g., glycosyl moieties), or composed of combinations thereof. Overlapping epitopes include at least one common amino acid residue, glycosyl group, phosphate group, sulfate group, or other molecular feature.

Calculations of “homology” or “sequence identity” between two sequences (the terms are used interchangeably herein) are performed as follows. The sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in one or both of a first and a second amino acid or nucleic acid sequence for optimal alignment and non-homologous sequences can be

disregarded for comparison purposes). The optimal alignment is determined as the best score using the GAP program in the GCG software package with a Blossum 62 scoring matrix with a gap penalty of 12, a gap extend penalty of 4, and a frameshift gap penalty of 5. The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position (as used herein amino acid or nucleic acid “identity” is equivalent to amino acid or nucleic acid “homology”). The percent identity between the two sequences is a function of the number of identical positions shared by the sequences.

In a preferred embodiment, the length of a reference sequence aligned for comparison purposes is at least 30%, preferably at least 40%, more preferably at least 50%, even more preferably at least 60%, and even more preferably at least 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% of the length of the reference sequence. For example, the reference sequence may be the length of the immunoglobulin variable domain sequence.

As used herein, the term “substantially identical” (or “substantially homologous”) is used herein to refer to a first amino acid or nucleic acid sequence that contains a sufficient number of identical or equivalent (e.g., with a similar side chain, e.g., conserved amino acid substitutions) amino acid residues or nucleotides to a second amino acid or nucleic acid sequence such that the first and second amino acid or nucleic acid sequences have (or encode proteins having) similar activities, e.g., a binding activity, a binding preference, or a biological activity. In the case of antibodies, the second antibody has the same specificity and has at least 50%, at least 25%, or at least 10% of the affinity relative to the same antigen.

Sequences similar or homologous (e.g., at least about 85% sequence identity) to the sequences disclosed herein are also part of this application. In some embodiments, the sequence identity can be about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or higher. In addition, substantial identity exists when the nucleic acid segments hybridize under selective hybridization conditions (e.g., highly stringent hybridization conditions), to the complement of the strand. The nucleic acids may be present in whole cells, in a cell lysate, or in a partially purified or substantially pure form.

As used herein, the term “hybridizes under low stringency, medium stringency, high stringency, or very high stringency conditions” describes conditions for hybridization and washing. Guidance for performing hybridization reactions can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. Aqueous and nonaqueous methods are described in that reference and either can be used. Specific hybridization conditions referred to herein are as follows: (1) low stringency hybridization conditions in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by two washes in 0.2X SSC, 0.1% SDS at least at 50°C (the temperature of the washes can be increased to 55°C for low stringency conditions); (2) medium stringency hybridization conditions in 6X SSC at about 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 60°C; (3) high stringency hybridization conditions in 6X SSC at about 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 65°C; and (4) very high stringency hybridization conditions are 0.5M sodium phosphate, 7% SDS at 65°C, followed by one or more washes at 0.2X SSC, 1% SDS at 65°C. Very high stringency conditions (4) are the preferred conditions and the ones that should be used unless otherwise specified. The disclosure includes nucleic acids that hybridize with low, medium, high, or very high stringency to a nucleic acid described herein or to a complement thereof, e.g., nucleic acids encoding a binding protein described herein. The nucleic acids can be the same length or within 30, 20, or 10% of the length of the reference nucleic acid. The nucleic acid can correspond to a region encoding an immunoglobulin variable domain sequence described herein.

An MMP-12 binding protein may have mutations (e.g., at least one, two, or four, and/or less than 15, 10, 5, or 3) relative to a binding protein described herein (e.g., conservative or non-essential amino acid substitutions), which do not have a substantial effect on protein function. Whether or not a particular substitution will be tolerated, i.e., will not adversely affect biological properties, such as binding activity can be predicted, e.g., by evaluating whether the mutation is conservative or by the method of Bowie, et al. (1990) *Science* 247:1306-1310.

A “conservative amino acid substitution” is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline,

phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). It is possible for many framework and CDR amino acid residues to include one or more conservative substitutions.

Motif sequences for biopolymers can include positions which can be varied amino acids. For example, the symbol “X” in such a context generally refers to any amino acid (e.g., any of the twenty natural amino acids or any of the nineteen non-cysteine amino acids). Other allowed amino acids can also be indicated for example, using parentheses and slashes. For example, “(A/W/F/N/Q)” means that alanine, tryptophan, phenylalanine, asparagine, and glutamine are allowed at that particular position.

A “non-essential” amino acid residue is a residue that can be altered from the wild-type sequence of the binding agent, e.g., the antibody, without abolishing or more preferably, without substantially altering a biological activity, whereas changing an “essential” amino acid residue results in a substantial loss of activity.

The term “cognate ligand” refers to a naturally occurring ligand of an MMP-12, including naturally occurring variants thereof (e.g., splice variants, naturally occurring mutants, and isoforms).

Statistical significance can be determined by any art known method. Exemplary statistical tests include: the Students T-test, Mann Whitney U non-parametric test, and Wilcoxon non-parametric statistical test. Some statistically significant relationships have a P value of less than 0.05 or 0.02. Particular binding proteins may show a difference, e.g., in specificity or binding, that are statistically significant (e.g., P value < 0.05 or 0.02). The terms “induce”, “inhibit”, “potentiate”, “elevate”, “increase”, “decrease” or the like, e.g., which denote distinguishable qualitative or quantitative differences between two states, and may refer to a difference, e.g., a statistically significant difference, between the two states.

MMP-12 Binding Proteins

The disclosure provides proteins that bind to MMP-12 (e.g., human MMP-12 and/or murine MMP-12) and include at least one immunoglobulin variable region. For example, the MMP-12 binding protein includes a heavy chain (HC) immunoglobulin variable domain

sequence and a light chain (LC) immunoglobulin variable domain sequence. A number of exemplary MMP-12 binding proteins are described herein.

The MMP-12 binding protein may be an isolated protein (e.g., at least 70, 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% free of other proteins).

The MMP-12 binding protein may additionally inhibit MMP-12, e.g., human and/or murine MMP-12. The binding protein can inhibit the catalytic activity of MMP-12 (e.g., human MMP-12). In one embodiment, the protein binds the catalytic domain of human MMP-12, e.g., the protein contacts residues in or near the active site of MMP-12. In some embodiments, the protein does not contact residues in or near the active site of MMP-12 but instead binds elsewhere on MMP-12 and causes a steric change in MMP-12 that affects (e.g., inhibits) its activity.

Exemplary MMP-12 binding proteins include M0134-A02, M134-A05, M134-A07, M134-A09, M134-A10, M134-A11, M0134-B01, M134-B04, M0134-B08, M0134-B11, M0134-C01, M0134-C02, M0134-C06, M0134-C09, M0134-C10, M0134-C11, M0134-C12, M0134-D02, M0134-D03, M0134-E04, M0134-E07, M0134-E08, M134-E11, M0134-F01, M0134-F05, M0134-G02, M0134-G04, M0134-G07, M0135-A03, M0135-A05, M0135-A06, M0135-A07, M0135-B02, M0135-B08, M0135-C01, M0135-C11, M0135-E03, M0135-F03, M0135-F11, M0135-G02, M0135-G03, M0135-G07, M0135-G11, M0135-H03, M0135-H10, M0105-C05, M0105-E11, M0105-F08, M0107-A12, M0108-A02, M0109-G11, M0110-G05, M0129-B11, M0130-A01, M0130-C12, M0130-F06, M0130-H04, M0131-A06, M0131-D03, M0132-A04, M0133-B08, M0133-E05, M0121-E07, M0118-F11, M0125-G07, M0124-E07, M0119-D01, M0119-A02, M0122-C06, M0123-G07, M0063-A02, M0063-A04, M0063-B01, M0063-B11, M0063-C07, M0063-G01, M0065-E12, M0065-G03, M0065-H05, M0067-A02, M0067-B06, M0067-B09, M0067-C10, M0067-F02, M0067-F06, M0069-A04, M0069-A11, M0069-C02, M0069-D10, M0069-G07, M0071-A01, M0071-B07, M0071-D05, M0071-D09, M0071-H03, M0071-H06, M0087-F09, M0088-F07, M0088-G10, M0088-H10, M0089-C01, M0089-F05, M0089-B07, M0089-H11, , M0034-C04, M0039-F01, M0041-B05, M0041-G01, M0042-B06, M0006-B10, M0007-H06, M0008-H09, M0009-H08, M0011-H11, M0015-F02, M0016-D01, M0013-D11, M0013-G12, M0013-H06, M0014-C09, M0014-G11, M0016-A11, M0016-H05, M0019-C05, M0020-B01, M0022-C07, M0025-D04 and M0027-E11. Preferably, the MMP-12 binding protein is M0030-A10, M0008-H09, M0032-H09, M0038-A03, M0038-

H04, M0039-B02, M0040-B05, M0041-A05, R011-B11, M0007-A10 (also referred to as M7A10) or M0008-E08 (also referred to as M8E8).

MMP-12 binding proteins may be antibodies. MMP-12 binding antibodies may have their HC and LC variable domain sequences included in a single polypeptide (e.g., scFv), or on different polypeptides (e.g., IgG or Fab).

Matrix Metalloproteinase 12 (MMP-12)

MMP-12 Sequences. MMP-12 is encoded by a gene designated as *MMP12* with full name Matrix metalloproteinase-12 precursor. Synonyms for MMP-12 include matrix metalloproteinase 12, macrophage elastase, macrophage metalloelastase. The DNA sequence is known for *Homo sapiens* and *Mus musculus*. An exemplary cDNA sequence encoding human *MMP12* and the amino acid sequence are shown below. Exemplary cDNA sequences encoding murine *MMP12* and amino acid sequences are also shown below. An exemplary MMP-12 protein can include the human or mouse MMP-12 amino acid sequence, a sequence that is 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to one of these sequences, or a fragment thereof, e.g., a fragment without the signal sequence or prodomain.

cDNA and amino acid sequences of human *MMP12*

```
>embl|BC112301|BC112301 Homo sapiens matrix metalloproteinase 12
(matrix metalloproteinase), mRNA (cDNA clone MGC:138506 IMAGE:8327769),
complete cds
atgaagtttcttctaataactgct
cctgcaggccactgcttctggagctcttccctgaacagctctacaagcctggaaaaaa
taatgtgctatattggtgaaagatacttagaaaaattttatggccttgagataaacaact
tccagtgcacaaaaatgaaatatagtggaacttaatgaaggaaaaaatccaagaaatgca
gcacttcttgggtctgaaagtgaccgggcaactggacacatctaccctggagatgatgca
cgcacctcgatgtggagtccccgatgtccatcatttcagggaaatgccaggggggcccgt
atggaggaaacattatatcacctacagaatcaataattacacacctgacatgaaccgtga
ggatgttgactacgcaatccggaaagctttccaagtatggagtaattgttacccttgaa
attcagcaagattaacacaggcatggctgacattttggtggtttttgcccgtggagctca
tggagacttccatgcttttgatggcaaaggtggaatcctagcccatgcttttgacctgg
atctggcattggaggggatgcacatttcgatgaggacgaattctggactacacattcagg
aggcacaacttggttcctcactgctgttcacgagattggccattccttaggtcttgcca
```

ttctagtgatccaaaggccgtaatgttccccacctacaaatatgttgacatcaacacatt
 tcgcctctctgctgatgacatacgtggcattcagtcctgtatggagacccaaaagagaa
 ccaacgcttgccaaatcctgacaattcagaaccagctctctgtgaccccaatttgagttt
 tgatgctgtcactaccgtgggaaataagatctttttcttcaaagacaggttcttctggct
 gaaggtttctgagagaccaaagaccagtggttaatttaatttcttccttatggccaacctt
 gccatctggcattgaagctgcttatgaaattgaagccagaaatcaagtttttctttttaa
 agatgacaaatactgggttaattagcaatttaagaccagagccaaattatcccaagagcat
 acattcttttggttttcctaactttgtgaaaaaattgatgcagctgtttttaaccacg
 tttttataggacctacttctttgtagataaccagttatggagggtatgatgaaaggagaca
 gatgatggacctgggttatcccaaactgattaccaagaacttccaaggaatcgggcctaa
 aattgatgcagctcttctactctaaaaacaaatactactatttcttccaaggatctaacca
 atttgaatatgacttctactccaacgtatcaccaaaacactgaaaagcaatagctgggt
 tgggttgtagaaatgggtgtaattaatgggtttttgtagttcacttcagcttaataagtat
 ttattgcataatttgctatgtcctcagtgtagcactacttagagatatgtatcataaaaat
 aaaatctgtaaaccataggtaatgattatataaaatacataatatttttcaattttgaaa
 actctaattgtccattcttgcttgactctactattaagtttgaaaatagttaccttcaaa
 ggccaagagaattctatttgaagcatgctctgtaagttgcttcctaacat

>Amino acid sequence of human MMP12 (AAI12302.1)

MKFLLILLQATASGALPLNSSTSLEKNNVLFGERYLEKFYGLEINKLPVTKMKYSGNLM
 KEKIQEMQHFLGLKVTGQLDSTLEMMHAPRCGVPDVHFFREMPGGPVWRKHYITYRINN
 YTPDMNREDVDYAIRKAFQVWSNVTPFKFSKINTGMADILVVFARGAHGDFHAFDGKGGI
 LAHAFGPGSGIGGDAHFEDEFWTHSGGTNLFLTAVHEIGHSLGLGHSSDPKAVMFPTY
 KYVDINTFRLSADDIRGIQSLYGDPKENQRLPNPDNSEPALCDPNLSFDAVTTVGNKIFF
 FKDRFFWLKVSRPKTSVNLISLWPTLPSGIEAAYEIEARNQVFLFKDDKYWLISNLRP
 EPNYPKSIHSEFGFPNFVKKIDA AVFNPRFYRTYFFVDNQYWRYDERRQMMDPGYPKLITK
 NFQGIGPKIDAVFYSKNKYYYFFQGSNQFEYDFLLQRITKTLKSNSWFGC

Polymorphisms in the MMP-12 gene are described, for example, in (2002) *J Am Coll Cardiol.* 3:40(1):43-8, (2002) *Hum Mol Genet.* 1:11(5):569-76., (2001) *Stroke* 32(9):2198-202., and (2000) *Circ Res.* 86(9):998-1003.

cDNA and amino acid sequences of mouse *MMP12*

> Mouse MMP-12 cDNA sequence (NM_008605)

1 ACTCTGCTGAAAGGAGTCTGCACAATGAAATTTCTCATGATGATTGTGTTCTTACAGGTA
 61 TCTGCCTGTGGGGCTGCTCCCATGAATGACAGTGAATTTGCTGAATGGTACTTGTCAAGA
 121 TTTTATGATTATGGAAAGGACAGAATTCCAATGACAAAAACAAAAACCAATAGAACTTC

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181      CTAAAAGAAAACTCCAGGAAATGCAGCAGTTCTTTGGGCTAGAAGCAACTGGGCAACTG
241      GACAACTCAACTCTGGCAATAATGCACATCCCTCGATGTGGAGTGCCCGATGTACAGCAT
301      CTTAGAGCAGTGCCCCAGAGGTCAAGATGGATGAAGCGGTACCTCACTTACAGGATCTAT
361      AATTACACTCCGGACATGAAGCGTGAGGATGTAGACTACATATTTTCAGAAAGCTTTCCAA
421      GTCTGGAGTGATGTGACTCCTCTAAGATTCAGAAAGCTTCATAAAGATGAGGCTGACATT
481      ATGATACTTTTTTGCATTTGGAGCTCACGGAGACTTCAACTATTTTGATGGCAAAGGTGGT
541      AACTAGCCCATGCTTTTTTATCCTGGACCTGGTATTCAAGGAGATGCACATTTTGATGAG
601      GCAGAAACGTGGACTAAAAGTTTTCAAGGCACAAACCTCTTCCTTGTTGCTGTTTCATGAA
661      CTTGGCCATTCTTGTTGGGGCTGCAGCATTCCTCAATAATCCAAAGTCAATAATGTACCCACC
721      TACAGATACCTTAACCCAGCACATTTTCGCTCTCTGCTGATGACATACGTAACATTCAG
781      TCCCTCTATGGAGCCCCAGTGAAACCCCATCCTTGACAAAACCTAGCAGTCCACCATCA
841      ACTTTCTGTCACCAAAGCTTGAGTTTTGATGCTGTCACAACAGTGGGAGAGAAAATCTTT
901      TTCTTTAAAGACTGGTTCTTCTGGTGGAAGCTTCCTGGGAGTCCAGCCACCAACATTACT
961      TCTATTTCTTCCATATGGCCAAGCATCCCATCTGGTATTCAAGCTGCTTACGAAATTGAA
1021     AGCAGAAATCAACTTTTCTTTTAAAGATGAGAAGTACTGGTTAATAAACAACCTTAGTA
1081     CCAGAGCCACACTATCCCAGGAGCATATATTCCTGGGCTTCTCTGCATCTGTGAAGAAG
1141     GTTGATGCAGCTGTCTTTGACCCACTTCGCCAAAAGGTTTATTTCTTTGTGGATAAACAC
1201     TACTGGAGGTATGATGTGAGGCAGGAGCTCATGGACCCTGCTTACCCCAAGCTGATTTCC
1261     ACACACTTCCCAGGAATCAAGCCTAAAATTGATGCAGTCCTCTATTTCAAAGACACTAC
1321     TACATCTTCCAAGGAGCCTATCAATTGGAATATGACCCCCTGTTCCGTCGTGTCACCAAA
1381     ACATTGAAAAGTACAAGCTGGTTTGGTTGT

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**>Amino acid sequence of mouse MMP12 (based on accession number
NM_008605)**

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MKFLMMIVFLQVSACGAAPMNDSEFAEWYLSRFYDYGKDRI PMTKTKTN
RNFLKEKLQEMQQFFGLEATGQLDNSTLAIMHIPRCGVDPDVQHLRAVPQ
RSRWMKRYLTYRIYNYTPDMKREDVDYIFQKAFQVWSDVTPLRFRKLHK
DEADIMILFAFGAHGDFNYFDGKGGTLAHAFYPGPGLQGDHFDDEAETW
TKSFQGTNLFLVAVHELGHSLGLQHSNNPKSIMYPTYRYLNPSTFRLSA
DDIRNIQSLYGAPVKPPSLTKPSSPPSTFCHQSLSFDAVTTVGEKIFFF
KDWFFWWKLPGPSATNITSISSIWPSIPSGIQAAYEIESRNQLFLFKDE
KYWLINNVLVPEPHYPRSIYSLGFSASVKKVDAVFDPLRQKVYFFVDKH
YWRYDVRQELMDPAYPKLISTHFPGIKPKIDAVLYFKRHYYIFQGAYQL
EYDPLFRRVTKTLKSTSWFGC

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Factors that regulate MMP-12. Expression of MMP-12 is regulated by many factors.

Reports of upregulation include: Oncogene. 2004 Jan 22;23(3):845-51. (recurrence in stage I

lung cancer, 2/10 cases), *Ann Neurol.* 2003 Jun;53(6):731-42. (collagenase-induced rat model of intracerebral hemorrhage), *Cancer Res.* 2005 May 15;65(10):4261-72. (protein kinase C/p53 resistant cells), *Br J Dermatol.* 2005 Apr;152(4):720-6. (Samples from nine patients with squamous cell carcinoma), *Cardiovasc Res.* 2005 May 1;66(2):410-9. (Aging), *J Immunol.* 2005 Apr 15;174(8):4953-9. (Surfactant protein D -/- mice), *J Biol Chem.* 2005 Jun 3;280(22):21653-60. (Corneal wound repair), *Surgery.* 2005 Apr;137(4):457-62. (periaortic application of CaCl₂ in mice), *J Virol.* 2005 Apr;79(8):4764-73. (murine viral encephalitis), *Biochem Biophys Res Commun.* 2005 Apr 29;330(1):194-203. (cigarette smoke condensate in mice), *Inflamm Res.* 2005 Jan;54(1):31-6. (bronchoalveolar lavage and lung tissue from COPD patients), *Am J Respir Cell Mol Biol.* 2005 Apr;32(4):311-8. (Induction of human IL-1beta in transgenic mice), *Toxicol Pathol.* 2004 May-Jun;32(3):351-6. (Cigarette smoke in mice), *Am J Physiol Lung Cell Mol Physiol.* 2004 Apr;286(4):L801-7. (lysosomal acid lipase gene knockout mice), *J Neurosci.* 2004 Feb 11;24(6):1521-9. (A1 adenosine receptor null mice), *J Neuroimmunol.* 1998 Jul 1;87(1-2):62-72. (experimentally-induced delayed type hypersensitivity model of MS), *Scand J Immunol.* 2005 Jan;61(1):10-7. (IL-4), *J Pediatr Gastroenterol Nutr.* 2005 Jan;40(1):60-6. (Enterocolitis), *J Cell Physiol.* 2005 Jul;204(1):139-45. (Statins), *J Immunol.* 2004 Oct 15;173(8):5209-18. (experimental autoimmune encephalomyelitis), *J Cardiovasc Pharmacol.* 2004 Jul;44(1):57-65. (hypercholesterolemic hamsters with endothelial injury in the carotid artery), *Cancer Metastasis Rev.* 2004 Jan-Jun;23(1-2):101-17. (colorectal cancer), *Free Radic Biol Med.* 2004 Mar 15;36(6):782-801. (oxidative stress), *Chest.* 2004 Feb;125(2):466-72. (Wood smoke, cigarette smoke, CPOD).

Down regulation or no upregulation is reported in Inflammation. 2003 Apr;27(2):107-13. (Mice immunized with type II collagen), *Cancer Res.* 2003 Jan 1;63(1):256-62. (Epstein-Barr virus proteins; nasopharyngeal carcinoma), *Curr Eye Res.* 1998 Feb;17(2):132-40. (human interphotoreceptor matrix and vitreous from postmortem human eyes), and *Scand J Immunol.* 2005 Jan;61(1):10-7 (dexamethasone).

Endogenous inhibitors of MMP-12. MMP-12 has a number of endogenous inhibitors. Like other MMPs, MMP-12 is inhibited by TIMPs (Murphy, G., and Willenbrock, F. (1995) *Methods Enzymol.* 248, 496-510).

Small molecule inhibitors of MMP-12. Small molecule inhibitors of MMP-12 have been synthesized and tested. Most of these have either insufficient potency or insufficient specificity, or both. The reports include: Proc Natl Acad Sci USA. 2005 Apr 12;102(15):5334-9. (acetohydroxamic acid and N-isobutyl-N-[4-methoxyphenylsulfonyl]glycyl hydroxamic acid); Arthritis Rheum. 2004 Oct;50(10):3275-85. (a general hydroxamate inhibitor of MMP activity); Arch Biochem Biophys. 2003 Jan 15;409(2):335-40. (peptide lin24); J Mol Biol. 2001 Sep 28;312(4):743-51. (hydroxamic acid inhibitor, CGS27023A); J Mol Biol. 2001 Sep 28;312(4):731-42. (batimastat (BB-94)); Anticancer Res. 2001 Jan-Feb;21(1A):145-55. (AE-941, an orally bioavailable extract made of cartilage); J Comb Chem. 2000 Nov-Dec;2(6):624-38. (XXX-Gpsi(PO2H-CH2)L-XXX library on beads); Biochim Biophys Acta. 2000 Mar 16;1478(1):51-60. (green tea polyphenols); J Leukoc Biol. 1984 May;35(5):449-57. (peptide chloromethyl ketone); Am Rev Respir Dis. 1982 Feb;125(2):203-7. (a battery of elastase inhibitors); Mem Inst Oswaldo Cruz. 2005 Mar;100:167-172. (marimastat); J Mol Biol. 2004 Aug 20;341(4):1063-76. (CP-271485, PF-00356231, and PD-0359601); Inflamm Res. 2003 Mar;52(3):95-100.¹; Bioorg Med Chem Lett. 2004 Oct 4;14(19):4935-9. (inhibitors with novel oxazoline zinc binding groups); and J Cardiovasc Pharmacol. 2004 Jul;44(1):57-65. (ONO-4817). Other small molecule inhibitors of MMP-12 are described, e.g., in US Patent Application No: 20050014817 (Fluorothiophene derivatives), US Patent Application No.: 20050014816 (Thiophene amino acid derivatives), US Patent 6,770,640 (1-Carboxymethyl-2-oxo-azepan derivatives), PCT Publication No.: WO200040577 (1-Carboxymethyl-2-Oxo-Azepan Derivatives), PCT Publication No.: WO 200532541 (Substituted Heterocyclic Mercaptosulfide Inhibitors), PCT Publication No.: WO 200183431, US Patent Application 20030158155, European Patent No.: 1288199, PCT Publication No.: WO 200040600 and US Patent 6,352,976, US Patent 6,350,907, US Patent 6,924,276, US Patent 6,916,807, US Patent 6,686,355, US Patent 6,548,477 and US Patent 5,506,242. The small molecule can be administered to inhibit MMP-12, e.g., in combination with a MMP-12 binding protein described herein.

Small interfering RNA inhibitors of MMP-12. MMP-12 can be inhibited by small interfering RNA (siRNA). Examples of siRNA that can be used are described in US Patent Publication No.: 20040087533 and PCT Publication No.: WO 200409098. The siRNA can be

administered to inhibit MMP-12, e.g., in combination with a MMP-12 binding protein described herein.

Drug Conjugates

The MMP-12 binding proteins described herein can be conjugated to a drug (e.g., a cytotoxic, cytostatic, or immunomodulatory agent). The conjugates can be used therapeutically or prophylactically, e.g., the binding protein can target the drug, e.g., *in vivo*, e.g., to a site of disease (e.g., a tumor or site of inflammation), e.g., such that the drug affects the site of disease (e.g., causes a cytostatic or cytotoxic effect on targeted cells).

In some embodiments, the binding protein itself has therapeutic or prophylactic efficacy (e.g., the protein can modulate (e.g., antagonize) MMP-12, or cause a cytostatic or cytotoxic effect on a cell that expresses MMP-12 (e.g., an endothelial cell or tumor cell)). The binding protein-drug conjugate can be used such that the binding protein and drug both contribute (e.g., additively or synergistically) to an effect on MMP-12 (e.g., a therapeutic effect, e.g., *in vivo*, e.g., to a site of disease (e.g., a tumor or site of undesired angiogenesis or vascularization)). The drug and/or binding protein can be, for example, cytotoxic, cytostatic or otherwise prevent or reduce the ability of a targeted cell to divide and/or survive (e.g., when the drug is taken up or internalized by the targeted cell and/or upon binding of the binding protein to MMP-12). For example, if the targeted cell is a cancer cell, the drug and/or binding protein can prevent or reduce the ability of the cell to divide and/or metastasize.

Useful classes of drugs that can be used in the binding protein-drug conjugates described herein include cytotoxic or immunomodulatory agents such as, for example, antitubulin agents, auristatins, DNA minor groove binders, DNA replication inhibitors, alkylating agents (e.g., platinum complexes such as cis-platin, mono(platinum), bis(platinum) and tri-nuclear platinum complexes and carboplatin), anthracyclines, antibiotics, antifolates, antimetabolites, chemotherapy sensitizers, duocarmycins, etoposides, fluorinated pyrimidines, ionophores, lexitropsins, nitrosoureas, platinols, pre-forming compounds, purine antimetabolites, puromycins, radiation sensitizers, steroids, taxanes, topoisomerase inhibitors, vinca alkaloids, or the like.

Individual cytotoxic or immunomodulatory agents include, for example, an androgen, anthramycin (AMC), asparaginase, 5-azacytidine, azathioprine, bleomycin, busulfan, buthionine

sulfoximine, camptothecin, carboplatin, carmustine (BSNU), CC-1065, chlorambucil, cisplatin, colchicine, cyclophosphamide, cytarabine, cytidine arabinoside, cytochalasin B, dacarbazine, dactinomycin (actinomycin), daunorubicin, decarbazine, docetaxel, doxorubicin, an estrogen, 5-fluorodeoxyuridine, 5-fluorouracil, gramicidin D, hydroxyurea, idarubicin, ifosfamide, irinotecan, lomustine (CCNU), mechlorethamine, melphalan, 6-mercaptopurine, methotrexate, mithramycin, mitomycin C, mitoxantrone, nitroimidazole, paclitaxel, plicamycin, procarbazine, rapamycin (Sirolimus), streptozotocin, tenoposide, 6-thioguanine, thioTEPA, topotecan, vinblastine, vincristine, vinorelbine, VP-16 and VM-26.

In some typical embodiments, the drug comprises a cytotoxic agent. Suitable cytotoxic agents include, for example, dolastatins (e.g., auristatin E, AFP, MMAF, MMAE), DNA minor groove binders (e.g., enediynes and lexitropsins), duocarmycins, taxanes (e.g., paclitaxel and docetaxel), puromycins, vinca alkaloids, CC-1065, SN-38, topotecan, morpholino-doxorubicin, rhizoxin, cyanomorpholino-doxorubicin, echinomycin, combretastatin, netropsin, epothilone A and B, estramustine, cryptophysins, cemadotin, maytansinoids, discodermolide, eleutherobin, and mitoxantrone.

In some embodiments, the drug is a cytotoxic agent such as AFP, MMAF, MMAE, AEB, AEVB, auristatin E, paclitaxel, docetaxel, CC-1065, SN-38, topotecan, morpholino-doxorubicin, rhizoxin, cyanomorpholino-doxorubicin, dolastatin-10, echinomycin, combretastatin, calicheamicin, maytansine, DM-1, or netropsin.

In some embodiments, the drug is a cytotoxic agent that comprises a conventional chemotherapeutic such as, for example, doxorubicin, paclitaxel, melphalan, vinca alkaloids, methotrexate, mitomycin C or etoposide. In some embodiments, the drug can be a combined therapy, such as CHOP (Cyclophosphamide, Doxorubicin, Prednisolone and Vincristine), CHOP-R (Cyclophosphamide, Doxorubicin Vincristine, Prednisolone, and rituximab) or ABVD (Doxorubicin, Bleomycin, Vinblastine and Dacarbazine). Agents such as CC-1065 analogues (e.g., DC1), calicheamicin, maytansine, analogues of dolastatin 10, rhizoxin, and palytoxin can also be used.

In specific embodiments, the drug can be a cytotoxic or cytostatic agent that comprises auristatin E (also known in the art as dolastatin-10) or a derivative thereof. Typically, the auristatin E derivative is, e.g., an ester formed between auristatin E and a keto acid. For example, auristatin E can be reacted with paraacetyl benzoic acid or benzoylvaleric acid to

produce AEB and AEVB, respectively. Other auristatin derivatives include AFP, MMAF, and MMAE. The synthesis and structure of auristatin E and its derivatives are described in US 20030083263 and US 20050009751, and U.S. Pat. Nos. 6,323,315; 6,239,104; 6,034,065; 5,780,588; 5,665,860; 5,663,149; 5,635,483; 5,599,902; 5,554,725; 5,530,097; 5,521,284; 5,504,191; 5,410,024; 5,138,036; 5,076,973; 4,986,988; 4,978,744; 4,879,278; 4,816,444; and 4,486,414. In some preferred embodiments, MMAF or AFP is used.

In specific embodiments, the drug is a cytotoxic agent that comprises a DNA minor groove binding agent. See, e.g., U.S. Pat. No. 6,130,237. For example, in some embodiments, the minor groove binding agent is a CBI compound. In other embodiments, the minor groove binding agent is an enediyne (e.g., calicheamicin).

Examples of anti-tubulin agents that can be used in the MMP-12 binding protein-drug conjugates include, but are not limited to, taxanes (e.g., TAXOL® (paclitaxel), TAXOTERE® (docetaxel)), T67 (Tularik), vinca alkyls (e.g., vincristine, vinblastine, vindesine, and vinorelbine), and dolastatins (e.g., auristatin E, AFP, MMAF, MMAE, AEB, AEVB). Other antitubulin agents include, for example, baccatin derivatives, taxane analogs (e.g., epothilone A and B), nocodazole, colchicine and colcimid, estramustine, cryptophysins, cemadotin, maytansinoids, combretastatins, discodermolide, eleutherobin, rhizoxin/maytansine, auristatin dolastatin 10 MMAE, and peloruside A.

In some embodiments, the drug is a cytotoxic agent such as an anti-tubulin agent. In some embodiments, the anti-tubulin agent is an auristatin, a vinca alkaloid, a podophyllotoxin, a taxane, a baccatin derivative, a cryptophysin, a maytansinoid, a combretastatin, or a dolastatin. In some embodiments, the antitubulin agent is AFP, MMAP, MMAE, AEB, AEVB, auristatin E, vincristine, vinblastine, vindesine, vinorelbine, VP-16, camptothecin, paclitaxel, docetaxel, epothilone A, epothilone B, nocodazole, colchicines, colcimid, estramustine, cemadotin, discodermolide, maytansine, DM1, DM2, DM3, DM4, or eleutherobin.

In some embodiments, the cytotoxic agent comprises a maytansinoid, another group of anti-tubulin agents. For example, in specific embodiments, the maytansinoid is maytansine or DM-1 (ImmunoGen, Inc.; see also Chari et al. *Cancer Res.* 52:127-131 (1992)). In some embodiments, sterically hindered thiol and disulfide-containing maytansinoids in which the alpha-carbon atom bearing the sulfur atom bears one or two alkyl substituents are used in the binding protein-drug conjugate, e.g., US 2007-0292422; US 2007-0264266.

In some embodiments, the drug comprises an agent that acts to disrupt DNA. The drug may be selected from enediynes (e.g., calicheamicin and esperamicin) and non-enediyne small molecule agents (e.g., bleomycin, methidiumpropyl-EDTA-Fe(II)). Other useful drugs include daunorubicin, doxorubicin, distamycin A, cisplatin, mitomycin C, ecteinascidins, duocarmycin/CC-1065, and bleomycin/pepleomycin.

In other embodiments, the drug can comprise an alkylating agent such as Asaley NSC 167780, AZQ NSC 182986, BCNU NSC 409962, Busulfan NSC 750, carboxyphthalatoplatinum NSC 271674, CBDCA NSC 241240, CCNU NSC 79037, CHIP NSC 256927, chlorambucil NSC 3088, chlorozotocin NSC 178248, cis-platinum NSC 119875, clomesone NSC 338947, cyanomorpholinodoxorubicin NSC 357704, cyclodisone NSC 348948, dianhydrogalactitol NSC 132313, fluorodopan NSC 73754, hepsulfam NSC 329680, hycanthone NSC 142982, melphalan NSC 8806, methyl CCNU NSC 95441, mitomycin C NSC 26980, mitozolamide NSC 353451, nitrogen mustard NSC 762, PCNU NSC 95466, piperazine NSC 344007, piperazinedione NSC 135758, pipobroman NSC 25154, porfiromycin NSC 56410, spirohydantoin mustard NSC 172112, teroxirone NSC 296934, tetraplatin NSC 363812, thio-tepa NSC 6396, triethylenemelamine NSC 9706, uracil nitrogen mustard NSC 34462, or Yoshi-864 NSC 102627.

In some embodiments, the drug can comprise an antimitotic agent such as allocolchicine NSC 406042, Halichondrin B NSC 609395, colchicine NSC 757, colchicine derivative NSC 33410, dolastatin 10 NSC 376128 (NG--auristatin derived), maytansine NSC 153858, rhizoxin NSC 332598, taxol NSC 125973, taxol derivative NSC 608832, thiocolchicine NSC 361792, trityl cysteine NSC 83265, vinblastine sulfate NSC 49842, or vincristine sulfate NSC 67574.

In other embodiments, the drug can comprise an topoisomerase I inhibitor such as camptothecin NSC 94600, camptothecin, Na salt NSC 100880, aminocamptothecin NSC 603071, camptothecin derivative NSC 95382, camptothecin derivative NSC 107124, camptothecin derivative NSC 643833, camptothecin derivative NSC 629971, camptothecin derivative NSC 295500, camptothecin derivative NSC 249910, camptothecin derivative NSC 606985, camptothecin derivative NSC 374028, camptothecin derivative NSC 176323, camptothecin derivative NSC 295501, camptothecin derivative NSC 606172, camptothecin derivative NSC 606173, camptothecin derivative NSC 610458, camptothecin derivative NSC 618939, camptothecin derivative NSC 610457, camptothecin derivative NSC 610459, camptothecin derivative NSC 606499, camptothecin derivative NSC 610456, camptothecin

derivative NSC 364830, camptothecin derivative NSC 606497, or morpholinodoxorubicin NSC 354646.

In other embodiments, the drug can comprise an topoisomerase II inhibitor such as doxorubicin NSC 123127, amonafide NSC 308847, m-AMSA NSC 249992, anthrapyrazole derivative NSC 355644, pyrazoloacridine NSC 366140, bisantrene HCL NSC 337766, daunorubicin NSC 82151, deoxydoxorubicin NSC 267469, mitoxantrone NSC 301739, menogaril NSC 269148, N,N-dibenzyl daunomycin NSC 268242, oxanthrazole NSC 349174, rubidazone NSC 164011, VM-26 NSC 122819, or VP-16 NSC 141540.

In other embodiments, the drug can comprise an RNA or DNA antimetabolite such as L-alanosine NSC 153353, 5-azacytidine NSC 102816, 5-fluorouracil NSC 19893, acivicin NSC 163501, aminopterin derivative NSC 132483, aminopterin derivative NSC 184692, aminopterin derivative NSC 134033, an antifol NSC 633713, an antifol NSC 623017, Baker's soluble antifol NSC 139105, dichlorallyl lawsone NSC 126771, brequinar NSC 368390, ftorafur (pro-drug) NSC 148958, 5,6-dihydro-5-azacytidine NSC 264880, methotrexate NSC 740, methotrexate derivative NSC 174121, N-(phosphonoacetyl)-L-aspartate (PALA) NSC 224131, pyrazofurin NSC 143095, trimetrexate NSC 352122, 3-HP NSC 95678, 2'-deoxy-5-fluorouridine NSC 27640, 5-HP NSC 107392, alpha-TGDR NSC 71851, aphidicolin glycinate NSC 303812, ara-C NSC 63878, 5-aza-2'-deoxycytidine NSC 127716, beta-TGDR NSC 71261, cyclocytidine NSC 145668, guanazole NSC 1895, hydroxyurea NSC 32065, inosine glycodialdehyde NSC 118994, macbecin 11 NSC 330500, pyrazoloimidazole NSC 51143, thioguanine NSC 752, or thiopurine NSC 755. See also US 2007-0292441.

The abbreviation "AFP" refers to dimethylvaline-valine-dolaisoleuine-dolaproine-phenylalanine-p-phenylened-iamine (e.g., see Formula XVI in US 2006-0233794).

The abbreviation "MAE" refers to monomethyl auristatin E (see Formula XI in US 2006-0233794).

The abbreviation "AEB" refers to an ester produced by reacting auristatin E with paraacetyl benzoic acid (e.g., see Formula XX in US 2006-0233794)

The abbreviation "AEVB" refers to an ester produced by reacting auristatin E with benzoylvaleric acid (e.g., see Formula XXI in US 2006-0233794).

The abbreviation "MMAF" refers to dovaline-valine-dolaisoleunine-dolaproine-phenylalanine (e.g., see Formula IVIV in US 2006-0233794).

The abbreviations "fk" and "phe-lys" refer to the linker phenylalanine-lysine.

The abbreviations "vc" and "val-cit" refer to the linker valine-citrulline.

In some embodiments, the drug is a cytotoxic agent selected from the group consisting of an auristatin, a DNA minor groove binding agent, a DNA minor groove alkylating agent, an enediyne, a lexitropsin, a duocarmycin, a taxane, a puromycin, a dolastatin, a maytansinoid, and a vinca alkaloid.

In some embodiments, the drug is a cytotoxic agent such as AFP or MMAF.

In some embodiments, the drug is an immunosuppressive agent such as gancyclovir, etanercept, cyclosporine, tacrolimus, rapamycin, cyclophosphamide, azathioprine, mycophenolate mofetil, methotrexate, cortisol, aldosterone, dexamethasone, a cyclooxygenase inhibitor, a 5-lipoxygenase inhibitor, or a leukotriene receptor antagonist.

See generally US 2007-0292441; US 2007-0292422; US 2007-0264266; and US 2006-0233794.

Linkers

The binding proteins described herein can be associated with a drug to form a binding protein-drug conjugate by being linked to the drug directly. In some embodiments, the binding protein is directly conjugated to the drug. Alternatively, the binding proteins described herein can be associated with a drug to form a binding protein-drug conjugate by use of a linker region between the drug and the binding protein. In some embodiments, the binding protein is conjugated to the drug via a linker. The linker can be cleavable under intracellular conditions, e.g., such that cleavage of the linker releases the drug from the binding protein in the intracellular environment. In some embodiments, the cleavable linker is a peptide linker cleavable by an intracellular protease. In some embodiments, the peptide linker is a dipeptide linker.

In some embodiments, the dipeptide linker is a val-cit (vc) linker or a phe-lys (fk) linker. In some embodiments, the cleavable linker is hydrolyzable at a pH of less than 5.5. In some embodiments, the hydrolyzable linker is a hydrazone linker. In some embodiments, the cleavable linker is a disulfide linker.

For example, in some embodiments, the linker is cleavable by a cleaving agent that is present in the intracellular environment (e.g., within a lysosome or endosome or caveolea). The

linker can be, e.g., a peptidyl linker that is cleaved by an intracellular peptidase or protease enzyme, including, but not limited to, a lysosomal or endosomal protease. In some embodiments, the peptidyl linker is at least two amino acids long or at least three amino acids long. Cleaving agents can include cathepsins B and D and plasmin, which are known to hydrolyze dipeptide drug derivatives resulting in the release of active drug inside target cells (see, e.g., Dubowchik and Walker *Pharm. Therapeutics* 83:67-123 (1999)). In some embodiments, peptidyl linkers are cleavable by enzymes that are present in targeted cells (e.g., cancer cells). For example, a peptidyl linker that is cleavable by the thiol-dependent protease cathepsin-B, which is highly expressed in cancerous tissue, can be used (e.g., a Phe-Leu or a Gly-Phe-Leu-Gly linker). Other such linkers are described, e.g., in U.S. Pat. No. 6,214,345. In some embodiments, the peptidyl linker cleavable by an intracellular protease is a Val-Cit (vc) linker or a Phe-Lys linker (fk) (see, e.g., U.S. Pat. No. 6,214,345, which describes the synthesis of doxorubicin with the val-cit linker). One advantage of using intracellular proteolytic release of the drug is that the drug can be attenuated when conjugated and the serum stabilities of the conjugates are typically high.

In some preferred embodiments, a vc linker is used in the binding protein-drug conjugates described herein. For example, a binding protein-vcAFP or a binding protein-vcMMAF conjugate (e.g., a MMP-12 binding protein-vcAFP or a MMP-12 binding protein-vcMMAF conjugate) is prepared.

In other embodiments, the cleavable linker is pH-sensitive, i.e., sensitive to hydrolysis at certain pH values. For example, the pH-sensitive linker is hydrolyzable under acidic conditions. For example, an acid-labile linker that is hydrolyzable in the lysosome (e.g., a hydrazone, semicarbazone, thiosemicarbazone, cis-aconitic amide, orthoester, acetal, ketal, or the like) can be used. See, e.g., U.S. Pat. Nos. 5,122,368; 5,824,805; 5,622,929; Dubowchik and Walker *Pharm. Therapeutics* 83:67-123 (1999); Neville et al. *Biol. Chem.* 264:14653-14661 (1989). Such linkers are relatively stable under neutral pH conditions, such as those in the blood, but are unstable at below pH 5.5 or 5.0, the approximate pH of the lysosome. In certain embodiments, the hydrolyzable linker is a thioether linker (such as, e.g., a thioether attached to the therapeutic agent via an acylhydrazone bond (see, e.g., U.S. Pat. No. 5,622,929)).

In yet other embodiments, the linker is cleavable under reducing conditions (e.g., a disulfide linker). A variety of disulfide linkers are known in the art, including, for example,

those that can be formed using SATA (N-succinimidyl-S-acetylthioacetate), SPDP (N-succinimidyl-3-(2-pyridyldithio)propionate), SPDB (N-succinimidyl-3-(2-pyridyldithio)butyrate) and SMPT (N-succinimidyl-oxycarbonyl-alpha-methyl-alpha-(2-pyridyl-dithio)toluene)-, SPDB and SMPT (See, e.g., Thorpe et al. *Cancer Res.* 47:5924-5931 (1987); Wawrzynczak et al., In *Immunoconjugates: Antibody Conjugates in Radioimager and Therapy of Cancer* (C. W. Vogel ed., Oxford U. Press, 1987). See also U.S. Pat. No. 4,880,935.

In yet other embodiments, the linker is a malonate linker (Johnson et al. *Anticancer Res.* 15:1387-93 (1995)), a maleimidobenzoyl linker (Lau et al. *Bioorg-Med-Chem.* 3(10):1299-1304 (1995), or a 3'-N-amide analog (Lau et al. *Bioorg-Med-Chem.* 3(10):1305-12 (1995)).

In some embodiments, the linker is not substantially sensitive to the extracellular environment. As used herein, "not substantially sensitive to the extracellular environment," in the context of a linker, means that no more than about 20%, typically no more than about 15%, more typically no more than about 10%, and even more typically no more than about 5%, no more than about 3%, or no more than about 1% of the linkers, in a sample of a binding protein-drug conjugate, are cleaved when the binding protein-drug conjugate is present in an extracellular environment (e.g., in plasma). Whether a linker is not substantially sensitive to the extracellular environment can be determined, for example, by incubating independently with plasma both (a) the binding protein-drug conjugate (the "conjugate sample") and (b) an equal molar amount of unconjugated binding protein or drug (the "control sample") for a predetermined time period (e.g., 2, 4, 8, 16, or 24 hours) and then comparing the amount of unconjugated binding protein or drug present in the conjugate sample with that present in control sample, as measured, for example, by high performance liquid chromatography.

In other, non-mutually exclusive embodiments, the linker promotes cellular internalization. In certain embodiments, the linker promotes cellular internalization when conjugated to the drug (i.e., in the milieu of the linker-drug moiety of the binding protein-drug conjugate described herein). In yet other embodiments, the linker promotes cellular internalization when conjugated to both the drug and the binding protein.

A variety of linkers that can be used with the present compositions and methods are described in WO 2004010957.

In some embodiments, the binding protein-drug conjugates described herein are used therapeutically in the treatment of a disorder (e.g., cancer or inflammation). In certain

embodiments, it is desirable to only target a binding protein-drug conjugate to a cell that expresses the target to which the binding protein binds (e.g., to only target a MMP-12 expressing cell to which a MMP-12 binding protein binds, and not target a nearby “bystander” cell), e.g., to minimize toxicity. In other embodiments, it is desirable to target a binding protein-drug conjugate to a cell expressing the target to which the binding protein binds and also to bystander cells (e.g., to elicit a “bystander effect”). In some embodiments, a binding protein-drug conjugate (e.g., a MMP-12 binding protein-drug conjugate can be engineered to exert a precise killing of only antigen-presenting cells without damaging proximal antigen-negative tissues, e.g., by preparing thioether-linked conjugates. Alternatively, it can be engineered to produce a bystander effect, e.g., by preparing disulfide-linked conjugates.

For example, many solid tumors express targets (e.g., antigens) in a heterogeneous fashion and are populated with both target-positive and target-negative cells. The bystander cytotoxicity associated with disulfide linker-containing conjugates provides a rationale for treatment of sites of a disorder (e.g., tumors) with binding protein-drug conjugates even if the sites exhibit heterogeneous target expression. The bystander effect adds a degree of nonselective killing activity. Potentially, this could be a drawback if normal cells in tissues surrounding the site of disorder (e.g., tumor) are affected. However, as a potential advantage, the bystander cytotoxicity may damage tissues intricately involved in supporting the disorder, such as endothelial cells and pericytes of tumor neovasculature, or tumor stromal cells, resulting, for example, in enhanced antitumor activity of the binding protein-drug conjugate against tumors expressing the antigen either homogeneously or heterogeneously. See also Kovtum et al. *Cancer Res.* 66:3214 (2006).

Techniques for conjugating therapeutic agents to proteins (such as binding proteins, e.g., MMP-12 binding proteins) are known. See, e.g., Arnon et al., “Monoclonal Antibodies For Immunotargeting Of Drugs In Cancer Therapy,” in *Monoclonal Antibodies And Cancer Therapy* (Reisfeld et al eds., Alan R. Liss, Inc., 1985); Hellstrom et al., “Antibodies For Drug Delivery,” in *Controlled Drug Delivery* (Robinson et al. eds., Marcel Dekker, Inc., 2nd ed. 1987); Thorpe, “Antibody Carriers Of Cytotoxic Agents In Cancer Therapy: A Review,” in *Monoclonal Antibodies '84: Biological And Clinical Applications* (Pinchera et al. eds., 1985); “Analysis, Results, and Future Prospective of the Therapeutic Use of Radiolabeled Antibody In Cancer Therapy,” in *Monoclonal Antibodies For Cancer Detection And Therapy* (Baldwin et al. eds.,

Academic Press, 1985); and Thorpe et al. *Immunol. Rev.* 62:119-58 (1982). See also, e.g., US 2006-0233794 and PCT publication WO 89/12624.

Display Libraries

A display library is a collection of entities; each entity includes an accessible polypeptide component and a recoverable component that encodes or identifies the polypeptide component. The polypeptide component is varied so that different amino acid sequences are represented. The polypeptide component can be of any length, e.g. from three amino acids to over 300 amino acids. A display library entity can include more than one polypeptide component, for example, the two polypeptide chains of a sFab. In one exemplary implementation, a display library can be used to identify proteins that bind to MMP-12. In a selection, the polypeptide component of each member of the library is probed with MMP-12 (e.g., the catalytic domain of MMP-12 or other fragment) and if the polypeptide component binds to the MMP-12, the display library member is identified, typically by retention on a support.

Retained display library members are recovered from the support and analyzed. The analysis can include amplification and a subsequent selection under similar or dissimilar conditions. For example, positive and negative selections can be alternated. The analysis can also include determining the amino acid sequence of the polypeptide component and purification of the polypeptide component for detailed characterization.

A variety of formats can be used for display libraries. Examples include the following.

Phage Display: The protein component is typically covalently linked to a bacteriophage coat protein. The linkage results from translation of a nucleic acid encoding the protein component fused to the coat protein. The linkage can include a flexible peptide linker, a protease site, or an amino acid incorporated as a result of suppression of a stop codon. Phage display is described, for example, in U.S. 5,223,409; Smith (1985) *Science* 228:1315-1317; WO 92/18619; WO 91/17271; WO 92/20791; WO 92/15679; WO 93/01288; WO 92/01047; WO 92/09690; WO 90/02809; de Haard *et al.* (1999) *J. Biol. Chem* 274:18218-30; Hoogenboom *et al.* (1998) *Immunotechnology* 4:1-20; Hoogenboom *et al.* (2000) *Immunol Today* 2:371-8 and Hoet *et al.* (2005) *Nat Biotechnol.* **23**(3)344-8. Bacteriophage displaying the protein component can be grown and harvested using standard phage preparatory methods, e.g. PEG precipitation from growth media. After selection of individual display phages, the nucleic acid encoding the

selected protein components can be isolated from cells infected with the selected phages or from the phage themselves, after amplification. Individual colonies or plaques can be picked, the nucleic acid isolated and sequenced.

Other Display Formats. Other display formats include cell based display (see, e.g., WO 03/029456), protein-nucleic acid fusions (see, e.g., US 6,207,446), ribosome display (See, e.g., Mattheakis *et al.* (1994) *Proc. Natl. Acad. Sci. USA* 91:9022 and Hanes *et al.* (2000) *Nat Biotechnol.* 18:1287-92; Hanes *et al.* (2000) *Methods Enzymol.* 328:404-30; and Schaffitzel *et al.* (1999) *J Immunol Methods.* 231(1-2):119-35), and *E. coli* periplasmic display (J Immunol Methods. 2005 Nov 22;PMID: 16337958).

Scaffolds. Scaffolds useful for display include: antibodies (e.g., Fab fragments, single chain Fv molecules (scFV), single domain antibodies, camelid antibodies, and camelized antibodies); T-cell receptors; MHC proteins; extracellular domains (e.g., fibronectin Type III repeats, EGF repeats); protease inhibitors (e.g., Kunitz domains, ecotin, BPTI, and so forth); TPR repeats; trifoil structures; zinc finger domains; DNA-binding proteins; particularly monomeric DNA binding proteins; RNA binding proteins; enzymes, e.g., proteases (particularly inactivated proteases), RNase; chaperones, e.g., thioredoxin and heat shock proteins; intracellular signaling domains (such as SH2 and SH3 domains); linear and constrained peptides; and linear peptide substrates. Display libraries can include synthetic and/or natural diversity. See, e.g., US 2004-0005709.

Display technology can also be used to obtain binding proteins (e.g., antibodies) that bind particular epitopes of a target. This can be done, for example, by using competing non-target molecules that lack the particular epitope or are mutated within the epitope, e.g., with alanine. Such non-target molecules can be used in a negative selection procedure as described below, as competing molecules when binding a display library to the target, or as a pre-elution agent, e.g., to capture in a wash solution dissociating display library members that are not specific to the target.

Iterative Selection. In one preferred embodiment, display library technology is used in an iterative mode. A first display library is used to identify one or more binding proteins for a target. These identified binding proteins are then varied using a mutagenesis method to form a second display library. Higher affinity binding proteins are then selected from the second library, e.g., by using higher stringency or more competitive binding and washing conditions.

In some implementations, the mutagenesis is targeted to regions at the binding interface. If, for example, the identified binding proteins are antibodies, then mutagenesis can be directed to the CDR regions of the heavy or light chains as described herein. Further, mutagenesis can be directed to framework regions near or adjacent to the CDRs. In the case of antibodies, mutagenesis can also be limited to one or a few of the CDRs, e.g., to make precise step-wise improvements. Exemplary mutagenesis techniques include: error-prone PCR, recombination, DNA shuffling, site-directed mutagenesis and cassette mutagenesis.

In one example of iterative selection, the methods described herein are used to first identify a protein from a display library that binds MMP-12 with at least a minimal binding specificity for a target or a minimal activity, e.g., an equilibrium dissociation constant for binding of less than 1 nM, 10 nM, or 100 nM. The nucleic acid sequence encoding the initial identified proteins are used as a template nucleic acid for the introduction of variations, e.g., to identify a second protein that has enhanced properties (e.g., binding affinity, kinetics, or stability) relative to the initial protein.

Off-Rate Selection. Since a slow dissociation rate can be predictive of high affinity, particularly with respect to interactions between polypeptides and their targets, the methods described herein can be used to isolate binding proteins with a desired (e.g., reduced) kinetic dissociation rate for a binding interaction to a target.

To select for slow dissociating binding proteins from a display library, the library is contacted to an immobilized target. The immobilized target is then washed with a first solution that removes non-specifically or weakly bound biomolecules. Then the bound binding proteins are eluted with a second solution that includes a saturating amount of free target or a target specific high-affinity competing monoclonal antibody, i.e., replicates of the target that are not attached to the particle. The free target binds to biomolecules that dissociate from the target. Rebinding is effectively prevented by the saturating amount of free target relative to the much lower concentration of immobilized target.

The second solution can have solution conditions that are substantially physiological or that are stringent. Typically, the solution conditions of the second solution are identical to the solution conditions of the first solution. Fractions of the second solution are collected in temporal order to distinguish early from late fractions. Later fractions include biomolecules that dissociate at a slower rate from the target than biomolecules in the early fractions.

Further, it is also possible to recover display library members that remain bound to the target even after extended incubation. These can either be dissociated using chaotropic conditions or can be amplified while attached to the target. For example, phage bound to the target can be contacted to bacterial cells.

Selecting or Screening for Specificity. The display library screening methods described herein can include a selection or screening process that discards display library members that bind to a non-target molecule. Examples of non-target molecules include streptavidin on magnetic beads, blocking agents such as bovine serum albumin, non-fat bovine milk, any capturing or target immobilizing monoclonal antibody, or non-transfected cells which do not express the human MMP-12 target.

In one implementation, a so-called “negative selection” step is used to discriminate between the target and related non-target molecule and a related, but distinct non-target molecules. The display library or a pool thereof is contacted to the non-target molecule. Members of the sample that do not bind the non-target are collected and used in subsequent selections for binding to the target molecule or even for subsequent negative selections. The negative selection step can be prior to or after selecting library members that bind to the target molecule.

In another implementation, a screening step is used. After display library members are isolated for binding to the target molecule, each isolated library member is tested for its ability to bind to a non-target molecule (e.g., a non-target listed above). For example, a high-throughput ELISA screen can be used to obtain this data. The ELISA screen can also be used to obtain quantitative data for binding of each library member to the target as well as for cross species reactivity to related targets or subunits of the target (e.g., mouse MMP-12) and also under different condition such as pH6 or pH 7.5. The non-target and target binding data are compared (e.g., using a computer and software) to identify library members that specifically bind to the target.

Other Exemplary Expression Libraries

Other types of collections of proteins (e.g., expression libraries) can be used to identify proteins with a particular property (e.g., ability to bind MMP-12 and/or ability to modulate

MMP-12), including, e.g., protein arrays of antibodies (see, e.g., De Wildt et al. (2000) Nat. Biotechnol. 18:989-994), lambda gt11 libraries, two-hybrid libraries and so forth.

Exemplary Libraries

It is possible to immunize a non-human primate and recover primate antibody genes that can be displayed on phage (see below). From such a library, one can select antibodies that bind the antigen used in immunization. See, for example, Vaccine. (2003) **22**(2):257-67 or Immunogenetics. (2005) **57**(10):730-8.. Thus one could obtain primate antibodies that bind and inhibit MMP-9 by immunizing a chimpanzee or macaque and using a variety of means to select or screen for primate antibodies that bind and inhibit MMP-12. One can also make chimeras of primatized Fabs with human constant regions, see Curr Opin Mol Ther. (2004) **6**(6):675-83. “PRIMATIZED antibodies, genetically engineered from cynomolgus macaque monkey and human components, are structurally indistinguishable from human antibodies. They may, therefore, be less likely to cause adverse reactions in humans, making them potentially suited for long-term, chronic treatment ” Curr Opin Investig Drugs. (2001) **2**(5):635-8.

One exemplary type of library presents a diverse pool of polypeptides, each of which includes an immunoglobulin domain, e.g., an immunoglobulin variable domain. Of interest are display libraries where the members of the library include primate or “primatized” (e.g., such as human, non-human primate or “humanized”) immunoglobulin domains (e.g., immunoglobulin variable domains) or chimeric primatized Fabs with human constant regions. Human or humanized immunoglobulin domain libraries may be used to identify human or “humanized” antibodies that, for example, recognize human antigens. Because the constant and framework regions of the antibody are human, these antibodies may avoid themselves being recognized and targeted as antigens when administered to humans. The constant regions may also be optimized to recruit effector functions of the human immune system. The in vitro display selection process surmounts the inability of a normal human immune system to generate antibodies against self-antigens.

A typical antibody display library displays a polypeptide that includes a VH domain and a VL domain. An “immunoglobulin domain” refers to a domain from the variable or constant domain of immunoglobulin molecules. Immunoglobulin domains typically contain two β -sheets formed of about seven β -strands, and a conserved disulphide bond (see, e.g., A. F. Williams and

A. N. Barclay, 1988, *Ann. Rev. Immunol.* 6:381-405). The display library can display the antibody as a Fab fragment (e.g., using two polypeptide chains) or a single chain Fv (e.g., using a single polypeptide chain). Other formats can also be used.

As in the case of the Fab and other formats, the displayed antibody can include one or more constant regions as part of a light and/or heavy chain. In one embodiment, each chain includes one constant region, e.g., as in the case of a Fab. In other embodiments, additional constant regions are displayed.

Antibody libraries can be constructed by a number of processes (see, e.g., de Haard et al., 1999, *J. Biol. Chem.* 274:18218-30; Hoogenboom et al., 1998, *Immunotechnology* 4:1-20; Hoogenboom et al., 2000, *Immunol. Today* 21:371-378, and Hoet et al. (2005) *Nat Biotechnol.* 23(3)344-8. Further, elements of each process can be combined with those of other processes. The processes can be used such that variation is introduced into a single immunoglobulin domain (e.g., VH or VL) or into multiple immunoglobulin domains (e.g., VH and VL). The variation can be introduced into an immunoglobulin variable domain, e.g., in the region of one or more of CDR1, CDR2, CDR3, FR1, FR2, FR3, and FR4, referring to such regions of either and both of heavy and light chain variable domains. The variation(s) may be introduced into all three CDRs of a given variable domain, or into CDR1 and CDR2, e.g., of a heavy chain variable domain. Any combination is feasible. In one process, antibody libraries are constructed by inserting diverse oligonucleotides that encode CDRs into the corresponding regions of the nucleic acid. The oligonucleotides can be synthesized using monomeric nucleotides or trinucleotides. For example, Knappik et al., 2000, *J. Mol. Biol.* 296:57-86 describe a method for constructing CDR encoding oligonucleotides using trinucleotide synthesis and a template with engineered restriction sites for accepting the oligonucleotides.

In another process, an animal, e.g., a rodent, is immunized with MMP-12. The animal is optionally boosted with the antigen to further stimulate the response. Then spleen cells are isolated from the animal, and nucleic acid encoding VH and/or VL domains is amplified and cloned for expression in the display library.

In yet another process, antibody libraries are constructed from nucleic acid amplified from naïve germline immunoglobulin genes. The amplified nucleic acid includes nucleic acid encoding the VH and/or VL domain. Sources of immunoglobulin-encoding nucleic acids are

described below. Amplification can include PCR, e.g., with primers that anneal to the conserved constant region, or another amplification method.

Nucleic acid encoding immunoglobulin domains can be obtained from the immune cells of, e.g., a primate (e.g., a human), mouse, rabbit, camel, or rodent. In one example, the cells are selected for a particular property. B cells at various stages of maturity can be selected. In another example, the B cells are naïve.

In one embodiment, fluorescent-activated cell sorting (FACS) is used to sort B cells that express surface-bound IgM, IgD, or IgG molecules. Further, B cells expressing different isotypes of IgG can be isolated. In another preferred embodiment, the B or T cell is cultured in vitro. The cells can be stimulated in vitro, e.g., by culturing with feeder cells or by adding mitogens or other modulatory reagents, such as antibodies to CD40, CD40 ligand or CD20, phorbol myristate acetate, bacterial lipopolysaccharide, concanavalin A, phytohemagglutinin, or pokeweed mitogen.

In another embodiment, the cells are isolated from a subject that has a disease of condition described herein, e.g., a cancer (e.g., metastatic cancer, e.g., metastatic breast cancer), an inflammatory disease (e.g., synovitis, atherosclerosis), rheumatoid arthritis, osteoarthritis, an ocular condition (e.g., macular degeneration), diabetes, Alzheimer's Disease, cerebral ischemia, endometriosis, fibrin-invasive activity, angiogenesis, or capillary tube formation. In another embodiment, the cells are isolated from a transgenic non-human animal that includes a human immunoglobulin locus.

In one preferred embodiment, the cells have activated a program of somatic hypermutation. Cells can be stimulated to undergo somatic mutagenesis of immunoglobulin genes, for example, by treatment with anti-immunoglobulin, anti-CD40, and anti-CD38 antibodies (see, e.g., Bergthorsdottir et al., 2001, *J. Immunol.* 166:2228). In another embodiment, the cells are naïve.

The nucleic acid encoding an immunoglobulin variable domain can be isolated from a natural repertoire by the following exemplary method. First, RNA is isolated from the immune cell. Full length (i.e., capped) mRNAs are separated (e.g. by degrading uncapped RNAs with calf intestinal phosphatase). The cap is then removed with tobacco acid pyrophosphatase and reverse transcription is used to produce the cDNAs.

The reverse transcription of the first (antisense) strand can be done in any manner with any suitable primer. See, e.g., de Haard et al., 1999, *J. Biol. Chem.* 274:18218-30. The primer binding region can be constant among different immunoglobulins, e.g., in order to reverse transcribe different isotypes of immunoglobulin. The primer binding region can also be specific to a particular isotype of immunoglobulin. Typically, the primer is specific for a region that is 3' to a sequence encoding at least one CDR. In another embodiment, poly-dT primers may be used (and may be preferred for the heavy-chain genes).

A synthetic sequence can be ligated to the 3' end of the reverse transcribed strand. The synthetic sequence can be used as a primer binding site for binding of the forward primer during PCR amplification after reverse transcription. The use of the synthetic sequence can obviate the need to use a pool of different forward primers to fully capture the available diversity.

The variable domain-encoding gene is then amplified, e.g., using one or more rounds. If multiple rounds are used, nested primers can be used for increased fidelity. The amplified nucleic acid is then cloned into a display library vector.

Secondary Screening Methods

After selecting candidate library members that bind to a target, each candidate library member can be further analyzed, e.g., to further characterize its binding properties for the target, e.g., MMP-12, or for binding to other protein, e.g., another metalloproteinase. Each candidate library member can be subjected to one or more secondary screening assays. The assay can be for a binding property, a catalytic property, an inhibitory property, a physiological property (e.g., cytotoxicity, renal clearance, immunogenicity), a structural property (e.g., stability, conformation, oligomerization state) or another functional property. The same assay can be used repeatedly, but with varying conditions, e.g., to determine pH, ionic, or thermal sensitivities.

As appropriate, the assays can use a display library member directly, a recombinant polypeptide produced from the nucleic acid encoding the selected polypeptide, or a synthetic peptide synthesized based on the sequence of the selected polypeptide. In the case of selected Fabs, the Fabs can be evaluated or can be modified and produced as intact IgG proteins. Exemplary assays for binding properties include the following.

ELISA. Binding proteins can be evaluated using an ELISA assay. For example, each protein is contacted to a microtitre plate whose bottom surface has been coated with the target,

e.g., a limiting amount of the target. The plate is washed with buffer to remove non-specifically bound polypeptides. Then the amount of the binding protein bound to the target on the plate is determined by probing the plate with an antibody that can recognize the binding protein, e.g., a tag or constant portion of the binding protein. The antibody is linked to a detection system (e.g., an enzyme such as alkaline phosphatase or horse radish peroxidase (HRP) which produces a colorimetric product when appropriate substrates are provided).

Homogeneous Binding Assays. The ability of a binding protein described herein to bind a target can be analyzed using a homogenous assay, i.e., after all components of the assay are added, additional fluid manipulations are not required. For example, fluorescence resonance energy transfer (FRET) can be used as a homogenous assay (see, for example, Lakowicz et al., U.S. Patent No. 5,631,169; Stavrianopoulos, et al., U.S. Patent No. 4,868,103). A fluorophore label on the first molecule (e.g., the molecule identified in the fraction) is selected such that its emitted fluorescent energy can be absorbed by a fluorescent label on a second molecule (e.g., the target) if the second molecule is in proximity to the first molecule. The fluorescent label on the second molecule fluoresces when it absorbs to the transferred energy. Since the efficiency of energy transfer between the labels is related to the distance separating the molecules, the spatial relationship between the molecules can be assessed. In a situation in which binding occurs between the molecules, the fluorescent emission of the ‘acceptor’ molecule label in the assay should be maximal. A binding event that is configured for monitoring by FRET can be conveniently measured through standard fluorometric detection means, e.g., using a fluorimeter. By titrating the amount of the first or second binding molecule, a binding curve can be generated to estimate the equilibrium binding constant.

Another example of a homogenous assay is ALPHASCREEN™ (Packard Bioscience, Meriden CT). ALPHASCREEN™ uses two labeled beads. One bead generates singlet oxygen when excited by a laser. The other bead generates a light signal when singlet oxygen diffuses from the first bead and collides with it. The signal is only generated when the two beads are in proximity. One bead can be attached to the display library member, the other to the target. Signals are measured to determine the extent of binding.

Surface Plasmon Resonance (SPR). The interaction of binding protein and a target can be analyzed using SPR. SPR or Biomolecular Interaction Analysis (BIA) detects biospecific interactions in real time, without labeling any of the interactants. Changes in the mass at the

binding surface (indicative of a binding event) of the BIA chip result in alterations of the refractive index of light near the surface (the optical phenomenon of surface plasmon resonance (SPR)). The changes in the refractivity generate a detectable signal, which are measured as an indication of real-time reactions between biological molecules. Methods for using SPR are described, for example, in U.S. Patent No. 5,641,640; Raether, 1988, *Surface Plasmons* Springer Verlag; Sjolander and Urbaniczky, 1991, *Anal. Chem.* 63:2338-2345; Szabo et al., 1995, *Curr. Opin. Struct. Biol.* 5:699-705 and on-line resources provide by BIAcore International AB (Uppsala, Sweden). BIAcore Flexchip can be used to compare and rank interactions in real time, in terms of kinetics, affinity or specificity without the use of labels.

Information from SPR can be used to provide an accurate and quantitative measure of the equilibrium dissociation constant (K_d), and kinetic parameters, including K_{on} and K_{off} , for the binding of a binding protein to a target. Such data can be used to compare different biomolecules. For example, selected proteins from an expression library can be compared to identify proteins that have high affinity for the target or that have a slow K_{off} . This information can also be used to develop structure-activity relationships (SAR). For example, the kinetic and equilibrium binding parameters of matured versions of a parent protein can be compared to the parameters of the parent protein. Variant amino acids at given positions can be identified that correlate with particular binding parameters, e.g., high affinity and slow K_{off} . This information can be combined with structural modeling (e.g., using homology modeling, energy minimization, or structure determination by x-ray crystallography or NMR). As a result, an understanding of the physical interaction between the protein and its target can be formulated and used to guide other design processes.

Cellular Assays. Binding proteins can be screened for ability to bind to cells which transiently or stably express and display the target of interest on the cell surface. For example, MMP-12 binding proteins can be fluorescently labeled and binding to MMP-12 in the presence of absence of antagonistic antibody can be detected by a change in fluorescence intensity using flow cytometry e.g., a FACS machine.

Other Exemplary Methods for Obtaining MMP-12 binding antibodies

In addition to the use of display libraries, other methods can be used to obtain a MMP-12 binding antibody. For example, MMP-12 protein or a region thereof can be used as an antigen in a non-human animal, e.g., a rodent.

In one embodiment, the non-human animal includes at least a part of a human immunoglobulin gene. For example, it is possible to engineer mouse strains deficient in mouse antibody production with large fragments of the human Ig loci. Using the hybridoma technology, antigen-specific monoclonal antibodies (Mabs) derived from the genes with the desired specificity may be produced and selected. See, e.g., XENOMOUSE™, Green et al., 1994, *Nat. Gen.* 7:13-21; U.S. 2003-0070185, WO 96/34096, published Oct. 31, 1996, and PCT Application No. PCT/US96/05928, filed Apr. 29, 1996.

In another embodiment, a monoclonal antibody is obtained from the non-human animal, and then modified, e.g., humanized or deimmunized. Winter describes a CDR-grafting method that may be used to prepare the humanized antibodies (UK Patent Application GB 2188638A, filed on March 26, 1987; US Patent No. 5,225,539. All of the CDRs of a particular human antibody may be replaced with at least a portion of a non-human CDR or only some of the CDRs may be replaced with non-human CDRs. It is only necessary to replace the number of CDRs required for binding of the humanized antibody to a predetermined antigen.

Humanized antibodies can be generated by replacing sequences of the Fv variable region that are not directly involved in antigen binding with equivalent sequences from human Fv variable regions. General methods for generating humanized antibodies are provided by Morrison, S. L., 1985, *Science* 229:1202-1207, by Oi et al., 1986, *BioTechniques* 4:214, and by Queen et al. US Patent Nos. 5,585,089, US 5,693,761 and US 5,693,762. Those methods include isolating, manipulating, and expressing the nucleic acid sequences that encode all or part of immunoglobulin Fv variable regions from at least one of a heavy or light chain. Numerous sources of such nucleic acid are available. For example, nucleic acids may be obtained from a hybridoma producing an antibody against a predetermined target, as described above. The recombinant DNA encoding the humanized antibody, or fragment thereof, can then be cloned into an appropriate expression vector.

Reducing Immunogenicity of MMP-12 Binding Proteins

Immunoglobulin MMP-12 binding proteins (*e.g.*, IgG or Fab MMP-12 binding proteins) may be modified to reduce immunogenicity. Reduced immunogenicity is desirable in MMP-12 binding proteins intended for use as therapeutics, as it reduces the chance that the subject will develop an immune response against the therapeutic molecule. Techniques useful for reducing immunogenicity of MMP-12 binding proteins include deletion/modification of potential human T cell epitopes and ‘germlining’ of sequences outside of the CDRs (*e.g.*, framework and Fc).

An MMP-12-binding antibody may be modified by specific deletion of human T cell epitopes or "deimmunization" by the methods disclosed in WO 98/52976 and WO 00/34317. Briefly, the heavy and light chain variable regions of an antibody are analyzed for peptides that bind to MHC Class II; these peptides represent potential T-cell epitopes (as defined in WO 98/52976 and WO 00/34317). For detection of potential T-cell epitopes, a computer modeling approach termed “peptide threading” can be applied, and in addition a database of human MHC class II binding peptides can be searched for motifs present in the VH and VL sequences, as described in WO 98/52976 and WO 00/34317. These motifs bind to any of the 18 major MHC class II DR allotypes, and thus constitute potential T cell epitopes. Potential T-cell epitopes detected can be eliminated by substituting small numbers of amino acid residues in the variable regions, or preferably, by single amino acid substitutions. As far as possible conservative substitutions are made, often but not exclusively, an amino acid common at this position in human germline antibody sequences may be used. Human germline sequences are disclosed in Tomlinson, I.A. et al., 1992, *J. Mol. Biol.* 227:776-798; Cook, G. P. et al., 1995, *Immunol. Today* Vol. 16 (5): 237-242; Chothia, D. et al., 1992, *J. Mol. Bio.* 227:799-817. The V BASE directory provides a comprehensive directory of human immunoglobulin variable region sequences (compiled by Tomlinson, I.A. et al. MRC Centre for Protein Engineering, Cambridge, UK). After the deimmunizing changes are identified, nucleic acids encoding V_H and V_L can be constructed by mutagenesis or other synthetic methods (*e.g.*, de novo synthesis, cassette replacement, and so forth). Mutagenized variable sequence can, optionally, be fused to a human constant region, *e.g.*, human IgG1 or κ constant regions.

In some cases a potential T cell epitope will include residues which are known or predicted to be important for antibody function. For example, potential T cell epitopes are usually biased towards the CDRs. In addition, potential T cell epitopes can occur in framework

residues important for antibody structure and binding. Changes to eliminate these potential epitopes will in some cases require more scrutiny, e.g., by making and testing chains with and without the change. Where possible, potential T cell epitopes that overlap the CDRs were eliminated by substitutions outside the CDRs. In some cases, an alteration within a CDR is the only option, and thus variants with and without this substitution should be tested. In other cases, the substitution required to remove a potential T cell epitope is at a residue position within the framework that might be critical for antibody binding. In these cases, variants with and without this substitution should be tested. Thus, in some cases several variant deimmunized heavy and light chain variable regions were designed and various heavy/light chain combinations tested in order to identify the optimal deimmunized antibody. The choice of the final deimmunized antibody can then be made by considering the binding affinity of the different variants in conjunction with the extent of deimmunization, i.e., the number of potential T cell epitopes remaining in the variable region. Deimmunization can be used to modify any antibody, e.g., an antibody that includes a non-human sequence, e.g., a synthetic antibody, a murine antibody other non-human monoclonal antibody, or an antibody isolated from a display library.

MMP-12 binding antibodies are “germlined” by reverting one or more non-germline amino acids in framework regions to corresponding germline amino acids of the antibody, so long as binding properties are substantially retained. Similar methods can also be used in the constant region, e.g., in constant immunoglobulin domains.

Antibodies that bind to MMP-12, e.g., an antibody described herein, may be modified in order to make the variable regions of the antibody more similar to one or more germline sequences. For example, an antibody can include one, two, three, or more amino acid substitutions, e.g., in a framework, CDR, or constant region, to make it more similar to a reference germline sequence. One exemplary germlining method can include identifying one or more germline sequences that are similar (e.g., most similar in a particular database) to the sequence of the isolated antibody. Mutations (at the amino acid level) are then made in the isolated antibody, either incrementally or in combination with other mutations. For example, a nucleic acid library that includes sequences encoding some or all possible germline mutations is made. The mutated antibodies are then evaluated, e.g., to identify an antibody that has one or more additional germline residues relative to the isolated antibody and that is still useful (e.g.,

has a functional activity). In one embodiment, as many germline residues are introduced into an isolated antibody as possible.

In one embodiment, mutagenesis is used to substitute or insert one or more germline residues into a framework and/or constant region. For example, a germline framework and/or constant region residue can be from a germline sequence that is similar (e.g., most similar) to the non-variable region being modified. After mutagenesis, activity (e.g., binding or other functional activity) of the antibody can be evaluated to determine if the germline residue or residues are tolerated (i.e., do not abrogate activity). Similar mutagenesis can be performed in the framework regions.

Selecting a germline sequence can be performed in different ways. For example, a germline sequence can be selected if it meets a predetermined criteria for selectivity or similarity, e.g., at least a certain percentage identity, e.g., at least 75, 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 99.5% identity. The selection can be performed using at least 2, 3, 5, or 10 germline sequences. In the case of CDR1 and CDR2, identifying a similar germline sequence can include selecting one such sequence. In the case of CDR3, identifying a similar germline sequence can include selecting one such sequence, but may including using two germline sequences that separately contribute to the amino-terminal portion and the carboxy-terminal portion. In other implementations more than one or two germline sequences are used, e.g., to form a consensus sequence.

In one embodiment, with respect to a particular reference variable domain sequence, e.g., a sequence described herein, a related variable domain sequence has at least 30, 40, 50, 60, 70, 80, 90, 95 or 100% of the CDR amino acid positions that are not identical to residues in the reference CDR sequences, residues that are identical to residues at corresponding positions in a human germline sequence (i.e., an amino acid sequence encoded by a human germline nucleic acid).

In one embodiment, with respect to a particular reference variable domain sequence, e.g., a sequence described herein, a related variable domain sequence has at least 30, 50, 60, 70, 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100% of the FR regions identical to FR sequence from a human germline sequence, e.g., a germline sequence related to the reference variable domain sequence.

Accordingly, it is possible to isolate an antibody which has similar activity to a given antibody of interest, but is more similar to one or more germline sequences, particularly one or more human germline sequences. For example, an antibody can be at least 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 99.5% identical to a germline sequence in a region outside the CDRs (e.g., framework regions). Further, an antibody can include at least 1, 2, 3, 4, or 5 germline residues in a CDR region, the germline residue being from a germline sequence of similar (e.g., most similar) to the variable region being modified. Germline sequences of primary interest are human germline sequences. The activity of the antibody (e.g., the binding activity as measured by K_A) can be within a factor of 100, 10, 5, 2, 0.5, 0.1, and 0.001 of the original antibody.

Germline sequences of human immunoglobulin genes have been determined and are available from a number of sources, including the international ImMunoGeneTics information system® (IMGT), available via the world wide web at imgt.cines.fr, and the V BASE directory (compiled by Tomlinson, I.A. et al. MRC Centre for Protein Engineering, Cambridge, UK, available via the world wide web at vbase.mrc-cpe.cam.ac.uk).

Exemplary germline reference sequences for V_{κ} include: O12/O2, O18/O8, A20, A30, L14, L1, L15, L4/18a, L5/L19, L8, L23, L9, L24, L11, L12, O11/O1, A17, A1, A18, A2, A19/A3, A23, A27, A11, L2/L16, L6, L20, L25, B3, B2, A26/A10, and A14. See, e.g., Tomlinson et al., 1995, *EMBO J.* 14(18):4628-3.

A germline reference sequence for the HC variable domain can be based on a sequence that has particular canonical structures, e.g., 1-3 structures in the H1 and H2 hypervariable loops. The canonical structures of hypervariable loops of an immunoglobulin variable domain can be inferred from its sequence, as described in Chothia et al., 1992, *J. Mol. Biol.* 227:799-817; Tomlinson et al., 1992, *J. Mol. Biol.* 227:776-798; and Tomlinson et al., 1995, *EMBO J.* 14(18):4628-38. Exemplary sequences with a 1-3 structure include: DP-1, DP-8, DP-12, DP-2, DP-25, DP-15, DP-7, DP-4, DP-31, DP-32, DP-33, DP-35, DP-40, 7-2, hv3005, hv3005f3, DP-46, DP-47, DP-58, DP-49, DP-50, DP-51, DP-53, and DP-54.

Protein Production

Standard recombinant nucleic acid methods can be used to express a protein that binds to MMP-12. Generally, a nucleic acid sequence encoding the protein is cloned into a nucleic acid expression vector. Of course, if the protein includes multiple polypeptide chains, each chain can

be cloned into an expression vector, e.g., the same or different vectors, that are expressed in the same or different cells.

Antibody Production. Some antibodies, e.g., Fabs, can be produced in bacterial cells, e.g., *E. coli* cells. For example, if the Fab is encoded by sequences in a phage display vector that includes a suppressible stop codon between the display entity and a bacteriophage protein (or fragment thereof), the vector nucleic acid can be transferred into a bacterial cell that cannot suppress a stop codon. In this case, the Fab is not fused to the gene III protein and is secreted into the periplasm and/or media.

Antibodies can also be produced in eukaryotic cells. In one embodiment, the antibodies (e.g., scFv's) are expressed in a yeast cell such as *Pichia* (see, e.g., Powers et al., 2001, *J. Immunol. Methods*. 251:123-35), *Hansenula*, or *Saccharomyces*.

In one preferred embodiment, antibodies are produced in mammalian cells. Preferred mammalian host cells for expressing the clone antibodies or antigen-binding fragments thereof include Chinese Hamster Ovary (CHO cells) (including dhfr- CHO cells, described in Urlaub and Chasin, 1980, *Proc. Natl. Acad. Sci. USA* 77:4216-4220, used with a DHFR selectable marker, e.g., as described in Kaufman and Sharp, 1982, *Mol. Biol.* 159:601-621), lymphocytic cell lines, e.g., NS0 myeloma cells and SP2 cells, COS cells, HEK293T cells (*J. Immunol. Methods* (2004) 289(1-2):65-80.), and a cell from a transgenic animal, e.g., a transgenic mammal. For example, the cell is a mammary epithelial cell.

In addition to the nucleic acid sequence encoding the diversified immunoglobulin domain, the recombinant expression vectors may carry additional sequences, such as sequences that regulate replication of the vector in host cells (e.g., origins of replication) and selectable marker genes. The selectable marker gene facilitates selection of host cells into which the vector has been introduced (see e.g., U.S. Patent Nos. 4,399,216, 4,634,665 and 5,179,017). For example, typically the selectable marker gene confers resistance to drugs, such as G418, hygromycin or methotrexate, on a host cell into which the vector has been introduced. Preferred selectable marker genes include the dihydrofolate reductase (DHFR) gene (for use in *dhfr*⁻ host cells with methotrexate selection/amplification) and the *neo* gene (for G418 selection).

In an exemplary system for recombinant expression of an antibody, or antigen-binding portion thereof, a recombinant expression vector encoding both the antibody heavy chain and the antibody light chain is introduced into *dhfr*⁻ CHO cells by calcium phosphate-mediated

transfection. Within the recombinant expression vector, the antibody heavy and light chain genes are each operatively linked to enhancer/promoter regulatory elements (e.g., derived from SV40, CMV, adenovirus and the like, such as a CMV enhancer/AdMLP promoter regulatory element or an SV40 enhancer/AdMLP promoter regulatory element) to drive high levels of transcription of the genes. The recombinant expression vector also carries a DHFR gene, which allows for selection of CHO cells that have been transfected with the vector using methotrexate selection/amplification. The selected transformant host cells are cultured to allow for expression of the antibody heavy and light chains and intact antibody is recovered from the culture medium. Standard molecular biology techniques are used to prepare the recombinant expression vector, transfect the host cells, select for transformants, culture the host cells and recover the antibody from the culture medium. For example, some antibodies can be isolated by affinity chromatography with a Protein A or Protein G coupled matrix.

For antibodies that include an Fc domain, the antibody production system may produce antibodies in which the Fc region is glycosylated. For example, the Fc domain of IgG molecules is glycosylated at asparagine 297 in the CH2 domain. This asparagine is the site for modification with biantennary-type oligosaccharides. It has been demonstrated that this glycosylation is required for effector functions mediated by Fcγ receptors and complement C1q (Burton and Woof, 1992, *Adv. Immunol.* 51:1-84; Jefferis et al., 1998, *Immunol. Rev.* 163:59-76). In one embodiment, the Fc domain is produced in a mammalian expression system that appropriately glycosylates the residue corresponding to asparagine 297. The Fc domain can also include other eukaryotic post-translational modifications.

Antibodies can also be produced by a transgenic animal. For example, U.S. Patent No. 5,849,992 describes a method of expressing an antibody in the mammary gland of a transgenic mammal. A transgene is constructed that includes a milk-specific promoter and nucleic acids encoding the antibody of interest and a signal sequence for secretion. The milk produced by females of such transgenic mammals includes, secreted-therein, the antibody of interest. The antibody can be purified from the milk, or for some applications, used directly.

Characterization of MMP-12 Binding Proteins

Binding of MMP-12 binding proteins to cells expressing MMP-12 can be characterized in a number assays known in the art, including FACS (Fluorescence Activated Cell Sorting),

ELISA, immunofluorescence, and immunocytochemistry. MMP-12 binding protein is contacted with cells and/or tissues which express or contain MMP-12, and binding is detected in accordance with the method being used. For example, a fluorescent detection system (e.g., fluorescent-labeled secondary antibody) employed for FACS and immunofluorescence analysis, or an enzymatic system is used for immunocytochemistry are generally used in these assays can be performed on non-perm. MMP-12 binding proteins can be characterized as to cellular binding by FACS (Fluorescence Activated Cell Sorting) using cells expressing MMP-12. Individual cells held in a thin stream of fluid are passed through one or more laser beams cause light to scatter and fluorescent dyes to emit light at various frequencies. Photomultiplier tubes (PMT) convert light to electrical signals and cell data is collected. Forward and side scatter are used for preliminary identification of cells. Forward and side scatter are used to exclude debris and dead cells. Fluorescent labeling allows investigation of cell structure and function. Cell autofluorescence is generated by labeling cell structures with fluorescent dyes. FACS collects fluorescence signals in one to several channels corresponding to different laser excitation and fluorescence emission wavelength. Immunofluorescence, the most widely used application, involves the staining of cells with antibodies conjugated to fluorescent dyes such as fluorescein and phycoerythrin (PE). This method can be used to label MMP-12 on permeabilized cells, e.g., using biotinylated MMP-12 binding proteins. Biotin is used in this two-step detection systems in concert with conjugated streptavidin. Biotin is typically conjugated to proteins via primary amines (i.e., lysines). Usually, between 1.5 and 3 biotin molecules are conjugated to each antibody. A second fluorescently conjugated antibody (streptavidin/PE) is added which is specific for biotin.

MMP-12 binding proteins can be characterized in cultured cells expressing the MMP-12 antigen. The method generally used is immunocytochemistry. Immunocytochemistry involves the use of antibodies that recognize parts of the protein that are exposed to the outside environment when expressed at the cell surface (the 'primary antibody') or that are accessible upon permeabilization of the cell. If the experiment is carried out in intact cells, such an antibody will only bind to surface expressed receptors. Biotinylated or non-biotinylated MMP-12 binding proteins can be used. The secondary antibody is then either a streptavidin/HRP antibody (for biotinylated MMP-12 binding protein) or an anti-human IgG/HRP (for non-biotinylated MMP-12 binding protein). The staining can then be detected using an inverted

microscope. The assay can be performed in the absence of MMP-12 binding protein and in presence of 10 μ g/mL of MMP-12 binding protein. Secreted MMP12 can be detected in samples of the medium in which MMP-12-expressing cells are cultured. For example, antibody based screening methods, e.g., using binding proteins described herein, can be used to detect secreted MMP-12. For example, immunoblot analysis or ELISA can be used.

MMP-12 binding proteins can be characterized in assays that measure their modulatory activity toward MMP-12 or fragments thereof *in vitro* or *in vivo*. For example, MMP-12 can be combined with a substrate such as Mca-Pro-Leu-Ala-Cys(Mob)-Trp-Ala-Arg-Dap(Dnp)-NH₂ under assay conditions permitting cleavage by MMP-12. The assay is performed in the absence of the MMP-12 binding protein, and in the presence of increasing concentrations of the MMP-12 binding protein. The concentration of binding protein at which 50% of the MMP-12 activity (e.g., binding to the substrate) is inhibited is the IC₅₀ value (Inhibitory Concentration 50%) or EC₅₀ (Effective Concentration 50%) value for that binding protein. Within a series or group of binding proteins, those having lower IC₅₀ or EC₅₀ values are considered more potent inhibitors of MMP-12 than those binding proteins having higher IC₅₀ or EC₅₀ values. Exemplary binding proteins have an IC₅₀ value of less than 800 nM, 400 nM, 100 nM, 25 nM, 5 nM, or 1 nM, e.g., as measured in an *in vitro* assay for inhibition of MMP-12 activity when the MMP-12 is at 2 pM.

MMP-12 binding proteins may also be characterized with reference to the activity of MMP-12 on substrates (e.g., lung extracellular matrix, elastin, gelatin, etc.). For example, cleavage of gelatin by MMP-12 can be detected in zymography. The method is based on a SDS gel impregnated with a substrate, which is degraded by the proteases resolved during the incubation period. Coomassie blue staining of the gels reveals proteolytic fragments as white bands on a dark blue background. Within a certain range, the band intensity can be related linearly to the amount of the protease loaded. Cells expressing MMP-12 are used in this assay. The assay is performed in the absence of the MMP-12 binding protein, and in the presence of increasing concentrations of the MMP-12 binding protein. The concentration of binding protein at which 50% of the MMP-12 activity (e.g., binding to the substrate) is inhibited is the IC₅₀ value (Inhibitory Concentration 50%) or EC₅₀ (Effective Concentration 50%) value for that binding protein. Within a series or group of binding proteins, those having lower IC₅₀ or EC₅₀ values are considered more potent inhibitors of MMP-12 than those binding proteins having higher IC₅₀ or EC₅₀ values. Exemplary binding proteins have an IC₅₀ value of less than 800 nM, 400 nM, 100

nM, 25 nM, 5 nM, or 1 nM, e.g., as measured in an *in vitro* assay for inhibition of MMP-12 activity.

The binding proteins can also be evaluated for selectivity toward MMP-12. For example, a MMP-12 binding protein can be assayed for its potency toward MMP-12 and a panel of MMPs and other enzymes, e.g., human and/or mouse enzymes, e.g., MMP-1, -2, -3, -7, -8, -9, -13, -14, -16, -17, -24, and TACE, and an IC₅₀ value or EC₅₀ value can be determined for each MMP. In one embodiment, a compound that demonstrates a low IC₅₀ value or EC₅₀ value for the MMP-12, and a higher IC₅₀ value or EC₅₀ value, e.g., at least 2-, 5-, or 10- fold higher, for another MMP within the test panel (e.g., MMP-1, -10) is considered to be selective toward MMP-12.

MMP-12 binding proteins can be evaluated for their ability to inhibit MMP-12 in a cell based assay, e.g., in situ zymography, e.g., in Colo205 cells or MCF-7 cells.

A pharmacokinetics study in rat, mice, or monkey can be performed with MMP-12 binding proteins for determining MMP-12 half-life in the serum. Likewise, the effect of the binding protein can be assessed *in vivo*, e.g., in an animal model for a disease, for use as a therapeutic, for example, to treat a disease or condition described herein, e.g., a cancer (e.g., metastatic cancer, e.g., metastatic colorectal, lung, or hepatocellular cancer), an inflammatory disease (e.g., chronic obstructive pulmonary disease (COPD), asthma, rhinitis (e.g., allergic rhinitis), atherosclerosis, multiple sclerosis, rheumatoid arthritis), cardiovascular disease, aneurysm, wound healing, aging and nerve damage associated with excess or inappropriate activity of MMP-12.

Pharmaceutical Compositions

In another aspect, the disclosure provides compositions, e.g., pharmaceutically acceptable compositions or pharmaceutical compositions, which include an MMP-12-binding protein, e.g., an antibody molecule, other polypeptide or peptide identified as binding to MMP-12 described herein. The MMP-12 binding protein can be formulated together with a pharmaceutically acceptable carrier. Pharmaceutical compositions include therapeutic compositions and diagnostic compositions, e.g., compositions that include labeled MMP-12 binding proteins for *in vivo* imaging.

A pharmaceutically acceptable carrier includes any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the

like that are physiologically compatible. Preferably, the carrier is suitable for intravenous, intramuscular, subcutaneous, parenteral, spinal, or epidermal administration (e.g., by injection or infusion), although carriers suitable for inhalation and intranasal administration are also contemplated. Depending on the route of administration, the MMP-12 binding protein may be coated in a material to protect the compound from the action of acids and other natural conditions that may inactivate the compound.

A pharmaceutically acceptable salt is a salt that retains the desired biological activity of the parent compound and does not impart any undesired toxicological effects (see e.g., Berge, S.M., et al., 1977, *J. Pharm. Sci.* 66:1-19). Examples of such salts include acid addition salts and base addition salts. Acid addition salts include those derived from nontoxic inorganic acids, such as hydrochloric, nitric, phosphoric, sulfuric, hydrobromic, hydroiodic, phosphorous, and the like, as well as from nontoxic organic acids such as aliphatic mono- and dicarboxylic acids, phenyl-substituted alkanolic acids, hydroxy alkanolic acids, aromatic acids, aliphatic and aromatic sulfonic acids, and the like. Base addition salts include those derived from alkaline earth metals, such as sodium, potassium, magnesium, calcium, and the like, as well as from nontoxic organic amines, such as N,N'-dibenzylethylenediamine, N-methylglucamine, chlorprocaine, choline, diethanolamine, ethylenediamine, procaine, and the like.

The compositions may be in a variety of forms. These include, for example, liquid, semi-solid and solid dosage forms, such as liquid solutions (e.g., injectable and infusible solutions), dispersions or suspensions, tablets, pills, powders, liposomes and suppositories. The form can depend on the intended mode of administration and therapeutic application. Many compositions are in the form of injectable or infusible solutions, such as compositions similar to those used for administration of humans with antibodies. An exemplary mode of administration is parenteral (e.g., intravenous, subcutaneous, intraperitoneal, intramuscular). In one embodiment, the MMP-12 binding protein is administered by intravenous infusion or injection. In another preferred embodiment, the MMP-12 binding protein is administered by intramuscular or subcutaneous injection.

The phrases "parenteral administration" and "administered parenterally" as used herein means modes of administration other than enteral and topical administration, usually by injection, and includes, without limitation, intravenous, intramuscular, intraarterial, intrathecal, intracapsular, intraorbital, intracardiac, intradermal, intraperitoneal, transtracheal, subcutaneous,

subcuticular, intraarticular, subcapsular, subarachnoid, intraspinal, epidural and intrasternal injection and infusion.

The composition can be formulated as a solution, microemulsion, dispersion, liposome, or other ordered structure suitable to high drug concentration. Sterile injectable solutions can be prepared by incorporating the binding protein in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and freeze-drying that yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof. The proper fluidity of a solution can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prolonged absorption of injectable compositions can be brought about by including in the composition an agent that delays absorption, for example, monostearate salts and gelatin.

An MMP-12 binding protein can be administered by a variety of methods, although for many applications, the preferred route/mode of administration is intravenous injection or infusion. For example, for therapeutic applications, the MMP-12 binding protein can be administered by intravenous infusion at a rate of less than 30, 20, 10, 5, or 1 mg/min to reach a dose of about 1 to 100 mg/m² or 7 to 25 mg/m². The route and/or mode of administration will vary depending upon the desired results. In certain embodiments, the active compound may be prepared with a carrier that will protect the compound against rapid release, such as a controlled release formulation, including implants, and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Many methods for the preparation of such formulations are available. See, e.g., Sustained and Controlled Release Drug Delivery Systems, J.R. Robinson, ed., 1978, Marcel Dekker, Inc., New York.

Pharmaceutical compositions can be administered with medical devices. For example, in one embodiment, a pharmaceutical composition disclosed herein can be administered with a device, e.g., a needleless hypodermic injection device, a pump, or implant.

In certain embodiments, an MMP-12 binding protein can be formulated to ensure proper distribution *in vivo*. For example, the blood-brain barrier (BBB) excludes many highly hydrophilic compounds. To ensure that the therapeutic compounds disclosed herein cross the BBB (if desired), they can be formulated, for example, in liposomes. For methods of manufacturing liposomes, see, e.g., U.S. Patent Nos. 4,522,811; 5,374,548; and 5,399,331. The liposomes may comprise one or more moieties that are selectively transported into specific cells or organs, thus enhance targeted drug delivery (see, e.g., V.V. Ranade, 1989, *J. Clin. Pharmacol.* 29:685).

Dosage regimens are adjusted to provide the optimum desired response (e.g., a therapeutic response). For example, a single bolus may be administered, several divided doses may be administered over time or the dose may be proportionally reduced or increased as indicated by the exigencies of the therapeutic situation. It is especially advantageous to formulate parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subjects to be treated; each unit contains a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms can be dictated by and directly dependent on (a) the unique characteristics of the active compound and the particular therapeutic effect to be achieved, and (b) the limitations inherent in the art of compounding such an active compound for the treatment of sensitivity in individuals.

An exemplary, non-limiting range for a therapeutically or prophylactically effective amount of an antibody disclosed herein is 0.1-20 mg/kg, more preferably 1-10 mg/kg. An anti-MMP-12 antibody can be administered, e.g., by intravenous infusion, e.g., at a rate of less than 30, 20, 10, 5, or 1 mg/min to reach a dose of about 1 to 100 mg/m² or about 5 to 30 mg/m². For binding proteins smaller in molecular weight than an antibody, appropriate amounts can be proportionally less. Dosage values may vary with the type and severity of the condition to be alleviated. For a particular subject, specific dosage regimens can be adjusted over time according to the individual need and the professional judgment of the person administering or supervising the administration of the compositions.

The pharmaceutical compositions disclosed herein may include a “therapeutically effective amount” or a “prophylactically effective amount” of an MMP-12 binding protein

disclosed herein. A “therapeutically effective amount” refers to an amount effective, at dosages and for periods of time necessary, to achieve the desired therapeutic result. A therapeutically effective amount of the composition may vary according to factors such as the disease state, age, sex, and weight of the individual, and the ability of the protein to elicit a desired response in the individual. A therapeutically effective amount is also one in which any toxic or detrimental effects of the composition is outweighed by the therapeutically beneficial effects.

A “therapeutically effective dosage” preferably modulates a measurable parameter, e.g., levels of circulating IgG antibodies or enzymatic activity, by a statistically significant degree or at least about 20%, more preferably by at least about 40%, even more preferably by at least about 60%, and still more preferably by at least about 80% relative to untreated subjects. The ability of a compound to modulate a measurable parameter, e.g., a disease-associated parameter, can be evaluated in an animal model system predictive of efficacy in human disorders and conditions, e.g., a cancer (e.g., metastatic cancer, e.g., metastatic colorectal, lung, or hepatocellular cancer), an inflammatory disease (e.g., chronic obstructive pulmonary disease (COPD), asthma, rhinitis (e.g., allergic rhinitis), atherosclerosis, multiple sclerosis, rheumatoid arthritis), cardiovascular disease, aneurysm, wound healing, aging and nerve damage associated with excess or inappropriate activity of MMP-12. Alternatively, this property of a composition can be evaluated by examining the ability of the compound to modulate a parameter in vitro.

A “prophylactically effective amount” refers to an amount effective, at dosages and for periods of time necessary, to achieve the desired prophylactic result. Typically, because 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.

Stabilization and Retention

In one embodiment, an MMP-12 binding protein is physically associated with a moiety that improves its stabilization and/or retention in circulation, e.g., in blood, serum, lymph, or other tissues, e.g., by at least 1.5, 2, 5, 10, or 50 fold. For example, an MMP-12 binding protein can be associated with a polymer, e.g., a substantially non-antigenic polymer, such as polyalkylene oxides or polyethylene oxides. Suitable polymers will vary substantially by weight. Polymers having molecular number average weights ranging from about 200 to about 35,000 (or about 1,000 to about 15,000, and 2,000 to about 12,500) can be used. For example, an MMP-12

binding protein can be conjugated to a water soluble polymer, e.g., hydrophilic polyvinyl polymers, e.g. polyvinylalcohol and polyvinylpyrrolidone. A non-limiting list of such polymers include polyalkylene oxide homopolymers such as polyethylene glycol (PEG) or polypropylene glycols, polyoxyethylenated polyols, copolymers thereof and block copolymers thereof, provided that the water solubility of the block copolymers is maintained.

An MMP-12 binding protein can also be associated with a carrier protein, e.g., a serum albumin, such as a human serum albumin. For example, a translational fusion can be used to associate the carrier protein with the MMP-12 binding protein.

Kits

An MMP-12 binding protein described herein can be provided in a kit, e.g., as a component of a kit. For example, the kit includes (a) an MMP-12 binding protein, e.g., a composition that includes an MMP-12 binding protein, and, optionally (b) informational material. The informational material can be descriptive, instructional, marketing or other material that relates to the methods described herein and/or the use of an MMP-12 binding protein for the methods described herein.

The informational material of the kits is not limited in its form. In one embodiment, the informational material can include information about production of the compound, molecular weight of the compound, concentration, date of expiration, batch or production site information, and so forth. In one embodiment, the informational material relates to using the binding protein to treat, prevent, or diagnosis of disorders and conditions, e.g., a cancer (e.g., metastatic cancer, e.g., metastatic colorectal, lung, or hepatocellular cancer), an inflammatory disease (e.g., chronic obstructive pulmonary disease (COPD), asthma, rhinitis (e.g., allergic rhinitis), atherosclerosis, multiple sclerosis, rheumatoid arthritis), cardiovascular disease, aneurysm, wound healing, aging and nerve damage associated with excess or inappropriate activity of MMP-12.

In one embodiment, the informational material can include instructions to administer an MMP-12 binding protein in a suitable manner to perform the methods described herein, e.g., in a suitable dose, dosage form, or mode of administration (e.g., a dose, dosage form, or mode of administration described herein). In another embodiment, the informational material can include instructions to administer an MMP-12 binding protein to a suitable subject, e.g., a human, e.g., a human having, or at risk for, a disorder or condition described herein, e.g., a cancer (e.g.,

metastatic cancer, e.g., metastatic colorectal, lung, or hepatocellular cancer), an inflammatory disease (e.g., chronic obstructive pulmonary disease (COPD), asthma, rhinitis (e.g., allergic rhinitis), atherosclerosis, multiple sclerosis, rheumatoid arthritis), cardiovascular disease, aneurysm, wound healing, aging and nerve damage associated with excess or inappropriate activity of MMP-12. For example, the material can include instructions to administer an MMP-12 binding protein to a patient with a disorder or condition described herein, e.g., a cancer (e.g., metastatic cancer, e.g., metastatic colorectal, lung, or hepatocellular cancer), an inflammatory disease (e.g., chronic obstructive pulmonary disease (COPD), asthma, rhinitis (e.g., allergic rhinitis), atherosclerosis, multiple sclerosis, rheumatoid arthritis), cardiovascular disease, aneurysm, wound healing, aging and nerve damage associated with excess or inappropriate activity of MMP-12. The informational material of the kits is not limited in its form. In many cases, the informational material, e.g., instructions, is provided in print but may also be in other formats, such as computer readable material.

An MMP-12 binding protein can be provided in any form, e.g., liquid, dried or lyophilized form. It is preferred that an MMP-12 binding protein be substantially pure and/or sterile. When an MMP-12 binding protein is provided in a liquid solution, the liquid solution preferably is an aqueous solution, with a sterile aqueous solution being preferred. When an MMP-9 binding protein is provided as a dried form, reconstitution generally is by the addition of a suitable solvent. The solvent, e.g., sterile water or buffer, can optionally be provided in the kit.

The kit can include one or more containers for the composition containing an MMP-12 binding protein. In some embodiments, the kit contains separate containers, dividers or compartments for the composition and informational material. For example, the composition can be contained in a bottle, vial, or syringe, and the informational material can be contained association with the container. In other embodiments, the separate elements of the kit are contained within a single, undivided container. For example, the composition is contained in a bottle, vial or syringe that has attached thereto the informational material in the form of a label. In some embodiments, the kit includes a plurality (e.g., a pack) of individual containers, each containing one or more unit dosage forms (e.g., a dosage form described herein) of an MMP-12 binding protein. For example, the kit includes a plurality of syringes, ampules, foil packets, or blister packs, each containing a single unit dose of an MMP-12 binding protein. The containers

of the kits can be air tight, waterproof (e.g., impermeable to changes in moisture or evaporation), and/or light-tight.

The kit optionally includes a device suitable for administration of the composition, e.g., a syringe, inhalant, dropper (e.g., eye dropper), swab (e.g., a cotton swab or wooden swab), or any such delivery device. In one embodiment, the device is an implantable device that dispenses metered doses of the binding protein. The disclosure also features a method of providing a kit, e.g., by combining components described herein.

Treatments

Proteins that bind to MMP-12 and identified by the method described herein and/or detailed herein have therapeutic and prophylactic utilities, particularly in human subjects. These binding proteins are administered to a subject to treat, prevent, and/or diagnose a variety of disorders, including e.g., a cancer (e.g., metastatic cancer, e.g., metastatic colorectal, lung, or hepatocellular cancer), an inflammatory disease (e.g., chronic obstructive pulmonary disease (COPD), asthma, rhinitis (e.g., allergic rhinitis), atherosclerosis, multiple sclerosis, rheumatoid arthritis), cardiovascular disease, aneurysm, wound healing, aging and nerve damage associated with excess or inappropriate activity of MMP-12, or even to cells in culture, e.g. *in vitro* or *ex vivo*. Treating includes administering an amount effective to alleviate, relieve, alter, remedy, ameliorate, improve or affect the disorder, the symptoms of the disorder or the predisposition toward the disorder. The treatment may also delay onset, e.g., prevent onset, or prevent deterioration of a disease or condition.

Exemplary disorders include a cancer (e.g., metastatic cancer, e.g., metastatic lung, colorectal or hepatocellular cancer), an inflammatory disease (e.g., chronic obstructive pulmonary disease (COPD), asthma, rhinitis (e.g., allergic rhinitis), atherosclerosis, multiple sclerosis, rheumatoid arthritis), cardiovascular disease, aneurysm, wound healing, aging and nerve damage associated with excess or inappropriate activity of MMP-12. Some of these disorders are discussed above. Still other disorders that can be treated using an MMP-12 binding protein include: aortic aneurysms, dermal photoaging.

As used herein, an amount of an target-binding agent effective to prevent a disorder, or a prophylactically effective amount of the binding agent refers to an amount of a target binding agent, e.g., an MMP-12 binding protein, e.g., an anti-MMP-12 antibody described herein, which

is effective, upon single- or multiple-dose administration to the subject, for preventing or delaying the occurrence of the onset or recurrence of a disorder, e.g., a disorder described herein.

A binding agent described herein can be used to reduce angiogenesis in a subject, e.g., to treat a cancer (e.g., a solid tumor) or an angiogenesis-associated disorder. The method includes administering the binding to the subject, e.g., in an amount effective to modulate angiogenesis, a symptom of the disorder, or progression of the disorder. The agent (e.g., an MMP-12 binding protein, e.g., an anti-MMP-12 antibody) may be administered multiple times (e.g., at least two, three, five, or ten times) before a therapeutically effective amount is attained.

Methods of administering MMP-12 binding proteins and other agents are also described in “Pharmaceutical Compositions.” Suitable dosages of the molecules used can depend on the age and weight of the subject and the particular drug used. The binding proteins can be used as competitive agents to inhibit, reduce an undesirable interaction, e.g., between a natural or pathological agent and the MMP-12. The dose of the MMP-12 binding protein can be the amount sufficient to block 90%, 95%, 99%, or 99.9% of the activity of MMP-12 in the patient, especially at the site of disease. Depending on the disease, this may require 0.1, 1.0, 3.0, 6.0, or 10.0 mg/Kg. For an IgG having a molecular mass of 150,000 g/mole (two binding sites), these doses correspond to approximately 18 nM, 180 nM, 540 nM, 1.08 μ M, and 1.8 μ M of binding sites for a 5 L blood volume.

In one embodiment, the MMP-12 binding proteins are used to inhibit an activity (e.g., inhibit at least one activity of, reduce proliferation, migration, growth or viability) of a cell, e.g., a cancer cell *in vivo*. The binding proteins can be used by themselves or conjugated to an agent, e.g., a cytotoxic drug, cytotoxin enzyme, or radioisotope. This method includes: administering the binding protein alone or attached to an agent (e.g., a cytotoxic drug), to a subject requiring such treatment. For example, MMP-12 binding proteins that do not substantially inhibit MMP-12 may be used to deliver nanoparticles containing agents, such as toxins, to MMP-12 associated cells or tissues, e.g., tumors.

Because the MMP-12 binding proteins recognize MMP-12-expressing cells and can bind to cells that are associated with (e.g., in proximity of or intermingled with) cancer cells, e.g., cancerous lung, liver, colon, breast, ovarian, epidermal, laryngeal, and cartilage cells, and particularly metastatic cells thereof, MMP-12 binding proteins can be used to inhibit (e.g., inhibit at least one activity, reduce growth and proliferation, or kill) any such cells and inhibit

carcinogenesis. Reducing MMP-12 activity near a cancer can indirectly inhibit (e.g., inhibit at least one activity, reduce growth and proliferation, or kill) the cancer cells which may be dependent on the MMP-12 activity for metastasis, activation of growth factors, and so forth.

Alternatively, the binding proteins bind to cells in the vicinity of the cancerous cells, but are sufficiently close to the cancerous cells to directly or indirectly inhibit (e.g., inhibit at least one activity, reduce growth and proliferation, or kill) the cancerous cells. Thus, the MMP-12 binding proteins (e.g., modified with a toxin, e.g., a cytotoxin) can be used to selectively inhibit cells in cancerous tissue (including the cancerous cells themselves and cells associated with or invading the cancer).

The binding proteins may be used to deliver an agent (e.g., any of a variety of cytotoxic and therapeutic drugs) to cells and tissues where MMP-12 is present. Exemplary agents include a compound emitting radiation, molecules of plants, fungal, or bacterial origin, biological proteins, and mixtures thereof. The cytotoxic drugs can be intracellularly acting cytotoxic drugs, such as toxins short range radiation emitters, e.g., short range, high energy α -emitters.

To target MMP-12 expressing cells, particularly cancerous cells, a prodrug system can be used. For example, a first binding protein is conjugated with a prodrug which is activated only when in close proximity with a prodrug activator. The prodrug activator is conjugated with a second binding protein, preferably one which binds to a non competing site on the target molecule. Whether two binding proteins bind to competing or non competing binding sites can be determined by conventional competitive binding assays. Exemplary drug prodrug pairs are described in Blakely et al., (1996) Cancer Research, 56:3287-3292.

The MMP-12 binding proteins can be used directly *in vivo* to eliminate antigen-expressing cells via natural complement-dependent cytotoxicity (CDC) or antibody dependent cellular cytotoxicity (ADCC). The binding proteins described herein can include complement binding effector domain, such as the Fc portions from IgG1, -2, or -3 or corresponding portions of IgM which bind complement. In one embodiment, a population of target cells is *ex vivo* treated with a binding agent described herein and appropriate effector cells. The treatment can be supplemented by the addition of complement or serum containing complement. Further, phagocytosis of target cells coated with a binding protein described herein can be improved by binding of complement proteins. In another embodiment target cells coated with the binding protein which includes a complement binding effector domain are lysed by complement.

Methods of administering MMP-12 binding proteins are described in “Pharmaceutical Compositions.” Suitable dosages of the molecules used will depend on the age and weight of the subject and the particular drug used. The binding proteins can be used as competitive agents to inhibit or reduce an undesirable interaction, e.g., between a natural or pathological agent and the MMP-12.

The MMP-12 binding protein can be used to deliver macro and micromolecules, e.g., a gene into the cell for gene therapy purposes into the endothelium or epithelium and target only those tissues expressing the MMP-12. The binding proteins may be used to deliver a variety of cytotoxic drugs including therapeutic drugs, a compound emitting radiation, molecules of plants, fungal, or bacterial origin, biological proteins, and mixtures thereof. The cytotoxic drugs can be intracellularly acting cytotoxic drugs, such as short range radiation emitters, including, for example, short range, high energy α emitters, as described herein.

In the case of polypeptide toxins, recombinant nucleic acid techniques can be used to construct a nucleic acid that encodes the binding protein (e.g., antibody or antigen-binding fragment thereof) and the cytotoxin (or a polypeptide component thereof) as translational fusions. The recombinant nucleic acid is then expressed, e.g., in cells and the encoded fusion polypeptide isolated.

Alternatively, the MMP-12 binding protein can be coupled to high energy radiation emitters, for example, a radioisotope, such as ^{131}I , a γ -emitter, which, when localized at a site, results in a killing of several cell diameters. See, e.g., S.E. Order, “Analysis, Results, and Future Prospective of the Therapeutic Use of Radiolabeled Antibody in Cancer Therapy”, *Monoclonal Antibodies for Cancer Detection and Therapy*, R.W. Baldwin et al. (eds.), pp 303 316 (Academic Press 1985). Other suitable radioisotopes include α emitters, such as ^{212}Bi , ^{213}Bi , and ^{211}At , and β emitters, such as ^{186}Re and ^{90}Y . Moreover, ^{177}Lu may also be used as both an imaging and cytotoxic agent.

Radioimmunotherapy (RIT) using antibodies labeled with ^{131}I , ^{90}Y , and ^{177}Lu is under intense clinical investigation. There are significant differences in the physical characteristics of these three nuclides and as a result, the choice of radionuclide is very critical in order to deliver maximum radiation dose to a tissue of interest. The higher beta energy particles of ^{90}Y may be good for bulky tumors. The relatively low energy beta particles of ^{131}I are ideal, but in vivo dehalogenation of radioiodinated molecules is a major disadvantage for internalizing antibody.

In contrast, ^{177}Lu has low energy beta particle with only 0.2-0.3 mm range and delivers much lower radiation dose to bone marrow compared to ^{90}Y . In addition, due to longer physical half-life (compared to ^{90}Y), the residence times are higher. As a result, higher activities (more mCi amounts) of ^{177}Lu labeled agents can be administered with comparatively less radiation dose to marrow. There have been several clinical studies investigating the use of ^{177}Lu labeled antibodies in the treatment of various cancers. (Mulligan T et al., 1995, *Clin. Canc. Res.* 1: 1447-1454; Meredith RF, et al., 1996, *J. Nucl. Med.* 37:1491-1496; Alvarez RD, et al., 1997, *Gynecol. Oncol.* 65: 94-101).

Exemplary Diseases and Conditions

The MMP-12 binding proteins described herein are useful to treat diseases or conditions in which MMP-12 is implicated, e.g., a disease or condition described herein, or to treat one or more symptoms associated therewith. In some embodiments, the MMP-12 binding protein (e.g., MMP-12 binding IgG or Fab) inhibits MMP-12 activity, e.g., catalytic activity.

Examples of such diseases and conditions include a cancer (e.g., metastatic cancer, e.g., metastatic colorectal, lung, or hepatocellular cancer), an inflammatory disease (e.g., chronic obstructive pulmonary disease (COPD), asthma, rhinitis (e.g., allergic rhinitis), atherosclerosis, multiple sclerosis, rheumatoid arthritis), cardiovascular disease, aneurysm, wound healing, aging and nerve damage associated with excess or inappropriate activity of MMP-12. A therapeutically effective amount of a MMP-12 binding protein is administered to a subject having or suspected of having a disorder in which MMP-12 is implicated, thereby treating (e.g., ameliorating or improving a symptom or feature of a disorder, slowing, stabilizing or halting disease progression) the disorder.

The MMP-12 binding protein is administered in a therapeutically effective amount. A therapeutically effective amount of an MMP-12 binding protein is the amount which is effective, upon single or multiple dose administration to a subject, in treating a subject, e.g., curing, alleviating, relieving or improving at least one symptom of a disorder in a subject to a degree beyond that expected in the absence of such treatment. A therapeutically effective amount of the composition may vary according to factors such as the disease state, age, sex, and weight of the individual, and the ability of the compound to elicit a desired response in the individual. A

therapeutically effective amount is also one in which any toxic or detrimental effects of the composition are outweighed by the therapeutically beneficial effects.

A therapeutically effective amount can be administered, typically an amount of the compound which is effective, upon single or multiple dose administration to a subject, in treating a subject, e.g., curing, alleviating, relieving or improving at least one symptom of a disorder in a subject to a degree beyond that expected in the absence of such treatment. A therapeutically effective amount of the composition may vary according to factors such as the disease state, age, sex, and weight of the individual, and the ability of the compound to elicit a desired response in the individual. A therapeutically effective amount is also one in which any toxic or detrimental effects of the composition are outweighed by the therapeutically beneficial effects. A therapeutically effective dosage preferably modulates a measurable parameter, favorably, relative to untreated subjects. The ability of a compound to inhibit a measurable parameter can be evaluated in an animal model system predictive of efficacy in a human disorder.

Dosage regimens can be adjusted to provide the optimum desired response (e.g., a therapeutic response). For example, a single bolus may be administered, several divided doses may be administered over time or the dose may be proportionally reduced or increased as indicated by the exigencies of the therapeutic situation. It is especially advantageous to formulate parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subjects to be treated; each unit contains a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier.

Cancer

Matrix metalloproteases (MMPs), such as MMP-12, are believed to contribute to cancer by cleaving components of the ECM and basement membranes, thereby allowing cancer cells to penetrate and infiltrate the subjacent stromal matrix. Additionally, a number of growth-factor receptors, cell adhesion molecules, chemokines, cytokines, apoptotic ligands, and angiogenic factors are substrates of MMPs. Hence, MMP activity may cause activation of growth factors, suppression of tumor cell apoptosis, destruction of chemokine gradients developed by host immune response, or release of angiogenic factors. MMPs may facilitate tumor growth by

promoting the release of cell proliferation factors such as insulin-like growth factors which are bound to specific binding proteins (IGFBPs) (Manes et al., 1997 J. Biol. Chem. 272: 25706-25712).

Collagenases, including MMP-12, have been found at elevated levels in cancers of the colon, lung, and liver. Usually, these elevated levels correlate with higher tumor grade and invasiveness.

Accordingly, the disclosure provides methods of treating (e.g., slowing, eliminating, or reversing tumor growth, preventing or reducing, either in number or size, metastases, reducing or eliminating tumor cell invasiveness, providing an increased interval to tumor progression, or increasing disease-free survival time) cancer (e.g., breast cancer, including Her2+, Her2-, ER+, ER-, Her2+/ER+, Her2+/ER-, Her2-/ER+, and Her2-/ER- breast cancer), head and neck cancer, oral cavity cancer, laryngeal cancer, chondrosarcoma, ovarian cancer, lung cancer (e.g., non-small cell lung cancer), prostate cancer, colon cancer, colorectal cancer, liver cancer (hepatocellular cancer), cervical cancer, testicular carcinoma, melanoma, brain tumors (e.g., astrocytomas, glioblastomas, gliomas)) by administering an effective amount of an MMP-12 binding protein (e.g., an anti-MMP-12 IgG or Fab). In some embodiments, the MMP-12 binding protein inhibits MMP-12 activity.

In certain embodiments, the MMP-12 binding protein is administered as a single agent treatment. In other embodiments, the MMP-12 binding protein is administered in combination with an additional anti-cancer agent.

Also provided are methods of preventing or reducing risk of developing cancer, by administering an effective amount of an MMP-12 binding protein to a subject at risk of developing cancer, thereby reducing the subject's risk of developing a cancer.

The disclosure further provides methods of modulating (e.g., reducing or preventing) angiogenesis at a tumor site by administering an effective amount of an MMP-12 binding protein, thereby reducing or preventing angiogenesis at the tumor site. The MMP-12 binding protein may be administered as a single agent therapy or in combination with additional agents.

Also provided are methods for reducing extracellular matrix (ECM) degradation by a tumor, comprising administering an effective amount of an MMP-12 binding protein to a subject, thereby reducing ECM degradation by a tumor in the subject.

The disclosed methods are useful in the prevention and treatment of solid tumors, soft tissue tumors, and metastases thereof. Solid tumors include malignancies (e.g., sarcomas, adenocarcinomas, and carcinomas) of the various organ systems, such as those of lung, breast, lymphoid, gastrointestinal (e.g., colon), and genitourinary (e.g., renal, urothelial, or testicular tumors) tracts, pharynx, prostate, and ovary. Exemplary adenocarcinomas include colorectal cancers, renal-cell carcinoma, liver cancer, non-small cell carcinoma of the lung, and cancer of the small intestine. Additional exemplary solid tumors include: fibrosarcoma, myxosarcoma, liposarcoma, chondrosarcoma, osteogenic sarcoma, chordoma, angiosarcoma, endotheliosarcoma, lymphangiosarcoma, lymphangioendotheliosarcoma, synovioma, mesothelioma, Ewing's tumor, leiomyosarcoma, rhabdomyosarcoma, gastrointestinal system carcinomas, colon carcinoma, pancreatic cancer, breast cancer, genitourinary system carcinomas, ovarian cancer, prostate cancer, squamous cell carcinoma, basal cell carcinoma, adenocarcinoma, sweat gland carcinoma, sebaceous gland carcinoma, papillary carcinoma, papillary adenocarcinomas, cystadenocarcinoma, medullary carcinoma, bronchogenic carcinoma, renal cell carcinoma, hepatoma, bile duct carcinoma, choriocarcinoma, seminoma, embryonal carcinoma, Wilms' tumor, cervical cancer, endocrine system carcinomas, testicular tumor, lung carcinoma, small cell lung carcinoma, non-small cell lung carcinoma, bladder carcinoma, epithelial carcinoma, glioma, astrocytoma, medulloblastoma, craniopharyngioma, ependymoma, pinealoma, hemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, melanoma, neuroblastoma, and retinoblastoma. Metastases of the aforementioned cancers can also be treated or prevented in accordance with the methods described herein.

Guidance for determination of a therapeutically effective amount for treatment of cancer may be obtained by reference to *in vivo* models of the cancer to be treated. For example, the amount of a MMP-12 binding protein that is a therapeutically effective amount in a rodent or Libechov minipig model of cancer may be used to guide the selection of a dose that is a therapeutically effective amount. A number of rodent models of human cancers are available, including nude mouse/tumor xenograft systems (e.g., melanoma xenografts; see, e.g., Trikha et al. Cancer Research 62:2824-2833 (2002)) and murine models of breast cancer or glioma (e.g., Kuperwasser et al., Cancer Research 65, 6130-6138, (2005); Bradford et al., Br J Neurosurg. 3(2):197-210 (1989)). A melanoblastoma-bearing Libechov minipig (MeLiM) is available as an

animal model of melanoma (e.g., Boisgard et al., Eur J Nucl Med Mol Imaging 30(6):826-34 (2003)).

Rheumatoid Arthritis and Associated Conditions

Rheumatoid arthritis (RA) is an autoimmune, chronic inflammatory disease that causes joint swelling and pain and normally results in joint destruction. RA generally follows a relapsing/remitting course, with “flares” of disease activity interspersed with remissions of disease symptoms. RA is associated with a number of additional inflammatory disorders, including Sjogren’s syndrome (dry eyes and mouth caused by inflammation of tear and saliva glands), pleuritis (inflammation of the pleura that causes pain upon deep breath and coughing), rheumatoid nodules (nodular sites of inflammation that develop within the lungs), pericarditis (inflammation of the pericardium that causes pain when lying down or leaning forward), Felty syndrome (splenomegaly and leucopenia observed in conjunction with RA, making the subject prone to infection), and vasculitis (an inflammation of the blood vessels which can block blood flow). MMP-12 has been implicated in rheumatoid arthritis.

Symptoms of active RA include fatigue, lack of appetite, low grade fever, muscle and joint aches, and stiffness. Muscle and joint stiffness are usually most notable in the morning and after periods of inactivity. During flares, joints frequently become red, swollen, painful, and tender, generally as a consequence of synovitis.

Treatment for rheumatoid arthritis involves a combination of medications, rest, joint strengthening exercises, and joint protection. Two classes of medications are used in treating rheumatoid arthritis: anti-inflammatory “first-line drugs,” and Disease-Modifying Antirheumatic Drugs (DMARDs).” The first-line drugs include NSAIDS (e.g., aspirin, naproxen, ibuprofen, and etodolac) and cortisone (corticosteroids). DMARDS, such as gold (e.g., gold salts, gold thioglucose, gold thiomalate, oral gold), methotrexate, sulfasalazine, D-penicillamine, azathioprine, cyclophosphamide, chlorambucil, and cyclosporine, leflunomide, etanercept, infliximab, anakinra, and adalimumab, and hydroxychloroquine, promote disease remission and prevent progressive joint destruction, but they are not anti-inflammatory agents.

Increased levels of MMP-12 have been found in subjects with arthritis (compared with normal individuals). The disclosure provides methods of treating (e.g., ameliorating, stabilizing, or eliminating one or more symptoms or ameliorating or stabilizing the subject’s score on a RA

scale) rheumatoid arthritis by administering a therapeutically effective amount of a MMP-12 binding protein to a subject having or suspected of having RA. Additionally provided are methods of treating RA by administering a therapeutically effective amount of a MMP-12 binding protein and at least one NSAID and/or DMARDS.

Further provided are methods of treating (e.g., ameliorating, stabilizing, or eliminating one or more symptoms) rheumatoid arthritis associated disorders (Sjogren's syndrome, pleuritis, pulmonary rheumatoid nodules, pericarditis, Felty syndrome, and vasculitis) by administering a therapeutically effective amount of an MMP-12 binding protein.

Scales useful for assessing RA and symptoms of RA include the Rheumatoid Arthritis Severity Scale (RASS; Bardwell et al., (2002) *Rheumatology* **41**(1):38-45), SF-36 Arthritis Specific Health Index (ASHI; Ware et al., (1999) *Med. Care.* **37**(5 Suppl):MS40-50), Arthritis Impact Measurement Scales or Arthritis Impact Measurement Scales 2 (AIMS or AIMS2; Meenan et al. (1992) *Arthritis Rheum.* **35**(1):1-10); the Stanford Health Assessment Questionnaire (HAQ), HAQII, or modified HAQ (see, e.g., Pincus et al. (1983) *Arthritis Rheum.* **26**(11):1346-53).

Guidance for the determination of the dosage that delivers a therapeutically effective amount of a MMP-12 binding protein may be obtained from animal models of rheumatoid arthritis, such as collagen-induced arthritis (CIA), which is induced, typically in rodents, by immunization with autologous or heterologous type II collagen in adjuvant (Williams et al. *Methods Mol Med.* 98:207-16 (2004)).

COPD

Chronic Obstructive Pulmonary Disease (COPD), also known as chronic obstructive airway disease (COAD), is a group of diseases characterized by the pathological limitation of airflow in the airway that is not fully reversible. COPD is the umbrella term for chronic bronchitis, emphysema and a range of other lung disorders. It is most often due to tobacco smoking, but can be due to other airborne irritants such as coal dust, asbestos or solvents, as well as congenital conditions such as alpha-1-antitrypsin deficiency.

The main symptoms of COPD include dyspnea (shortness of breath) lasting for months or perhaps years, possibly accompanied by wheezing, and a persistent cough with sputum production. It is possible the sputum may contain blood (hemoptysis) and become thicker,

usually due to damage of the blood vessels of the airways. Severe COPD could lead to cyanosis caused by a lack of oxygen in the blood. In extreme cases it could lead to cor pulmonale due to the extra work required by the heart to get blood to flow through the lungs.

COPD is particularly characterised by the spirometric measurement of a ratio of forced expiratory volume over 1 second (FEV_1) to forced vital capacity (FVC) being < 0.7 and the $FEV_1 < 80\%$ of the predicted value as measured by a plethysmograph. Other signs include a rapid breathing rate (tachypnea) and a wheezing sound heard through a stethoscope. Pulmonary emphysema is NOT the same as subcutaneous emphysema, which is a collection of air under the skin that may be detected by the crepitus sounds produced on palpation.

Treatment for COPD includes inhalers that dilate the airways (bronchodilators) and sometimes theophylline. The COPD patient must stop smoking. In some cases inhaled steroids are used to suppress lung inflammation, and, in severe cases or flare-ups, intravenous or oral steroids are given. Antibiotics are used during flare-ups of symptoms as infections can worsen COPD. Chronic, low-flow oxygen, non-invasive ventilation, or intubation may be needed in some cases. Surgery to remove parts of the diseased lung has been shown to be helpful for some patients with COPD. Lung rehabilitation programs may help some patients. Lung transplant is sometimes performed for severe cases. Bronchodilators that can be used include:

There are several types of bronchodilators used clinically with varying efficacy: for example, β_2 agonists, M_3 antimuscarinics, leukotriene antagonists, cromones, corticosteroids, and xanthines. These drugs relax the smooth muscles of the airway allowing for improved airflow. β_2 agonists include: Salbutamol (VENTOLIN®), Bambuterol, Clenbuterol, Fenoterol, and Formoterol, and long acting β_2 agonists (LABAs) such as Salmeterol. M_3 muscarinic antagonists (anticholinergics) include the quaternary M_3 muscarinic antagonist Ipratropium, which is widely prescribed with the β_2 agonist salbutamol, Ipratropium, and Tiotropium, which can be combined with a LABA and inhaled steroid. Cromones include Cromoglicic acid and Nedocromil. Leukotriene antagonists can be used and include Montelukast, Pranlukast, Zafirlukast. Xanthines include theophylline, methylxanthines, theobromine. More aggressive EMR interventions include IV H_1 antihistamines and IV dexamethasone. Phosphodiesterase-4 antagonists include roflumilast and cilomilast. Corticosteroids can be used and include glucocorticoids, beclomethasone, mometasone, and fluticasone. Corticosteroids are often combined with bronchodilators in a

single inhaler. Salmeterol and fluticasone can be combined (ADVAIR®). TNF antagonists include cachexin, cachectin infliximab, adalimumab and etanercept.

The disclosure provides methods of treating COPD (e.g., ameliorating symptoms or the worsening of COPD) by administering a therapeutically effective amount of a MMP-12 binding protein (e.g., an inhibitory MMP-12 binding protein, e.g., an anti-MMP-12 IgG or Fab) to a subject having or suspected of having COPD. Also provided are methods of treating COPD by administering a therapeutically effective amount of a MMP-12 binding protein with another COPD treatment (e.g., β_2 agonists, M_3 antimuscarinics, leukotriene antagonists, cromones, corticosteroids, and xanthines).

Guidance regarding the efficacy and dosage an MMP-12 binding protein which will deliver a therapeutically effective amount of the protein can be obtained from an animal model of COPD, see e.g., PCT publication WO 2007/084486 and references cited therein.

Emphysema

Emphysema is a chronic obstructive pulmonary disease (COPD), formerly termed a chronic obstructive lung disease (COLD). It is often caused by exposure to toxic chemicals or long-term exposure to tobacco smoke.

Emphysema is caused by loss of elasticity (increased compliance) of the lung tissue, from destruction of structures supporting the alveoli, and destruction of capillaries feeding the alveoli, due to the action of alpha 1 antitrypsin deficiency. Thus the small airways collapse during exhalation, although alveolar collapsibility has increased. This impedes airflow and traps air in the lungs, as with other obstructive lung diseases. Symptoms include shortness of breath on exertion and later at rest, hyperventilation, and an expanded chest.

Signs of emphysema include pursed-lipped breathing, central cyanosis and finger clubbing. The chest has increased percussion notes, particularly just above the liver, and a difficult to palpate apex beat, both due to hyperinflation. There may be decreased breath sounds and audible expiratory wheeze. In advanced disease, there are signs of fluid overload such as pitting peripheral edema. The face has a ruddy complexion if there is a secondary polycythemia. Sufferers who retain carbon dioxide have asterixis (metabolic flap) at the wrist.

Emphysema is an irreversible degenerative condition. An important measure to slow its progression is for the patient to stop smoking and avoid all exposure to cigarette smoke and lung

irritants. Pulmonary rehabilitation can be very helpful to optimize the patient's quality of life and teach the patient how to actively manage his or her care. Emphysema is also treated by supporting the breathing with anticholinergics, bronchodilators, steroid medication (inhaled or oral), and supplemental oxygen as required. Treating the patient's other conditions including gastric reflux and allergies can improve lung function. Supplemental oxygen used as prescribed (usually more than 20 hours per day) is the only non-surgical treatment which has been shown to prolong life in emphysema patients. Lung volume reduction surgery (LVRS) can improve the quality of life for certain carefully selected patients. Another treatment option is lung transplant, but few patients are strong enough physically to survive the surgery.

Cigarette smoke condensate induces MMP-12 gene expression in airway-like epithelia in mice (Lavigne et al. *Biochem biophys Res Commun.* 2005: 330:194). COPD patients produce greater quantities of MMP-12 than controls, which may be a critical step in the pathogenesis of emphysema (Molet et al. 2005: *Inflamm Res.* 2005: 54(1): 31). It has been shown that inflammatory lesions in the lungs of mice contain significantly more MMP-12 in macrophages at 10, 20, and 30 days than in controls of mice exposed to cigarette for 60 days (Valenca et al. *Toxicol Pathol.* 2004:32(3):351).

The disclosure provides methods of treating or preventing emphysema (e.g., ameliorating symptoms or the worsening of emphysema) by administering a therapeutically effective amount of a MMP-12 binding protein (e.g., an inhibitory MMP-12 binding protein, e.g., an anti-MMP-12 IgG or Fab) to a subject having or suspected of having emphysema. Also provided are methods of treating emphysema by administering a therapeutically effective amount of a MMP-12 binding protein with another emphysema treatment (e.g., anticholinergics, bronchodilators, steroid medication, oxygen supplementation, lung volume reduction surgery or lung transplant).

Guidance regarding the efficacy and dosage an MMP-12 binding protein which will deliver a therapeutically effective amount of the protein can be obtained from animal models of emphysema, see e.g., those described in Molet et al. 2005: *Inflamm Res.* 2005: 54(1): 31, Valenca et al. *Toxicol Pathol.* 2004:32(3):351, and references cited therein.

Asthma

Asthma is a chronic condition involving the respiratory system in which the airway occasionally constricts, becomes inflamed, and is lined with excessive amounts of mucus, often

in response to one or more triggers. These episodes may be triggered by such things as exposure to an environmental stimulant (or allergen) such as cold air, warm air, moist air, exercise or exertion, or emotional stress. In children, the most common triggers are viral illnesses such as those that cause the common cold. This airway narrowing causes symptoms such as wheezing, shortness of breath, chest tightness, and coughing. The airway constriction responds to bronchodilators.

In some individuals asthma is characterized by chronic respiratory impairment. In others it is an intermittent illness marked by episodic symptoms that may result from a number of triggering events, including upper respiratory infection, stress, airborne allergens, air pollutants (such as smoke or traffic fumes), or exercise. Some or all of the following symptoms may be present in those with asthma: dyspnea, wheezing, stridor, coughing, an inability for physical exertion. Some asthmatics who have severe shortness of breath and tightening of the lungs never wheeze or have stridor and their symptoms may be confused with a COPD-type disease.

An acute exacerbation of asthma is commonly referred to as an asthma attack. The clinical hallmarks of an attack are shortness of breath (dyspnea) and either wheezing or stridor.

During an asthma episode, inflamed airways react to environmental triggers such as smoke, dust, or pollen. The airways narrow and produce excess mucus, making it difficult to breathe. In essence, asthma is the result of an immune response in the bronchial airways.

The airways of asthmatics are "hypersensitive" to certain triggers/stimuli. In response to exposure to these triggers, the bronchi (large airways) contract into spasm (an "asthma attack"). Inflammation soon follows, leading to a further narrowing of the airways and excessive mucus production, which leads to coughing and other breathing difficulties.

The most effective treatment for asthma is identifying triggers, such as pets or aspirin, and limiting or eliminating exposure to them. Desensitization is currently the only known "cure" to the disease.

Symptomatic control of episodes of wheezing and shortness of breath is generally achieved with fast-acting bronchodilators.

Relief medication: Short-acting, selective beta₂-adrenoceptor agonists, such as salbutamol (*albuterol* USAN), levalbuterol, terbutaline and bitolterol, can be used. Older, less selective adrenergic agonists, such as inhaled epinephrine and ephedrine tablets, can be used. Anticholinergic medications, such as ipratropium bromide may be used.

Preventative medication: Current treatment protocols recommend prevention medications such as an inhaled corticosteroid, which helps to suppress inflammation and reduces the swelling of the lining of the airways, in anyone who has frequent (greater than twice a week) need of relievers or who has severe symptoms. If symptoms persist, additional preventive drugs are added until the asthma is controlled. With the proper use of prevention drugs, asthmatics can avoid the complications that result from overuse of relief medications. Preventive agents include: inhaled glucocorticoids (e.g., ciclesonide, beclomethasone, budesonide, flunisolide, fluticasone, mometasone, and triamcinolone), leukotriene modifiers (e.g., montelukast, zafirlukast, pranlukast, and zileuton), mast cell stabilizers (e.g., cromoglicate (cromolyn), and nedocromil), antimuscarinics/anticholinergics (e.g., ipratropium, oxitropium, and tiotropium), methylxanthines (e.g., theophylline and aminophylline), antihistamines, an IgE blocker such as omalizumab, methotrexate).

Long-acting beta₂-adrenoceptor agonists can be used and include salmeterol, formoterol, bambuterol, and sustained-release oral albuterol. Combinations of inhaled steroids and long-acting bronchodilators are becoming more widespread; the most common combination currently in use is fluticasone/salmeterol (Advair in the United States, and Seretide in the United Kingdom). Another combination is budesonide/formoterol which is commercially known as Symbicort.

Concentrations of MMP-12 are increased in asthmatic subjects as compared with normal individuals. The disclosure provides methods of treating asthma (e.g., ameliorating symptoms or the worsening of asthma) by administering a therapeutically effective amount of a MMP-12 binding protein (e.g., an inhibitory MMP-12 binding protein, e.g., an anti-MMP-12 IgG or Fab) to a subject having or suspected of having asthma. Also provided are methods of treating asthma by administering a therapeutically effective amount of a MMP-12 binding protein with another asthma treatment (e.g., glucocorticoids, leukotriene modifiers, mast cell stabilizers, antimuscarinics/anticholinergics, antihistamines, an IgE blocker, methotrexate).

Guidance regarding the efficacy and dosage an MMP-12 binding protein which will deliver a therapeutically effective amount of the protein can be obtained from an animal model of asthma, see e.g., US Pat. No. 5,602,302, or European Pat. No. EP1192944 B1, and references cited therein.

Atherosclerosis and cardiovascular disease

Atherosclerosis is a disease affecting arterial blood vessels. It is a chronic inflammatory response in the walls of arteries, in large part due to the accumulation of macrophage white blood cells and promoted by low density (especially small particle) lipoproteins (plasma proteins that carry cholesterol and triglycerides) without adequate removal of fats and cholesterol from the macrophages by functional high density lipoproteins(HDL). It is caused by the formation of multiple plaques within the arteries.

Atherosclerosis causes two main problems. First, the atheromatous plaques, though long compensated for by artery enlargement, eventually lead to plaque ruptures and stenosis (narrowing) of the artery and, therefore, an insufficient blood supply to the organ it feeds. If the compensating artery enlargement process is excessive, then an aneurysm results.

Commonly, soft plaque suddenly ruptures, causing the formation of a thrombus that will rapidly slow or stop blood flow, leading to death of the tissues fed by the artery. This event is called an infarction. One commonly recognized scenario is called coronary thrombosis of a coronary artery, causing myocardial infarction (a heart attack). Another common scenario is claudication from insufficient blood supply to the legs, typically due to a combination of both stenosis and aneurysmal segments narrowed with clots. Since atherosclerosis is a body-wide process, similar events also occur in the arteries to the brain, intestines, kidneys, legs, etc.

Atherosclerosis commonly becomes symptomatic when interfering with the coronary circulation supplying the heart or cerebral circulation supplying the brain, and is considered an underlying cause of strokes, heart attacks, various heart diseases including congestive heart failure, and most cardiovascular diseases, in general.

In human peripheral blood derived macrophages, MMP-12 mRNA is upregulated by several pro-atherosclerotic cytokines (Feinberg et al. J Biol Chem. 2000: 275(33):25766). Transcript levels of MMP-12 in carotid atherosclerotic plaques correlate with histological features and clinical manifestations (Morgan et al. Stroke. 2004: 35(6): 1310). MMP-12 mRNA was consistently demonstrated in atherosclerotic occlusive disease (AOD) tissues and may have a direct role in the pathogenesis of aortic aneurysms (Curci et al. J Clin Invest. 1998:102(11):1900). Epidemiological data and in vivo animal experiments have indicated that differentiation of macrophages into potentially plaque-forming foam cells accompanied significantly elevated levels of matrix-degrading MMP-12 (Vogel et al. Cardiovasc Toxicol.

2004;4(4):363). MMP-12 has been shown to play an important role in vascular stenosis in hypercholesterolemia in hypercholesterolemic hamsters (Matsuno et al. 2004: 44(1): 57). Deficiency in MMP-12 protected apolipoprotein E-deficient mice against atherosclerotic media destruction when MMP-12 deficiency mice were crossed in the atherosclerosis-prone apolipoprotein E-deficient background and fed a cholesterol-rich diet (Lutten et al. 2004: 109(11): 1408).

Smoking has been shown to be associated with increased macrophage immunoreactivity as well as elevated expression of MMP-12, which is a marker of inflammation and tissue destruction atherosclerotic plaques (Kangavari et al. J Cardiovasc Pharmacol Ther. 2004: 9(4):291). MMP-12 was detected in the lungs of rats treated with intraperitoneal nicotine and might play an important role in the development of cardiovascular and lung diseases in smokers (Valenca et al. Exp Toxicol Pathol. 2004: 55(5)393).

Treatment for atherosclerosis includes statins, primary and secondary prevention, diet and dietary supplements, surgical intervention and prophylaxis.

Some statins, e.g., rosuvastatin, have demonstrated regression of atherosclerotic plaque within the coronary arteries by IVUS (intravascular ultrasound evaluation). Combinations of statins, niacin, intestinal cholesterol absorption-inhibiting supplements (ezetimibe and others, and to a much lesser extent fibrates) have been a successful in changing common but sub-optimal lipoprotein patterns and group outcomes.

In addition, several classes of lipoprotein expression altering agents have consistently reduced not only heart attack, stroke and hospitalization but also mortality rates. Vitamin B3, AKA niacin, in pharmacologic doses, (generally 1,000 to 3,000 mg/day) tend to improve (a) HDL levels, size and function; (b) shift LDL particle distribution to larger particle size; and (c) lower lipoprotein (a), an atherosclerosis promoting genetic variant of LDL. The described MMP-12 binding proteins can be administered in combination with one or more of these treatments.

Other treatments include minimally invasive angioplasty procedures that can include stents to physically expand narrowed arteries, and major invasive surgery, such as bypass surgery, to create additional blood supply connections that go around the more severely narrowed areas.

Patients at risk for atherosclerosis-related diseases are increasingly being treated prophylactically with low-dose aspirin and a statin.

The disclosure provides methods of treating or preventing atherosclerosis and cardiovascular disease (e.g., ameliorating symptoms or the worsening of atherosclerosis and cardiovascular disease) by administering a therapeutically effective amount of a MMP-12 binding protein (e.g., an inhibitory MMP-12 binding protein, e.g., an anti-MMP-12 IgG or Fab) to a subject having or suspected of having atherosclerosis and cardiovascular disease. Also provided are methods of treating atherosclerosis and cardiovascular disease by administering a therapeutically effective amount of a MMP-12 binding protein with another atherosclerosis and cardiovascular disease treatment (e.g., statins, primary and secondary prevention, diet and dietary supplements, surgical intervention or prophylaxis)

Guidance regarding the efficacy and dosage an MMP-12 binding protein which will deliver a therapeutically effective amount of the protein can be obtained from animal models of atherosclerosis, see e.g., those described in Fan et al. Transgenic Res. 2004: 13(3): 261) and references cited therein.

Multiple sclerosis

Multiple sclerosis (MS) is an autoimmune condition in which the immune system attacks the central nervous system (CNS), leading to demyelination. It may cause numerous physical and mental symptoms, and often progresses to physical and cognitive disability. Disease onset usually occurs in young adults, is more common in women.

MS presents with a variety of symptoms, including changes in sensation (hypoesthesia); muscle weakness, abnormal muscle spasms, or difficulty in moving; difficulties with coordination and balance (ataxia); problems in speech (dysarthria) or swallowing (dysphagia); visual problems (nystagmus, optic neuritis, or diplopia); fatigue and acute or chronic pain syndromes; and bladder and bowel difficulties. Cognitive impairment of varying degrees, or emotional symptomatology in the form of depression or pseudobulbar affect are also common. Neuropathic pain is usual, and this can be in the form of Lhermitte's sign. Paraesthesias can be present and include pins and needles; tingling; shivering; burning pains; feelings of pressure; and areas of skin with heightened sensitivity to touch. The pains associated with these can be aching, throbbing, stabbing, shooting, gnawing, tingling, tightness and numbness. The main clinical measure of disability progression and severity of the symptoms is the Expanded Disability Status Scale or EDSS.

The initial attacks (also known as exacerbations or relapses) are often transient, mild (or asymptomatic), and self-limited. The common initial symptoms reported are: changes in sensation in the arms, legs or face (33%), complete or partial vision loss (optic neuritis) (16%), weakness (13%), double vision (7%), unsteadiness when walking (5%), and balance problems (3%); but many rare initial symptoms have been reported such as aphasia or psychosis. Optic neuritis or focal leg weakness may lead to falls and other serious accidents.

Several therapies have proven helpful for treatment of multiple sclerosis. The aims of treatment include returning function after an attack, preventing new attacks, and preventing disability. During symptomatic attacks administration of high doses of intravenous corticosteroids, such as methylprednisolone, is the routine therapy for acute relapses. Disease-modifying treatments including interferons (e.g., AVONEX®, REBIF®, BETAFERON®), glatiramer acetate (e.g., COPAXONE®), immunosuppressant (e.g., mitoxantrone) and natalizumab (e.g., TYSABRI®) are used for relapsing-remitting MS.

In human active demyelinating lesions, phagocytic macrophages are MMP-12 positive, suggesting a role for MMP-12 during demyelination in MS (Vos et al. J Neuroimmunol 2003: 138(1-2): 106).

The disclosure provides methods of treating or preventing MS (e.g., ameliorating symptoms or the worsening of MS) by administering a therapeutically effective amount of a MMP-12 binding protein (e.g., an inhibitory MMP-12 binding protein, e.g., an anti-MMP-12 IgG or Fab) to a subject having or suspected of having MS. Also provided are methods of treating MS by administering a therapeutically effective amount of a MMP-12 binding protein with another MS treatment (e.g., interferons (e.g., AVONEX®, REBIF®, BETAFERON®), glatiramer acetate (e.g., COPAXONE®), immunosuppressant (e.g., mitoxantrone) and natalizumab (e.g., TYSABRI®)).

Guidance regarding the efficacy and dosage an MMP-12 binding protein which will deliver a therapeutically effective amount of the protein can be obtained from animal models of MS, see e.g., those described in Toft-Hansen et al. J Immunol. 2004: 173(8): 5209, Tsutsui et al. J Neurosci 2004: 24: 1521, Anthony et al. J Neuroimmunol 1998: 87(1-2): 62 and references cited therein.

Abdominal aortic aneurysm

Abdominal aortic aneurysm (AAA) is a localized dilatation of the abdominal aorta, that exceeds the normal diameter by more than 50%. The normal diameter of the infrarenal aorta is approximately 2 cm. It is caused by a degenerative process of the aortic wall, however the exact etiology remains unknown. It is most commonly located below the kidneys (infrarenally; 90%), other possible locations are above or at the level of the kidneys (suprarenal and pararenal). The aneurysm can extend to include one or both of the iliac arteries. An aortic aneurysm may also occur in the thorax.

An abdominal aortic aneurysm occurs more commonly in older individuals (between 65 and 75), and more often in men and smokers.

A serious complication of an abdominal aortic aneurysm is rupture, which is often a fatal event. An abdominal aortic aneurysm weakens the walls of the blood vessel, leaving it vulnerable to rupturing. The clinical manifestation of ruptured AAA can include low back, flank, abdominal or groin pain, but the bleeding usually leads to a hypovolemic shock with hypotension, tachycardia, cyanosis, and altered mental status.

Some risk factors for AAA include genetic influences, hemodynamic influences, atherosclerosis, infection, trauma, arteritis, cystic medial necrosis and connective tissue disorders (e.g. Marfan syndrome, Ehlers-Danlos syndrome).

MMP-12 zymogen levels and proteolytic activities are increased in AAAs when compared with healthy aorta, suggesting that chronic aortic wall inflammation is mediated by macrophage infiltration, which may account for the destruction of medial elastin (Annabi et al. J Vasc Surg. 2002: 35(3): 539). MMP-12 is prominently expressed by aneurysm-infiltrating macrophages within the degenerating aortic media of AAA, where it is also bound to residual elastic fiber fragments. Because elastin represents a critical component of aortic wall structure and a matrix substrate for metalloelastases, MMP-12 may have a direct role in the pathogenesis of aortic aneurysms (Curci et al. 1998: 102(11): 1900).

The treatment options for asymptomatic AAA are immediate repair, surveillance with a view to eventual repair, and conservative management. There are currently two modes of repair available for an AAA: open aneurysm repair (OR), and endovascular aneurysm repair (EVAR).

The disclosure provides methods of treating or preventing AAA (e.g., ameliorating symptoms or the worsening of AAA) by administering a therapeutically effective amount of a

MMP-12 binding protein (e.g., an inhibitory MMP-12 binding protein, e.g., an anti-MMP-12 IgG or Fab) to a subject having or suspected of having AAA. Also provided are methods of treating AAA by administering a therapeutically effective amount of a MMP-12 binding protein with another AAA treatment (e.g., immediate repair, surveillance with a view to eventual repair, or conservative management).

Guidance regarding the efficacy and dosage an MMP-12 binding protein which will deliver a therapeutically effective amount of the protein can be obtained from animal models of AAA, see e.g., those described in Longo et al. *Surgery*. 2005: 137(4): 457, Shimizu et al. *J Clin Invest*. 2004: 114(2): 300 and references cited therein.

Sclerosis

Systemic sclerosis (SSc) is the generalized type of scleroderma, which is a chronic disease characterized by excessive deposits of collagen in the skin or other organs. SSc can be fatal as a result of heart, kidney, lung or intestinal damage autoimmune disease.

Scleroderma affects the skin, and in more serious cases it can affect the blood vessels and internal organs. The more evident symptom is usually the hardening of the skin and associated scarring. Blood vessels may also be more visible. Many SSc patients (over 80%) have vascular symptoms and Raynaud's phenomenon. During an attack, there is discoloration of the hands and feet in response to cold. Raynaud's normally affects the fingers and toes. SSc and Raynaud's can cause painful ulcers on the fingers or toes which are known as digital ulcers. Calcinosis is also common in SSc, and is often seen near the elbows, knees or other joints. Diffuse scleroderma can cause musculoskeletal, pulmonary, gastrointestinal, renal and other complications. Patients with larger amounts of cutaneous involvement are more likely to have involvement of the internal tissues and organs.

There appears to be a familial predisposition for autoimmune disease.

Overproduction of MMP-12 by SSc microvascular endothelial cells (MVECs) has been shown to account for the cleavage of urokinase-type plasminogen activator receptor (uPAR) and the impairment of angiogenesis in vitro and may contribute to reduced angiogenesis in SSc patients (D'Alessio et al. *Arthritis Rheum*. 2004: 50(10): 3275).

Treatment for some of the symptoms of scleroderma includes drugs that soften the skin and reduce inflammation. Topical treatment for the skin changes of scleroderma do not alter the

disease course, but may improve pain and ulceration. A range of NSAIDs (nonsteroidal anti-inflammatory drugs) can be used to ease painful symptoms, such as naproxen. Episodes of Raynaud's phenomenon sometimes respond to nifedipine or other calcium channel blockers; severe digital ulceration may respond to prostacyclin analogue iloprost, and the dual endothelin-receptor antagonist bosentan may be beneficial for Raynaud's phenomenon. The skin tightness may be treated systemically with methotrexate and cyclosporin. Scleroderma renal crisis, the occurrence of acute renal failure and malignant hypertension (very high blood pressure with evidence of organ damage) in people with scleroderma, is effectively treated with drugs from the class of the ACE inhibitors. Active alveolitis is often treated with pulses of cyclophosphamide, often together with a small dose of steroids. Pulmonary hypertension may be treated with epoprostenol, bosentan and possibly aerolized iloprost.

The disclosure provides methods of treating or preventing SSc (e.g., ameliorating symptoms or the worsening of SSc) by administering a therapeutically effective amount of a MMP-12 binding protein (e.g., an inhibitory MMP-12 binding protein, e.g., an anti-MMP-12 IgG or Fab) to a subject having or suspected of having SSc. Also provided are methods of treating SSc by administering a therapeutically effective amount of a MMP-12 binding protein with another SSc treatment (e.g., NSAIDs, calcium channel blockers, prostacyclin analogue, the dual endothelin-receptor antagonist, methotrexate, cyclosporin, ACE inhibitors, cyclophosphamide, epoprostenol, and bosentan).

Nephritis

Nephritis is inflammation of the kidney and is often caused by infections, toxins, and auto-immune diseases. Subtypes include glomerulonephritis, interstitial nephritis or tubulointerstitial nephritis, pyelonephritis and Lupus nephritis.

Nephritis is a common cause of glomerular injury. It is a disturbance of the glomerular structure with inflammatory cell proliferation. This can lead to: reduced glomerular blood flow leading to reduced urine output (oliguria) and retention of waste products (uremia). As a result, there can also be leakage of red blood cells from damaged glomerulus (hematuria). Low renal blood flow activates the renin-angiotensin-aldosterone system (RAAS), which therefore causes fluid retention and mild hypertension.

MMP-12 is one of the highly expressed genes in the kidneys on days 3 and 7 after the injection of anti-GBM (glomerular basement membrane) antiserum in a Rat crescentic glomerulonephritis model (Kaneko et al. J Immunol. 2003: 170(6): 3373).

As a subset of nephritis, e.g. pyelonephritis, are often due to bacterial infections, antibiotics are the mainstay of treatment.

The disclosure provides methods of treating or preventing nephritis (e.g., ameliorating symptoms or the worsening of nephritis) by administering a therapeutically effective amount of a MMP-12 binding protein (e.g., an inhibitory MMP-12 binding protein, e.g., an anti-MMP-12 IgG or Fab) to a subject having or suspected of having nephritis. Also provided are methods of treating nephritis by administering a therapeutically effective amount of a MMP-12 binding protein with another nephritis treatment (e.g. antibiotics).

Guidance regarding the efficacy and dosage an MMP-12 binding protein which will deliver a therapeutically effective amount of the protein can be obtained from animal models of nephritis, see e.g., those described in Kaneko et al. J Immunol. 2003: 170(6): 3373, and references cited therein.

Wound healing

Wound healing, or wound repair, is the process of regenerating dermal and epidermal tissue. When an individual is wounded, a set of complex biochemical events takes place in a closely orchestrated cascade to repair the damage. These events overlap in time and may be artificially categorized into separate steps: the inflammatory, proliferative, and remodeling phases.

By regulating the proliferation of corneal epithelial cells, MMP-12 appears to contribute to corneal wound healing (Lyu et al. J Biol Chem. 2005: 280(22): 21653). Epithelial expression of MMP-12 in chronic wounds provides a diagnostic clue for distinguishing squamous cell carcinoma (SCCs) from nonmalignant wounds (Impola et al. Br J Dermatol. 2005: 152(4): 720).

The disclosure provides methods of treating wound (e.g., ameliorating symptoms or the worsening of wound) by administering a therapeutically effective amount of a MMP-12 binding protein (e.g., an inhibitory MMP-12 binding protein, e.g., an anti-MMP-12 IgG or Fab) to a subject having or suspected of having wound. Also provided are methods of treating wound by

administering a therapeutically effective amount of a MMP-12 binding protein with another wound treatment.

Encephalomyelitis and neuroinflammatory disorders

Encephalomyelitis, e.g., experimental autoimmune encephalomyelitis, sometimes Experimental Allergic Encephalomyelitis (EAE), is an animal model of brain inflammation. It is an inflammatory demyelinating disease of the central nervous system (CNS). It is often used with rodents and is widely studied as an animal model of the human CNS demyelinating diseases, including the diseases multiple sclerosis and acute disseminated encephalomyelitis. EAE can be induced by inoculation with whole CNS tissue, purified myelin basic protein (MBP) or myelin proteolipid protein (PLP), together with adjuvants. It may also be induced by the passive transfer of T cells specifically reactive to these myelin antigens. EAE may have either an acute or a chronic relapsing course. Acute EAE closely resembles the human disease acute disseminated encephalomyelitis, while chronic relapsing EAE resembles multiple sclerosis. EAE is also the prototype for T-cell-mediated autoimmune disease in general.

MMP-12 is overexpressed in spinal cord from SJL/J mice and mice with adoptively transferred myelin basic protein (MBP)-specific EAE (Toft-Hansen et al. J. Immunol. 2004: 173(8): 5209). In human, aberrant expression of MMP-12 has been implicated in the pathogenesis of immune-mediated neuroinflammatory disorders (Hughes et al. Neuroscience. 2002: 113(2):273).

The disclosure provides methods of treating or preventing encephalomyelitis, e.g., EAE, and neuroinflammatory disorders (e.g., ameliorating symptoms or the worsening of encephalomyelitis and neuroinflammatory disorders) by administering a therapeutically effective amount of a MMP-12 binding protein (e.g., an inhibitory MMP-12 binding protein, e.g., an anti-MMP-12 IgG or Fab) to a subject having or suspected of having EAE and neuroinflammatory disorders. Also provided are methods of treating encephalomyelitis and neuroinflammatory disorders by administering a therapeutically effective amount of a MMP-12 binding protein with another nephritis treatment.

Guidance regarding the efficacy and dosage an MMP-12 binding protein which will deliver a therapeutically effective amount of the protein can be obtained from animal models of

encephalomyelitis and neuroinflammatory disorders, see e.g., those described in Toft-Hansen et al. J. Immunol. 2004: 173(8): 5209, and references cited therein.

Aging

In biology, senescence is the state or process of aging. Cellular senescence is a phenomenon where isolated cells demonstrate a limited ability to divide in culture, while organismal senescence is the aging of organisms.

Organismal senescence is characterized by the declining ability to respond to stress, increasing homeostatic imbalance and increased risk of disease. As genes that have an effect on aging are discovered, aging is increasingly being regarded in a similar fashion to other genetic conditions.

In humans and other animals, cellular senescence has been attributed to the shortening of telomeres with each cell cycle; when telomeres become too short, the cells die. Other genes are known to affect the aging process, the sirtuin family of genes have been shown to have a significant effect on the lifespan of yeast and nematodes. Over-expression of the RAS2 gene increases lifespan in yeast substantially. In addition to genetic ties to lifespan, diet has been shown to substantially affect lifespan in many animals.

The level of MMP-12 increases in the insoluble fraction of old mice, suggesting increased extracellular matrix (ECM) degradative capacity and MMP-12 may contribute to age-dependent ECM remodeling (Lindsey et al. Cardiovasc Res. 2005: 66(2):410.) Heat treatment increases MMP-12 mRNA and protein expression in human skin suggesting that MMP-12 may contribute to skin aging by accumulation of elastotic material in photoaged skin (Chen et al. J Invest Dermatol. 2005: 124(1):70). MMP-12 may also contribute to skin aging by remodeling of elastotic areas in sun-damaged skin (Saarialho-Kere et al. J Invest Dermatol. 1999: 113(4):664).

The disclosure provides methods of treating or preventing aging (e.g., ameliorating symptoms or the worsening of aging e.g. skin aging) by administering a therapeutically effective amount of a MMP-12 binding protein (e.g., an inhibitory MMP-12 binding protein, e.g., an anti-MMP-12 IgG or Fab) to a subject having or suspected of having aging (e.g. skin aging). Also provided are methods of treating aging by administering a therapeutically effective amount of a MMP-12 binding protein with another aging treatment.

Viral encephalitis

Viral encephalitis is an acute inflammation of the brain caused by a viral infection. Brain damage occurs as the inflamed brain pushes against the skull, and can lead to death.

Patients with encephalitis suffer from fever, headache and photophobia with weakness and seizures also common. Less commonly, stiffness of the neck can occur with rare cases of patients also suffering from stiffness of the limbs, slowness in movement and clumsiness depending on which specific part of the brain is involved. The symptoms of encephalitis are caused by the brain's defense mechanisms activating to get rid of the infection.

Treatment is usually symptomatic. Reliably tested specific antiviral agents are available only for a few viral agents (e.g. acyclovir for herpes simplex virus). In patients who are very sick, supportive treatment, such as mechanical ventilation, is also important.

Infection of the murine central nervous system (CNS) with a neurotropic coronavirus induces encephalitis associated with increased levels of mRNA encoding MMP-12 (Zhou et al. J Virol. 2005: 79(8):4764).

The disclosure provides methods of treating or preventing viral encephalitis (e.g., ameliorating symptoms or the worsening of viral encephalitis) by administering a therapeutically effective amount of a MMP-12 binding protein (e.g., an inhibitory MMP-12 binding protein, e.g., an anti-MMP-12 IgG or Fab) to a subject having or suspected of having viral encephalitis. Also provided are methods of treating viral encephalitis by administering a therapeutically effective amount of a MMP-12 binding protein with another viral encephalitis treatment (e.g., acyclovir, mechanical ventilation).

Guidance regarding the efficacy and dosage an MMP-12 binding protein which will deliver a therapeutically effective amount of the protein can be obtained from animal models of viral encephalitis, see e.g., those described in Zhou et al. J Virol. 2005: 79(8):4764, and references cited therein.

Stroke

Stroke is the rapidly developing loss of brain functions due to a disturbance in the blood vessels supplying blood to the brain. This can be due to ischemia (lack of blood supply) caused by thrombosis or embolism, or due to a hemorrhage. In an ischemic stroke, blood supply to part of the brain is decreased, leading to dysfunction and necrosis of the brain tissue in that area.

Intracranial hemorrhage is the accumulation of blood anywhere within the skull vault. A distinction is made between intra-axial hemorrhage (blood inside the brain) and extra-axial hemorrhage (blood inside the skull but outside the brain). Intra-axial hemorrhage is due to intraparenchymal hemorrhage or intraventricular hemorrhage (blood in the ventricular system). The main types of extra-axial hemorrhage are epidural hematoma (bleeding between the dura mater and the skull), subdural hematoma (in the subdural space) and subarachnoid hemorrhage (between the arachnoid mater and pia mater). Most of the hemorrhagic stroke syndromes have specific symptoms (e.g. headache, previous head injury).

Stroke symptoms typically develop rapidly (seconds to minutes). The symptoms of a stroke are related to the anatomical location of the damage; nature and severity of the symptoms can therefore vary widely. Ischemic strokes usually only affect regional areas of the brain perfused by the blocked artery. Hemorrhagic strokes can affect local areas, but often can also cause more global symptoms due to bleeding and increased intracranial pressure.

In mice MMP-12 expression following haemorrhagic stroke is deleterious and contributes to the development of secondary injury in this disease (Wells et al. *Eur J Neurosci.* 2005: 21(1):187). Transcript level of MMP-12 in carotid atherosclerotic plaques is correlated with histological features and clinical manifestations, supporting a role of MMP-12 in determining atherosclerotic plaque stability (Morgan et al. *Stroke.* 2001: 32(9):2198).

Treatment for stroke includes pharmacologic thrombolysis ("clot busting") with the drug tissue plasminogen activator, tPA, to dissolve the clot and unblock the artery. Another treatment for acute ischemic stroke is removal of the offending thrombus directly. This is accomplished by inserting a catheter into the femoral artery, directing it into the cerebral circulation, and deploying a corkscrew-like device to ensnare the clot, which is then withdrawn from the body. Anticoagulation can prevent recurrent stroke. Patients with bleeding into (intracerebral hemorrhage) or around the brain (subarachnoid hemorrhage), require neurosurgical evaluation to detect and treat the cause of the bleeding.

The disclosure provides methods of treating or preventing stroke (e.g., ameliorating symptoms or the worsening of stroke) by administering a therapeutically effective amount of a MMP-12 binding protein (e.g., an inhibitory MMP-12 binding protein, e.g., an anti-MMP-12 IgG or Fab) to a subject having or suspected of having stroke. Also provided are methods of treating stroke by administering a therapeutically effective amount of a MMP-12 binding protein with

another stroke treatment (e.g., thrombolysis, plasminogen activator, anticoagulation or surgical procedures).

Guidance regarding the efficacy and dosage an MMP-12 binding protein which will deliver a therapeutically effective amount of the protein can be obtained from animal models of stroke, see e.g., those described in Wells et al. Eur J Neurosci. 2005: 21(1):187), and references cited therein.

Enterocolitis

Enterocolitis (or "coloenteritis") is an inflammation of both the small and large intestine. Enteritis is the inflammation of the small intestine and colitis is inflammation of the large intestine, especially the colon.

Symptoms for enteritis may include abdominal pain, diarrhea, abdominal distension and hematochezia. General signs and symptoms of colitis include pain, tenderness in the abdomen, depression, rapid weight loss, aches and pains within the joints, fatigue, changes in bowel habits (increased frequency), fever; swelling of the colon tissue, erythema (redness) of the surface of the colon, ulcers on the colon (in ulcerative colitis) which can bleed, mucous in the stool, blood in stool and rectal bleeding. Other symptoms may include: diarrhea, gas, bloating, indigestion, heartburn, reflux, Gastro oesophageal reflux disease (GORD), cramps, urgency and many other uncomfortable aches in the gastrointestinal system.

MMP-12 is up-regulated in necrotizing enterocolitis (NEC), suggesting it might be a major factor in tissue destruction and remodeling in NEC (Bista et al. J Pediatr Gastroenterol Nutr. 2005:40(1):60).

Viral diarrhea is usually self-limiting and is treated with rehydration. When bacterial causes are suspected, antibiotics can be considered. Treatment of colitis includes administration of antibiotics and general non-steroidal anti-inflammatory (NSAIDS) medications such as Mesalamine (Asacol®) or its derivatives; Azathioprine or similar immunosuppressants; steroids such as prednisolone and prednisone; drugs that ameliorate inflammation and pain (buscopan).

The disclosure provides methods of treating or preventing enterocolitis (e.g., ameliorating symptoms or the worsening of enterocolitis) by administering a therapeutically effective amount of a MMP-12 binding protein (e.g., an inhibitory MMP-12 binding protein, e.g., an anti-MMP-12 IgG or Fab) to a subject having or suspected of having enterocolitis. Also provided are methods

of treating enterocolitis by administering a therapeutically effective amount of a MMP-12 binding protein with another enterocolitis treatment (e.g., rehydration, antibiotics, NSAIDS, Mesalamine (Asacol®) or its derivatives; Azathioprine or similar immunosuppressants; steroids such as prednisolone and prednisone; drugs that ameliorate inflammation and pain (buscopan)).

Celiac disease

Coeliac disease (CD), or celiac disease, is an autoimmune disorder of the small intestine that occurs in genetically predisposed people of all ages from middle infancy.

Symptoms include chronic diarrhoea, failure to thrive (in children), and fatigue, but these may be absent and symptoms in all other organ systems have been described.

CD is caused by a reaction to gliadin, a gluten protein found in wheat (and similar proteins of the tribe Triticeae which includes other cultivars such as barley and rye). Upon exposure to gliadin, the enzyme tissue transglutaminase modifies the protein, and the immune system cross-reacts with the bowel tissue, causing an inflammatory reaction. That leads to flattening of the lining of the small intestine, which interferes with the absorption of nutrients.

The presence of a peculiar MMP pattern in active CD strongly dominated by MMP-12 correlates either with IFN-gamma or the degree of mucosal damage (Ciccocioppo et al. J Pediatr Gastroenterol Nutr. 2005: 85(3):397).

Treatment for CD is a gluten-free diet.

The disclosure provides methods of treating or preventing CD (e.g., ameliorating symptoms or the worsening of CD) by administering a therapeutically effective amount of a MMP-12 binding protein (e.g., an inhibitory MMP-12 binding protein, e.g., an anti-MMP-12 IgG or Fab) to a subject having or suspected of having CD. Also provided are methods of treating CD by administering a therapeutically effective amount of a MMP-12 binding protein with another CD treatment (e.g., gluten-free diet).

Spinal cord injury

Spinal cord injury (SCI) causes myelopathy or damage to white matter or myelinated fiber tracts that carry sensation and motor signals to and from the brain. It also damages gray matter in the central part of the spinal cord, causing segmental losses of interneurons and motorneurons. Spinal cord injury can occur from many causes, including: trauma, tumor,

ischemia, developmental disorders, neurodegenerative diseases, demyelinating diseases, transverse myelitis, and vascular malformations.

MMP-12 expression after spinal cord trauma is deleterious in mice and contributes to the development of secondary injury in SCI (Wells et al. J Neurosci. 2003: 23(31): 10107).

Treatment for acute traumatic spinal cord injuries includes giving a high dose methylprednisolone if the injury occurred within 8 hours. The recommendation is primarily based on the National Acute Spinal Cord Injury Studies (NASCIS) II and III.

The disclosure provides methods of treating or preventing SCI (e.g., ameliorating symptoms or the worsening of SCI) by administering a therapeutically effective amount of a MMP-12 binding protein (e.g., an inhibitory MMP-12 binding protein, e.g., an anti-MMP-12 IgG or Fab) to a subject having or suspected of having SCI. Also provided are methods of treating SCI by administering a therapeutically effective amount of a MMP-12 binding protein with another SCI treatment (e.g., methylprednisolone).

Guidance regarding the efficacy and dosage of an MMP-12 binding protein which will deliver a therapeutically effective amount of the protein can be obtained from animal models of SCI, see e.g., those described in Wells et al. J Neurosci. 2003: 23(31): 10107), and references cited therein.

Acute lung injury in hyperoxia

Acute lung injury could be a side effect of therapy with a high concentration of inspired oxygen in patients.

Overexpression of Stat3C, a constitutive active form of STAT3, in respiratory epithelial cells of a doxycycline-controlled double-transgenic mouse system protects lung from inflammation and injury caused by hyperoxia. This protection is mediated at least partially through inhibition of hyperoxia-induced synthesis and release of MMP-12 by neutrophils and alveolar resident cells (Lian et al. J Immunol. 2005: 174(11):7250).

The disclosure provides methods of treating or preventing acute lung injury in hyperoxia (e.g., ameliorating symptoms or the worsening of acute lung injury in hyperoxia) by administering a therapeutically effective amount of a MMP-12 binding protein (e.g., an inhibitory MMP-12 binding protein, e.g., an anti-MMP-12 IgG or Fab) to a subject having or suspected of having acute lung injury in hyperoxia. Also provided are methods of treating acute

lung injury in hyperoxia by administering a therapeutically effective amount of a MMP-12 binding protein with another acute lung injury in hyperoxia treatment.

Guidance regarding the efficacy and dosage an MMP-12 binding protein which will deliver a therapeutically effective amount of the protein can be obtained from animal models of acute lung injury in hyperoxia, see e.g., those described in Lian et al. J Immunol. 2005: 174(11):7250, and references cited therein.

Pulmonary inflammatory diseases

Studies using animal models of acute and chronic pulmonary inflammatory diseases have given evidences that MMP-12 is an important mediator of the pathogenesis of these diseases. MMP inhibitor, marimastat could reverse some of these inflammatory events (Menan et al. Mem Inst Oswaldo Cruz. 2005: 100:167). MMP-12 also plays an important proinflammatory role in the development of allergic inflammation in a mouse model of allergic airway inflammation induced by cockroach antigen (CRA) (Warner et al. Am J Pathol. 2004:165(6):1921).

The disclosure provides methods of treating or preventing pulmonary inflammatory diseases (e.g., ameliorating symptoms or the worsening of pulmonary inflammatory diseases) by administering a therapeutically effective amount of a MMP-12 binding protein (e.g., an inhibitory MMP-12 binding protein, e.g., an anti-MMP-12 IgG or Fab) to a subject having or suspected of having pulmonary inflammatory diseases. Also provided are methods of treating pulmonary inflammatory diseases by administering a therapeutically effective amount of a MMP-12 binding protein with another pulmonary inflammatory diseases treatment (e.g. antibiotics).

Guidance regarding the efficacy and dosage an MMP-12 binding protein which will deliver a therapeutically effective amount of the protein can be obtained from animal models of pulmonary inflammatory diseases, see e.g., those described in Warner et al. Am J Pathol. 2004:165(6):1921, and references cited therein.

Combination Therapies

The MMP-12 binding proteins described herein, e.g., anti-MMP-12 Fabs or IgGs, can be administered in combination with one or more of the other therapies for treating a disease or condition associated with MMP-12 activity, e.g., a disease or condition described herein. For

example, an MMP-12 binding protein can be used therapeutically or prophylactically with surgery, another MMP-12 inhibitor, e.g., a small molecule inhibitor, another anti-MMP-12 Fab or IgG (e.g., another Fab or IgG described herein), peptide inhibitor, or small molecule inhibitor. Examples of MMP-12 inhibitors that can be used in combination therapy with an MMP-12 binding protein are described herein.

One or more small-molecule MMP inhibitors can be used in combination with one or more MMP-12 binding proteins described herein. For example, the combination can result in a lower dose of the small-molecule inhibitor being needed, such that side effects are reduced.

The MMP-12 binding proteins described herein can be administered in combination with one or more of the other therapies for treating cancers, including, but not limited to: surgery; radiation therapy, and chemotherapy. For example, proteins that inhibit MMP-12 or that inhibit a downstream event of MMP-12 activity can also be used in combination with other anti-cancer therapies, such as radiation therapy, chemotherapy, surgery, or administration of a second agent. For example, the second agent can be a Tie-1 inhibitor (e.g., Tie-1 binding proteins; see e.g., U.S. Ser. No. 11/199,739 and PCT/US2005/0284, both filed August 9, 2005). As another example, the second agent can be one that targets or negatively regulates the VEGF signaling pathway. Examples of this latter class include VEGF antagonists (e.g., anti-VEGF antibodies such as bevacizumab) and VEGF receptor antagonists (e.g., anti-VEGF receptor antibodies). One particularly preferred combination includes bevacizumab. As a further example, the second agent is an inhibitor of plasmin, such as a kunitz domain-containing protein or polypeptide (e.g., a plasmin-inhibiting kunitz domain disclosed in U.S. Patent No. 6,010,880, such as a protein or polypeptide comprising the amino acid sequence MHSFCAFK AETGPCRARFDRWFFNIFTRQCEEFIYGGCEGNQNR FESLEECKKMCTRD (SEQ ID NO:1)). As another example, the second agent is an agent that binds to Her2, such as a Her2-binding antibody (e.g., trastuzumab). The combination can further include 5-FU and leucovorin, and/or irinotecan.

Inhibitors of MMP-12 (e.g., the MMP-12 binding proteins disclosed herein) can potentiate the activity of an agent that targets Her2 (e.g., a Her2-binding antibody such as trastuzumab). Accordingly, in one combination therapy for the treatment of breast cancer, the second therapy is an agent that binds Her2, such as a Her2-binding antibody (e.g., trastuzumab). When an MMP-12 binding protein is used in a combination therapy with a Her2 binding agent, the dose of the

Her2 binding agent may be reduced from the dose of the Her2 binding agent when administered not in combination with an MMP-12 binding protein (e.g., is at least 10%, 25%, 40%, or 50% less than the dose of the Her2 binding agent when administered not in combination with a MMP-12 binding protein). For example, the dose of trastuzumab, when administered in a combination therapy with an MMP-12 binding protein is less than about 4.0, 3.6, 3.0, 2.4, or 2 mg/kg as an initial (loading) dose, and less than about 2.0, 1.8, 1.5, 1.2, or 1 mg/kg in subsequent doses.

The MMP-12 binding proteins described herein can also be administered in combination with one or more other therapies for treating ocular disorders, such as surgical or medical (e.g., administration of a second agent) therapies. For example, in treatment of age-related macular degeneration (e.g., wet age-related macular degeneration), an MMP-12 binding protein may be administered in conjunction with (e.g., before, during, or after) laser surgery (laser photocoagulation or photocoagulation therapy). As another example, the MMP-12 binding protein can be administered in combination with a second agent, such as a VEGF antagonist (e.g., an anti-VEGF antibody such as bevacizumab or ranibizumab) or a VEGF receptor antagonist (e.g., anti-VEGF receptor antibodies).

Other combinations are described above.

The term “combination” refers to the use of the two or more agents or therapies to treat the same patient, wherein the use or action of the agents or therapies overlap in time. The agents or therapies can be administered at the same time (e.g., as a single formulation that is administered to a patient or as two separate formulations administered concurrently) or sequentially in any order. Sequential administrations are administrations that are given at different times. The time between administration of the one agent and another agent can be minutes, hours, days, or weeks. The use of an MMP-12 binding protein described herein can also be used to reduce the dosage of another therapy, e.g., to reduce the side-effects associated with another agent that is being administered, e.g., to reduce the side-effects of an anti-VEGF antibody such as bevacizumab. Accordingly, a combination can include administering a second agent at a dosage at least 10, 20, 30, or 50% lower than would be used in the absence of the MMP-12 binding protein.

In addition, a subject can be treated for an angiogenesis-associated disorder, e.g., a cancer, by administering to the subject a first and second agent. For example, the first agent modulates early stage angiogenesis and the second agent modulates a subsequent stage of

angiogenesis or also modulates early stage angiogenesis. The first and second agents can be administered using a single pharmaceutical composition or can be administered separately. In one embodiment, the first agent is a VEGF pathway antagonist (e.g., an inhibitor of a VEGF (e.g., VEGF-A, -B, or -C) or a VEGF receptor (e.g., KDR or VEGF receptor III (Flt4)) or a bFGF pathway antagonist (e.g., an antibody that binds to bFGF or a bFGF receptor). Other VEGF pathway antagonists are also described, herein and elsewhere. In one embodiment, the second agent inhibits or decreases the mobility or invasiveness of tumor cells. For example, the second agent comprises an MMP-12 binding protein. For example, the second agent is an MMP-12 binding protein described herein.

Once a tumor reaches a certain size (e.g., ~ 1-2 mm), the tumor requires new vasculature prior to increasing its mass. An early stage of tumor angiogenesis can include a signal from the tumor, e.g., secretion of VEGF, to stimulate the growth of new blood vessels from the host and infiltration of the tumor by the vessels. VEGF can, for example, stimulate proliferation of endothelial cells that are then assembled into blood vessels. A late stage of tumor growth can include metastasis, mobility and invasiveness of tumor cells. This mobility and invasiveness may involve the action of matrix metalloproteinases, e.g., MMP-12. Thus, an effective therapy to treat angiogenesis-related disorders can involve a combination of an agent that modulates an early stage angiogenesis (e.g., VEGF pathway antagonists, e.g., anti-VEGF (e.g., bevacizumab) or anti-VEGF receptor (e.g., anti-KDR) antibodies; or antagonists of other pro-angiogenic pathways, e.g., anti-bFGF antibodies or anti-bFGF receptor (e.g., anti-bFGF receptor-1, -2, -3) antibodies) and an agent that modulates a late stage of tumor growth can include metastasis, mobility and invasiveness of tumor cells (e.g., antagonists of MMP-12 (e.g., anti-MMP-12 antibodies (e.g., an antibody disclosed herein)). One or more of these agents can be used in combination. One or more of these agents may also be used in combination with other anti-cancer therapies, such as radiation therapy or chemotherapy.

Exemplary VEGF receptor antagonists include inhibitors of a VEGF (e.g., VEGF-A, -B, or -C, for example bevacizumab), modulators of VEGF expression (e.g., INGN-241, oral tetrathiomolybdate, 2-methoxyestradiol, 2-methoxyestradiol nanocrystal dispersion, bevasiranib sodium, PTC-299, Veglin), inhibitors of a VEGF receptor (e.g., KDR or VEGF receptor III (Flt4), for example anti-KDR antibodies, VEGFR2 antibodies such as CDP-791, IMC-1121B, VEGFR2 blockers such as CT-322), VEGFR3 antibodies such as mF4-31C1 from Imclone

Systems, modulators of VEGFR expression (*e.g.*, VEGFR1 expression modulator Sirna-027) or inhibitors of VEGF receptor downstream signaling.

Exemplary inhibitors of VEGF include bevacizumab, pegaptanib, ranibizumab, NEOVASTAT[®], AE-941, VEGF Trap, and PI-88.

Exemplary VEGF receptor antagonists include inhibitors of VEGF receptor tyrosine kinase activity. 4-[4-(1-Amino-1-methylethyl)phenyl]-2-[4-(2-morpholin-4-yl-ethyl)phenylamino]pyrimidine-5-carbonitrile (JNJ-17029259) is one of a structural class of 5-cyanopyrimidines that are orally available, selective, nanomolar inhibitors of the vascular endothelial growth factor receptor-2 (VEGF-R2). Additional examples include: PTK-787/ZK222584 (Astra-Zeneca), SU5416, SU11248 (Pfizer), and ZD6474 ([N-(4-bromo-2-fluorophenyl)-6-methoxy-7-[(1-methylpiperidin-4-yl)methoxy]quinazolin-4-amine]), vandetanib, cediranib, AG-013958, CP-547632, E-7080, XL-184, L-21649, and ZK-304709. Other VEGF antagonist agents are broad specificity tyrosine kinase inhibitors, *e.g.*, SU6668 (see, *e.g.*, Bergers, B. et al., 2003 J. Clin. Invest. 111:1287-95), sorafenib, sunitinib, pazopanib, vatalanib, AEE-788, AMG-706, axitinib, BIBF-1120, SU-14813, XL-647, XL-999, ABT-869, BAY-57-9352, BAY-73-4506, BMS-582664, CEP-7055, CHIR-265, OSI-930, and TKI-258. Also useful are agents that down regulate VEGF receptors on the cell surface, such as fenretinide, and agents which inhibit VEGF receptor downstream signaling, such as squalamine

The second agent or therapy can also be another anti-cancer agent or therapy. Non-limiting examples of anti-cancer agents include, *e.g.*, anti-microtubule agents, topoisomerase inhibitors, antimetabolites, mitotic inhibitors, alkylating agents, intercalating agents, agents capable of interfering with a signal transduction pathway, agents that promote apoptosis, radiation, and antibodies against other tumor-associated antigens (including naked antibodies, immunotoxins and radioconjugates). Examples of the particular classes of anti-cancer agents are provided in detail as follows: antitubulin/antimicrotubule, *e.g.*, paclitaxel, vincristine, vinblastine, vindesine, vinorelbin, taxotere; topoisomerase I inhibitors, *e.g.*, irinotecan, topotecan, camptothecin, doxorubicin, etoposide, mitoxantrone, daunorubicin, idarubicin, teniposide, amsacrine, epirubicin, merbarone, piroxantrone hydrochloride; antimetabolites, *e.g.*, 5 fluorouracil (5 FU), methotrexate, 6 mercaptopurine, 6 thioguanine, fludarabine phosphate, cytarabine/Ara C, trimetrexate, gemcitabine, acivicin, alanosine, pyrazofurin, N-Phosphoracetyl-

L-Asparate=PALA, pentostatin, 5 azacitidine, 5 Aza 2' deoxycytidine, ara A, cladribine, 5 fluorouridine, FUDR, tiazofurin, N-[5-[N-(3,4-dihydro-2-methyl-4-oxoquinazolin-6-ylmethyl)-N-methylamino]-2-thenoyl]-L-glutamic acid; alkylating agents, e.g., cisplatin, carboplatin, mitomycin C, BCNU=Carmustine, melphalan, thiotepa, busulfan, chlorambucil, plicamycin, dacarbazine, ifosfamide phosphate, cyclophosphamide, nitrogen mustard, uracil mustard, pipobroman, 4 ipomeanol; agents acting via other mechanisms of action, e.g., dihydrolenperone, spiromustine, and desipeptide; biological response modifiers, e.g., to enhance anti-tumor responses, such as interferon; apoptotic agents, such as actinomycin D; and anti-hormones, for example anti-estrogens such as tamoxifen or, for example antiandrogens such as 4'-cyano-3-(4-fluorophenylsulphonyl)-2-hydroxy-2-methyl-3'-(trifluoromethyl) propionanilide.

A combination therapy can include administering an agent that reduces the side effects of other therapies. The agent can be an agent that reduces the side effects of anti-cancer treatments. For example, the agent can be leucovorin.

Combination therapies that include administering an MMP-12 binding protein or other binding protein described herein can also be used to treat a subject having or at risk for another angiogenesis related disorder (e.g., a disorder other than cancer, e.g., disorders that include undesired endothelial cell proliferation or undesirable inflammation, e.g., rheumatoid arthritis).

Diagnostic Uses

Proteins that bind to MMP-12 and identified by the method described herein and/or detailed herein have *in vitro* and *in vivo* diagnostic utilities. The MMP-12 binding proteins described herein (e.g., the proteins that bind and inhibit, or the proteins that bind but do not inhibit MMP-12) can be used, e.g., for *in vivo* imaging, e.g., during a course of treatment for a disease or condition in which MMP-12 is active, e.g., a disease or condition described herein, or in diagnosing a disease or condition described herein.

In one aspect, the disclosure provides a diagnostic method for detecting the presence of an MMP-12, *in vitro* or *in vivo* (e.g., *in vivo* imaging in a subject). The method can include localizing MMP-12 within a subject or within a sample from a subject. With respect to sample evaluation, the method can include, for example: (i) contacting a sample with MMP-12 binding protein; and (ii) detecting location of the MMP-12 binding protein in the sample.

An MMP-12 binding protein can also be used to determine the qualitative or quantitative level of expression of MMP-12 in a sample. The method can also include contacting a reference sample (e.g., a control sample) with the binding protein, and determining a corresponding assessment of the reference sample. A change, e.g., a statistically significant change, in the formation of the complex in the sample or subject relative to the control sample or subject can be indicative of the presence of MMP-12 in the sample. In one embodiment, the MMP-12 binding protein does not cross react with another metalloproteinase.

The MMP-12 binding proteins are also useful for *in vivo* tumor imaging. Better clinical endpoints are needed to monitor the efficacy of drugs, such as MMP-inhibitors, that are designed to block enzymatic function (Zucker et al, 2001, Nature Medicine 7:655- 656). Imaging of tumors *in vivo* by using labeled MMP-12 binding proteins could be of help to target the delivery of the binding protein to tumors for cancer diagnosis, intraoperative tumor detection, and for investigations of drug delivery and tumor physiology. MMP-12 binding proteins can be used to monitor native enzymatic activity *in vivo* at invasive sites. Another exemplary method includes: (i) administering the MMP-12 binding protein to a subject; and (iii) detecting location of the MMP-12 binding protein in the subject. The detecting can include determining location or time of formation of the complex.

The MMP-12 binding protein can be directly or indirectly labeled with a detectable substance to facilitate detection of the bound or unbound antibody. Suitable detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials and radioactive materials.

Complex formation between the MMP-12 binding protein and MMP-12 can be detected by evaluating the binding protein bound to the MMP-12 or unbound binding protein. Conventional detection assays can be used, e.g., an enzyme-linked immunosorbent assays (ELISA), a radioimmunoassay (RIA) or tissue immunohistochemistry. Further to labeling the MMP-12 binding protein, the presence of MMP-12 can be assayed in a sample by a competition immunoassay utilizing standards labeled with a detectable substance and an unlabeled MMP-12 binding protein. In one example of this assay, the biological sample, the labeled standards, and the MMP-12 binding protein are combined and the amount of labeled standard bound to the unlabeled binding protein is determined. The amount of MMP-12 in the sample is inversely proportional to the amount of labeled standard bound to the MMP-12 binding protein.

Fluorophore and chromophore labeled proteins can be prepared. Because antibodies and other proteins absorb light having wavelengths up to about 310 nm, the fluorescent moieties should be selected to have substantial absorption at wavelengths above 310 nm and preferably above 400 nm. A variety of suitable fluorescers and chromophores are described by Stryer, 1968, *Science* 162:526 and Brand, L. et al., 1972, *Annu. Rev. Biochem.* 41:843-868. The proteins can be labeled with fluorescent chromophore groups by conventional procedures such as those disclosed in U.S. Patent Nos. 3,940,475, 4,289,747, and 4,376,110. One group of fluorescers having a number of the desirable properties described above is the xanthene dyes, which include the fluoresceins and rhodamines. Another group of fluorescent compounds are the naphthylamines. Once labeled with a fluorophore or chromophore, the protein can be used to detect the presence or localization of the MMP-12 in a sample, e.g., using fluorescent microscopy (such as confocal or deconvolution microscopy).

Histological Analysis. Immunohistochemistry can be performed using the proteins described herein. For example, in the case of an antibody, the antibody can be synthesized with a label (such as a purification or epitope tag), or can be detectably labeled, e.g., by conjugating a label or label-binding group. For example, a chelator can be attached to the antibody. The antibody is then contacted to a histological preparation, e.g., a fixed section of tissue that is on a microscope slide. After an incubation for binding, the preparation is washed to remove unbound antibody. The preparation is then analyzed, e.g., using microscopy, to identify if the antibody bound to the preparation.

Of course, the antibody (or other polypeptide or peptide) can be unlabeled at the time of binding. After binding and washing, the antibody is labeled in order to render it detectable.

Protein Arrays. The MMP-12 binding protein can also be immobilized on a protein array. The protein array can be used as a diagnostic tool, e.g., to screen medical samples (such as isolated cells, blood, sera, biopsies, and the like). Of course, the protein array can also include other binding proteins, e.g., that bind to MMP-12 or to other target molecules.

Methods of producing polypeptide arrays are described, e.g., in De Wildt et al., 2000, *Nat. Biotechnol.* 18:989-994; Lueking et al., 1999, *Anal. Biochem.* 270:103-111; Ge, 2000, *Nucleic Acids Res.* 28, e3, I-VII; MacBeath and Schreiber, 2000, *Science* 289:1760-1763; WO 01/40803 and WO 99/51773A1. Polypeptides for the array can be spotted at high speed, e.g., using commercially available robotic apparatus, e.g., from Genetic Microsystems or BioRobotics.

The array substrate can be, for example, nitrocellulose, plastic, glass, e.g., surface-modified glass. The array can also include a porous matrix, e.g., acrylamide, agarose, or another polymer.

For example, the array can be an array of antibodies, e.g., as described in De Wildt, *supra*. Cells that produce the proteins can be grown on a filter in an arrayed format. Polypeptide production is induced, and the expressed polypeptides are immobilized to the filter at the location of the cell. A protein array can be contacted with a labeled target to determine the extent of binding of the target to each immobilized polypeptide. Information about the extent of binding at each address of the array can be stored as a profile, e.g., in a computer database. The protein array can be produced in replicates and used to compare binding profiles, e.g., of a target and a non-target.

FACS (Fluorescence Activated Cell Sorting). The MMP-12 binding protein can be used to label cells, e.g., cells in a sample (e.g., a patient sample). The binding protein is also attached (or attachable) to a fluorescent compound. The cells can then be sorted using fluorescence activated cell sorter (e.g., using a sorter available from Becton Dickinson Immunocytometry Systems, San Jose CA; see also U.S. Patent Nos. 5,627,037; 5,030,002; and 5,137,809). As cells pass through the sorter, a laser beam excites the fluorescent compound while a detector counts cells that pass through and determines whether a fluorescent compound is attached to the cell by detecting fluorescence. The amount of label bound to each cell can be quantified and analyzed to characterize the sample.

The sorter can also deflect the cell and separate cells bound by the binding protein from those cells not bound by the binding protein. The separated cells can be cultured and/or characterized.

***In Vivo* Imaging.** Also featured is a method for detecting the presence of a MMP-12 expressing tissues *in vivo*. The method includes (i) administering to a subject (e.g., a patient having, e.g., a cancer (e.g., metastatic cancer, e.g., metastatic breast cancer), an inflammatory disease (e.g., chronic obstructive pulmonary disease (COPD), asthma, rhinitis (e.g., allergic rhinitis), inflammatory bowel disease, synovitis, rheumatoid arthritis), heart failure, septic shock, neuropathic pain, osteoarthritis, or an ocular condition (e.g., macular degeneration)) an anti-MMP-12 antibody, conjugated to a detectable marker; (ii) exposing the subject to a means for detecting said detectable marker to the MMP-12 expressing tissues or cells. For example, the subject is imaged, e.g., by NMR or other tomographic means.

Examples of labels useful for diagnostic imaging include radiolabels such as ^{131}I , ^{111}In , ^{123}I , $^{99\text{m}}\text{Tc}$, ^{32}P , ^{125}I , ^3H , ^{14}C , and ^{188}Rh , fluorescent labels such as fluorescein and rhodamine, nuclear magnetic resonance active labels, positron emitting isotopes detectable by a positron emission tomography (“PET”) scanner, chemiluminescers such as luciferin, and enzymatic markers such as peroxidase or phosphatase. Short range radiation emitters, such as isotopes detectable by short range detector probes can also be employed. The protein can be labeled with such reagents; for example, see Wensel and Meares, 1983, *Radioimmunoimaging and Radioimmunotherapy*, Elsevier, New York for techniques relating to the radiolabeling of antibodies and D. Colcher et al., 1986, *Meth. Enzymol.* 121: 802 816.

The binding protein can be labeled with a radioactive isotope (such as ^{14}C , ^3H , ^{35}S , ^{125}I , ^{32}P , ^{131}I). A radiolabeled binding protein can be used for diagnostic tests, e.g., an in vitro assay. The specific activity of a isotopically-labeled binding protein depends upon the half life, the isotopic purity of the radioactive label, and how the label is incorporated into the antibody.

In the case of a radiolabeled binding protein, the binding protein is administered to the patient, is localized to cells bearing the antigen with which the binding protein reacts, and is detected or “imaged” in vivo using known techniques such as radionuclear scanning using e.g., a gamma camera or emission tomography. See e.g., A.R. Bradwell et al., “Developments in Antibody Imaging”, *Monoclonal Antibodies for Cancer Detection and Therapy*, R.W. Baldwin et al., (eds.), pp 65 85 (Academic Press 1985). Alternatively, a positron emission transaxial tomography scanner, such as designated Pet VI located at Brookhaven National Laboratory, can be used where the radiolabel emits positrons (e.g., ^{11}C , ^{18}F , ^{15}O , and ^{13}N).

MRI Contrast Agents. Magnetic Resonance Imaging (MRI) uses NMR to visualize internal features of living subject, and is useful for prognosis, diagnosis, treatment, and surgery. MRI can be used without radioactive tracer compounds for obvious benefit. Some MRI techniques are summarized in EP-A-0 502 814. Generally, the differences related to relaxation time constants T1 and T2 of water protons in different environments is used to generate an image. However, these differences can be insufficient to provide sharp high resolution images.

The differences in these relaxation time constants can be enhanced by contrast agents. Examples of such contrast agents include a number of magnetic agents paramagnetic agents (which primarily alter T1) and ferromagnetic or superparamagnetic (which primarily alter T2 response). Chelates (e.g., EDTA, DTPA and NTA chelates) can be used to attach (and reduce

toxicity) of some paramagnetic substances (e.g., Fe^{+3} , Mn^{+2} , Gd^{+3}). Other agents can be in the form of particles, e.g., less than 10 μm to about 10 nm in diameter). Particles can have ferromagnetic, antiferromagnetic, or superparamagnetic properties. Particles can include, e.g., magnetite (Fe_3O_4), $\gamma\text{-Fe}_2\text{O}_3$, ferrites, and other magnetic mineral compounds of transition elements. Magnetic particles may include: one or more magnetic crystals with and without nonmagnetic material. The nonmagnetic material can include synthetic or natural polymers (such as sepharose, dextran, dextrin, starch and the like).

The MMP-12 binding protein can also be labeled with an indicating group containing of the NMR active ^{19}F atom, or a plurality of such atoms inasmuch as (i) substantially all of naturally abundant fluorine atoms are the ^{19}F isotope and, thus, substantially all fluorine containing compounds are NMR active; (ii) many chemically active polyfluorinated compounds such as trifluoroacetic anhydride are commercially available at relatively low cost; and (iii) many fluorinated compounds have been found medically acceptable for use in humans such as the perfluorinated polyethers utilized to carry oxygen as hemoglobin replacements. After permitting such time for incubation, a whole body MRI is carried out using an apparatus such as one of those described by Pykett, 1982, *Sci. Am.* 246:78 88 to locate and image tissues expressing MMP-12.

The contents of all references, pending patent applications and published patents, cited throughout this application are hereby expressly incorporated by reference. The following examples provide further illustrate and are not limiting.

EXAMPLES

Example 1: Selection and Screening of Anti-MMP-12 Fabs and IgGs

Selection strategies employed to identify anti-MMP-12 antibodies are:

- (1) Selection with capture of a biotinylated form of MMP-12 catalytic domain on a streptavidin coated surface;
- (2) Selection with capture of a biotinylated form of proMMP-12 (APMA-activated) on a streptavidin coated surface;
- (3) Phage, suitably depleted (e.g., previous contact with streptavidin) were allowed to interact with the target, unbound phage washed away and the output sampled and/or

amplified for the next round of selection. This was repeated until the output phage in ELISA analysis indicate a high percentage of binders. The phage clones were converted into sFabs. 88/518 unique sFab were identified by ELISA and sequencing (campaign A) and 168 by sequencing (campaign B). Their ability to inhibit human MMP-12, murine MMP-12 and other MMPs (1, 2, 3, 7, 8, 9, 10, 13, 14, 16, 17 and 24) was determined by usual means. The sFabs were converted to IgG1s.

Table I:

	<u>Unique</u> <u>Positive hits</u>	<u>Inhibitors</u>	<u>IC50 (nM)</u>	<u>Specificity/</u> <u>Crossreactivity</u>
MMP12 Campaign A	88	12 (14 %)	6<sFab<90	100%
MMP12 Campaign B	168	7 (4%)	10<sFab<150	100% m/hu

Campaign A:Table II. hMMP-12 inhibition Screen: IC₅₀ Values:

Antibody name	IC₅₀ (nM)	
	Large scale purified Fabs	IgGs
539A-M0013-D11	20.3	13.3
539A-M0013-G12	6.7	4.1
539A-M0013-H06	11.9	5.3
539A-M0014-C09	36.9	43.3
539A-M0014-G11	35.0	12.3
539A-M0016-A11	8.8	2.1
539A-M0016-H05	56.6	32.9
539A-M0019-C05	93.0	24.5
539A-M0020-B01	74.8	34.6
539A-M0022-C07	24.2	13.2
539A-M0027-E11	23.9	23.7

There was no crossreactivity to mouse MMP12.

Table III: Ki values of four of the Campaign A MMP-12 binding proteins that act as inhibitors:

	IC50 values	Ki (nM)
539A-M0016-A11	2.1	0.7+/- 0.1
539A-M0013-D11	13.3	4.97 +/- 1.4
539A-M0013-G12	4.1	2.05+/- 1.4
539A-M0013-H06	5.3	2.7 +/- 1.6

The Campaign A MMP-12 binding proteins were crossreacted against other human proteases. The results are provided in Table IV.

Table IV:

<u>Anti MMP-12 IgG</u>	<u>MMP-9</u>	<u>MMP-14</u>	<u>hTACE</u>
539A-M0013-D11	no	no	No
539A-M0013-G12	no	no	No
539A-M0013-H06	no	no	No
539A-M0014-C09	no	no	No
539A-M0014-G11	no	no	no
539A-M0016-A11	no	no	no
539A-M0016-H05	no	no	no
539A-M0019-C05	no	no	no
539A-M0020-B01	no	no	no
539A-M0022-C07	no	no	no
539A-M0025-D04	no	no	no
539A-M0027-E11	no	no	no

Cross-reactivity of some of the campaign A MMP-12 binding proteins was assessed against other human proteases. The results are provided below.

Table V:

	<u>539A- M0016-A11</u>	<u>539A- M0013-D11</u>	<u>539A- M0013-G12</u>	<u>539A- M0013-H06</u>
MMP-1	no	no	no	no
MMP-2	no	no	no	no
MMP-3	no	no	no	no
MMP-7	no	no	no	no
MMP-8	no	no	no	no
MMP-10	no	no	no	no
MMP-13	no	no	no	no
MMP-16	no	no	no	no
MMP-17	no	no	no	no
MMP-24	no	no	no	no

Campaign B:

Three selection strategies were used. When the phage outputs in ELISA analysis indicate a high percentage of binders, the phage outputs were converted to sFabs. A high through-put sequencing campaign was done instead of high through-put ELISA and unique sFabs were recovered:

1. Three rounds on mouse MMP12: HT sequencing : 153 unique clones
2. Alternation (human-mouse MMP12): HT sequencing : 120 unique clones
3. Alternation (5 human peptides-mouse MMP12): not pursued

13 inhibitors of mouse MMP-12 were identified including 1 that is cross reactive with human MMP-12.

The following peptides were designed:

Table VI:

<u>Peptide</u>	<u>Size</u>	<u>location</u>
GDAHFDEDEFWT	12AA	13AA upstream the Zn binding site
GTNLFLTA VHEIGHSLGL	18AA	Overlap with Zn binding site
HEIGHSLGLGHS	12AA	Zn binding <u>motif</u>
TYRINNYTPDMNREDVDY	18AA	N'term part of the catalytic domain
TFRLSADDIRGIQSLYG	17AA	17AA downstream the Zn binding <u>motif</u>

BIOTIN - CG XXXXXXXXXXXXXXXXXXXXX - COOH

Several MMP-12 non-inhibitor antibodies were identified for Campaign B. These antibodies are described in FIGURE 1.

In addition, several MMP-12 antibody inhibitors of huMMP12 were identified (100 nM):

Table VII:

<u>REARRAY PLATE</u> <u>NAME & WELL #</u>	<u>MASTER PLATE NAME</u> <u>& WELL #</u>	<u>% of activity left</u> with 100 nM in assay <u>04/10/06</u>	<u>% of activity left</u> with 100 nM in assay <u>29/08/06</u>
539B-R0060-A06	539B-M0031-A06	126,3	ND
539B-R0060-C04	539B-M0034-C04	38,6	39,1
539B-R0060-G03	539B-M0039-F01	69,4	57,8
539B-R0061-A09	539B-M0041-B05	35,1	ND
539B-R0061-B04	539B-M0041-G01	108,6	84,8
539B-R0061-B07	539B-M0042-B06	53,6	ND

539B-R0062-A02	539B-M0006-B10	68,9	65,5
539B-R0062-B08	539B-M0007-H06	55,5	55,0
539B-R0062-C10	539B-M0008-H09	4,6	30,0
539B-R0062-D07	539B-M0009-H08	102,7	ND
539B-R0062-E11	539B-M0011-H11	12,2	ND
539B-R0062-F10	539B-M0015-F02	84,1	ND
539B-R0062-F11	539B-M0016-D01	48,1	ND

As shown in FIGURE 2, 539B-M0008-H09 is cross reactive with human MMP-12 and murine MMP-12. 539B-M0008-H09 showed a linear relationship between IC_{50} and concentration (μ M) for both human MMP-12 and murine MMP-12, see FIGURE 3. The K_i of 539B-M0008-H09 for human MMP-12 is 2.8 ± 0.8 nM and the K_m is 16 ± 6 μ M. The K_i of 539B-M0008-H09 for murine MMP-12 is 2.2 ± 0.6 nM and the K_m is 42 ± 17 μ M.

In addition, 539B-M0011-H11 was found to be an inhibitor of murine MMP-12 but not human MMP-12. This is shown in FIGURE 4.

The cross reactivity of several MMP-12 binding proteins from Campaign B was assessed for cross reactivity with other MMPs.

Table VIII:

	<u>M0016-A11 IgG</u> <u>a-huMMP12</u>	<u>M0013-G12 IgG</u> <u>a-huMMP12</u>	<u>M08H09 IgG, 400nM</u> <u>crossreactive</u>
MMP-1	N	N	N
MMP-2	N	N	N
MMP-3	N	N	N
MMP-7	N	N	N
MMP-8	N	N	N
MMP-9 (m/hu)	N	N	N
MMP-10	N	N	N
MMP-12	Y*	Y*	Y*

MMP-13	N	N	N
MMP-14	N	N	N
MMP-15	N	N	N
MMP-16	N	N	N
MMP-17	N	N	N
MMP-24	N	N	N

As shown in FIGURE 5, using ELIA competition binding assays, it was shown that M08H09 cross reacts with human and murine MMP-12, M0013-G12 and M0016-A11 inhibit human MMP-12 and R0062-E11 inhibits murine MMP-12.

Example 2: Evaluation of M08-H09 on Inflammation

The purpose of the following experiments was to determine the effect of 539B-M008-H09 (M08-H09) on inflammation and specifically on inflammatory cell infiltration into the carrageenan-stimulated mouse air pouch and on the OVA-challenged mouse model.

For the OVA-challenged mouse model, the mice were sensitized by IP administration of OVA/Alum on day 0 and day 7. Six hours prior to OVA challenge, M08-H09 was administered IP to the mice. The mice were challenged by pulmonary administration of OVA. On day 26, metacholine induction and airway hyperresponsiveness was measured. Six different groups were tested. Group 1 was a control group that received PBS. Groups 2, 3, 4 and 5 were administered M08-H09 at doses of 1 mg/kg, 5 mg/kg, 10 mg/kg and 25 mg/kg. Group 6 was administered 25 mg/kg of M11-H11.

The OVA challenged mice were assessed for BAL inflammation based upon differential cell counts, lung histology by quantifying global inflammation, measurement of airway responsiveness to metacholine challenge, IL-4, IL-5 and IL-13 ELISA measurement of BAL or protein lung extracts, serum specific IgE measurement, lung histology using congo red staining to determine eosinophil counts around bronchi and measurement of MMP-12 activity in the lungs using a fluorogenic substrate.

As shown in FIGURE 6, M08-H09 at all doses resulted in a decrease in the peribronchial inflammation score. A significant decrease was seen at 10 mg/kg and 25 mg/kg doses of M08-H09.

As shown in FIGURE 7, the differential cell counts showed that M08-H09 results in eosinophil percentages that are decreased.

For the carrageenan-stimulated mouse air pouch model, subcutaneous injection of air into the hind flank or back of mice produces an air pouch in a week, the interior surface of which contains both fibroblast-like and macrophage-like cells. Inflammatory stimulation of the pouch results in leukocyte recruitment to the pouch and release of mediators (cytokines) into the exudate. Preventing inflammatory cell infiltration into the air pouch may translate into preventing inflammation of the synovium in rheumatoid arthritis.

The effect of M08-H09 on inflammatory cell infiltration was compared to inflammatory cell infiltration indomethacin and a control (PBS). In addition, inflammatory cell recruitment was compared to an unstimulated mouse. As shown in FIGURE 8, M08-H09 significantly decreased total white blood cell infiltration and specifically neutrophil and lymphocyte infiltration.

Example 3: Affinity Matured Variants of M08-H09

Table IX summarizes cycle 1 of the affinity maturation of M08-H09.

Table IX:

Initial Name	Selection method	HV-CDR1	HV-CDR2	N-Gly	Inhibition assays (sFAB)		BIAcore (coated Fab)	
					IC50hu (nM)	IC50m	KD hu	koff m (1/s)
539B-M0008-H09		DYNMH	YIGPSGGYTHYADSVKG	1	12.1+2.5	<10	1.77E-08	4.00E-03
539B-M0063-B01	straight human	WYWMG	SISPSGGYTFYADSVKG	1	0.7+0.1	>10	1.71E-10	2.50E-03
539B-M0063-B11	straight human	PYWMH	GIGPSGGLTFYADSVKG	1	0.7+0.1	>10	1.20E-10	3.11E-03
539B-M0063-C07	straight human	PYWMS	GISPSGGITFYADSVKG	1	1.0+0.1	<10	2.29E-09	2.00E-03
539B-M0063-G01	straight human	WYWMV	SIGPSGGDTYYADSVKG	1	0.8+0.1	>10	1.58E-09	6.54E-03
539B-M0065-E12	straight mouse	WYNMH	GISPSGGNTMYADSVKG	1	1.4+0.1	<10	ND	ND
539B-M0065-G03	straight mouse	WYGMG	VIVSSGGFTQYADSVKG	1	3.0+0.2	<10	ND	ND
539B-M0065-H05	straight mouse	YYGMG	VISSSGGFTFYADSVKG	1	0.7+0.1	ND	2.19E-09	ND
539B-M0067-B06	alternate	WYWMH	GIVSSGGTTIYADSVKG	1	0.7+0.1	<10	6.20E-10	ND
539B-M0067-F06	alternate	WYNMS	RISPSGGDTGYADSVKG	2	0.7+0.1	<10	2.03E-10	2.50E-04
539B-M0069-C02	TIMP+MMP12	YYNMH	GIGPSGGGTLYADSVKG	1	1.6+0.2	~10	6.97E-09	ND
539B-M0069-D10	TIMP+MMP12	LYHMH	GIGPSGGWTIYADSVKG	1	2.3+0.1	<10	ND	ND
539B-M0071-A01	Lead+MMP12	EYWMT	GISPSGGMTFYADSVKG	1	0.3+0.1	>10	1.10E-09	1.00E-02
539B-M0071-D09	Lead+MMP12	PYWMH	GISSSGGDTLYADSVKG	1	2.4+0.2	<10	ND	ND
539B-M0071-H03	Lead+MMP12	PYWMH	GIGPSGGPTFYADSIKG	1	0.2+0.1	<10	1.03E-09	ND

KD_{huMMP12} improvement ~10-100x

Koff_{mMMP12} improvement ~2-10x

In cycle II of the affinity maturation, 109 Fabs were analyzed and 26 Fabs were selected as improved inhibitors. The IC₅₀ on human and murine MMP-12 was measured and an affinity ranking on human and murine MMP-12 was performed. For this analysis, 4 Fabs were selected and reformatted as IgGs. These four IgGs are described below in Table X:

Table X:

Name	Specie	Sequence																				Human MMP12			Mouse MMP12																				
		HC-CDR1				HC-CDR2				HC-CDR3				IC50	Kd (nM)	off rate	IC50	Kd (nM)	off rate																										
M08-H03	Fab	D	Y	N	N	H				I	C	P	S	C	G	Y	T	H	Y	A	D	S	V	K	G	D	I	R	G	A	Y	S	S	C	L	F	D	Y	14	18	9.54E-03	<10			4.00E-03
M131-A06	Fab	D	Y	N	N	H				I	C	P	S	C	G	Y	T	H	Y	A	D	S	V	K	G	D	I	V	G	P	Y	S	A	G	L	F	D	Y	0.299	0.18	1.91E-04	<10			4.84E-05
M121-E07	Fab	D	Y	N	N	H				I	C	P	S	C	G	Y	T	H	Y	A	D	S	V	K	G	D	I	R	G	V	F	L	S	C	L	F	D	H	0.006	0.197	1.41E-04	<10			1.15E-04
M118-F11	Fab	D	Y	N	N	H				I	C	P	S	C	G	Y	T	H	Y	A	D	S	V	K	G	D	I	T	C	A	Y	S	A	G	L	F	D	L	0.914	1.17	4.13E-04	<10			1.93E-04
M130-C12	Fab	D	Y	N	N	H				I	C	P	S	C	G	Y	T	H	Y	A	D	S	V	K	G	D	I	R	G	A	Y	S	A	G	I	F	D	Y	0.688			<10			

Inhibition assays of the affinity matured clones were performed. The results are provided below in Table XI.

Table XI:

KD huMMP12 (nM)		0.62	2.2	0.68	0.18	0.197	1.17
		Substrate used					
	Dilution of enzyme	533B-M067-B06	533B-M065-H05	533B-M130-C12	533B-M131-A06	533B-M121-E07	533B-M118-F11
		IgG at 1µM	IgG at 0.5µM	Fab at 1µM	Fab at 1µM	Fab at 1µM	Fab at 1µM
hMMP1	1/300	99	121	125	159	148	133
hMMP2	1/500	95	105	113	128	108	120
hMMP3	1/200	104	ND	121	110	97	102
hMMP7	1/500	102	128	117	115	113	112
hMMP8	1/1000	106	114	131	107	107	127
hMMP9	1/500	77	96	117	107	111	116
hMMP10	1/100	109	ND	106	124	123	127
hMMP12	1/500	0	0	0	2	3	1
hMMP12	1/400	2	ND	1	0	0	0
hMMP13	1/5000	102	ND	88	100	89	103
hMMP14	1/1000	90	ND	135	120	143	124

539B-M131A06 was cross reactive with human and murine MMP-12. It has a IC₅₀ or K_i of <0.3 nM and a K_D of 180 pM for human MMP-12 and 73-150 pM for murine MMP-12.

Example 4: Modification of 539B-M131-A06 (M131A06) to remove a glycosylation site in CDR1 of the variable light chain.

As shown in FIGURE 9, CDR 1 of the variable light chain of M131A06 was modified to remove a glycosylation site. Removal of the glycosylation site in CDR1 did not effect binding of M131A06 to MMP-12. The MMP-12 antibody with the glycosylation site removed is referred to as 539B-M131A06-GA-S.

Example 5

FIGURE 10 summarizes the identification of amino acid changes in affinity matured variant HV-CDRs (cycles 1 and 2) that contribute to improvement in affinity and inhibition properties.

Table. XII:

DX number	ID NO.	Clone origin
DX-2712	1	539B-M0131-A06-GA-S
	2	539B-M0008-H09-GA-S
	3	539B-M0121-E07-GA-S

ID NO.	VL
1	DIQMTQSPSSLSASVGDRTTITCRASQSIYTYLWNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQAQIFGQGTKLEIK
2	DIQMTQSPSSLSASVGDRTTITCRASQSIYTYLWNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQAQIFGQGTKLEIK
3	DIQMTQSPSSLSASVGDRTTITCRASQSIYTYLWNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQAQIFGQGTKLEIK

ID NO.	CL
1	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
2	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
3	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

ID NO.	VH
1	EVQLLESGGGLVQPGGSLRLSCAASGFTFSWYMMHWVRQAPGKGLVWVSGISPSGGMTMYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIVGPIYSAGLFDYWGRGTLVTVSS
2	EVQLLESGGGLVQPGGSLRLSCAASGFTFSQDYNMHWVRQAPGKGLVWVSYIGPSGGYTHYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
3	EVQLLESGGGLVQPGGSLRLSCAASGFTFSWYGMHWVRQAPGKGLVWVSGIVSSGGETFYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDIRGVFLSGLFDHWGRGTLVTVSS

ID NO.	CH
1	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVWTPVSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKD

	TLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QOPEN NYKTTPPVLDSDGSFFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
2	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTSPSSLSGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKD TLMIS RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PEN NYKTTPPVLDSDGSFFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
3	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTSPSSLSGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKD TLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QOPEN NYKTTPPVLDSDGSFFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Cycle 1 Fab Inhibitor Sequences- Light Chain

Initial Name	LV-FR1	LV-CDR1	LV-FR2	LV-CDR2	LV-FR3	LV-CDR3	LV-FR4	L-Constant
539B-M0063-A02	QDIQMTQSPSSLSASVGDRTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0063-A04	QDIQMTQSPSSLSASVGDRTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0063-B01	QDIQMTQSPSSLSASVGDRTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0063-B11	QDIQMTQSPSSLSASVGDRTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0063-C07	QDIQMTQSPSSLSASVGDRTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0063-G01	QDIQMTQSPSSLSASVGDRTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0065-E12	QDIQMTQSPSSLSASVGDRTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0065-G03	QDIQMTQSPSSLSASVGDRTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0065-H05	QDIQMTQSPSSLSASVGDRTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0067-A02	QDIQMTQSPSSLSASVGDRTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0067-B06	QDIQMTQSPSSLSASVGDRTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0067-B09	QDIQMTQSPSSLSASVGDRTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0067-C10	QDIQMTQSPSSLSASVGDRTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0067-F02	QDIQMTQSPSSLSASVGDRTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0067-F06	QDIQMTQSPSSLSASVGDRTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0069-A04	QDIQMTQSPSSLSASVGDRTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0069-A11	QDIQMTQSPSSLSASVGDRTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0069-C02	QDIQMTQSPSSLSASVGDRTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0069-D10	QDIQMTQSPSSLSASVGDRTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0069-G07	QDIQMTQSPSSLSASVGDRTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0071-	QDIQMTQSPSSLSASVGDRTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS

EVQLLESGGGLVQPPGSLRLSCAASGFTFS	WYNMH	WVRQAPGKGLEWVS	GISPSGNTMYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGLFDY	WGRGTLVTVSS
EVQLLESGGGLVQPPGSLRLSCAASGFTFS	WYGMG	WVRQAPGKGLEWVS	VIVSSGGFTQYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGLFDY	WGRGTLVTVSS
EVQLLESGGGLVQPPGSLRLSCAASGFTFS	YYGMG	WVRQAPGKGLEWVS	VISSSGGFTFYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGLFDY	WGRGTLVTVSS
EVQLLESGGGLVQPPGSLRLSCAASGFTFS	QYWMS	WVRQAPGKGLEWVS	SISPSGGETFYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGLFDY	WGRGTLVTVSS
EVQLLESGGGLVQPPGSLRLSCAASGFTFS	WYWMH	WVRQAPGKGLEWVS	GIVSSGGTTIYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGLFDY	WGRGTLVTVSS
EVQLLESGGGLVQPPGSLRLSCAASGFTFS	RYNMH	WVRQAPGKGLEWVS	GIVPSGGTTHYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGLFDY	WGRGTLVTVSS
EVQLLESGGGLVQPPGSLRLSCAASGFTFS	VYGMS	WVRQAPGKGLEWVS	RIVPSGGRTGYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGLFDY	WGRGTLVTVSS
EVQLLESGGGLVQPPGSLRLSCAASGFTFS	EYWMA	WVRQAPGKGLEWVS	SISPSGGHTFYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGLFDY	WGRGTLVTVSS
EVQLLESGGGLVQPPGSLRLSCAASGFTFS	WYNMS	WVRQAPGKGLEWVS	RISPSGGDTGYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGLFDY	WGRGTLVTVSS
EVQLLESGGGLVQPPGSLRLSCAASGFTFS	EYWMG	WVRQAPGKGLEWVS	SIYPSGGN TIYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGLFDY	WGRGTLVTVSS
EVQLLESGGGLVQPPGSLRLSCAASGFTFS	YYNMS	WVRQAPGKGLEWVS	GISPSGGPTGYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGLFDY	WGRGTLVTVSS
EVQLLESGGGLVQPPGSLRLSCAASGFTFS	YYNMH	WVRQAPGKGLEWVS	GIGPSGGGLYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGLFDY	WGRGTLVTVSS
EVQLLESGGGLVQPPGSLRLSCAASGFTFS	LYHMH	WVRQAPGKGLEWVS	GIGPSGGWTIYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGLFDY	WGRGTLVTVSS
EVQLLESGGGLVQPPGSLRLSCAASGFTFS	EYNMH	WVRQAPGKGLEWVS	GISPSGGMTHYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGLFDY	WGRGTLVTVSS
EVQLLESGGGLVQPPGSLRLSCAASGFTFS	EYWMT	WVRQAPGKGLEWVS	GISPSGGMTFYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGLFDY	WGRGTLVTVSS
EVQLLESGGGLVQPPGSLRLSCAASGFTFS	HYWMH	WVRQAPGKGLEWVS	GISPSGGMTMYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGLFDY	WGRGTLVTVSS
EVQLLESGGGLVQPPGSLRLSCAASGFTFS	QYNMH	WVRQAPGKGLEWVS	GIGPSGGITIYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGLFDY	WGRGTLVTVSS
EVQLLESGGGLVQPPGSLRLSCAASGFTFS	PYWMH	WVRQAPGKGLEWVS	GISSGGDTLYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGLFDY	WGRGTLVTVSS
EVQLLESGGGLVQPPGSLRLSCAASGFTFS	PYWMH	WVRQAPGKGLEWVS	GIGPSGGPTFYADSIKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGLFDY	WGRGTLVTVSS
EVQLLESGGGLVQPPGSLRLSCAASGFTFS	AYGMS	WVRQAPGKGLEWVS	RISPSGGITGYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGLFDY	WGRGTLVTVSS
EVQLLESGGGLVQPPGSLRLSCAASGFTFS	WYYMG	WVRQAPGKGLEWVS	SISPSGGWTRYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGLFDY	WGRGTLVTVSS
EVQLLESGGGLVQPPGSLRLSCAASGFTFS	FYWMD	WVRQAPGKGLEWVS	SISPSGGTTIYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGLFDY	WGRGTLVTVSS
EVQLLESGGGLVQPPGSLRLSCAASGFTFS	DYNMH	WVRQAPGKGLEWVS	YIGPSGGYTHYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGLFDY	WGRGTLVTVSS
EVQLLESGGGLVQPPGSLRLSCAASGFTFS	WYWMV	WVRQAPGKGLEWVS	SIVPSGGFTIYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGLFDY	WGRGTLVTVSS
EVQLLESGGGLVQPPGSLRLSCAASGFTFS	RYMMH	WVRQAPGKGLEWVS	YISSSGGTTIYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGLFDY	WGRGTLVTVSS
EVQLLESGGGLVQPPGSLRLSCAASGFTFS	HYWMQ	WVRQAPGKGLEWVS	GIVPSGGLTMYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGLFDY	WGRGTLVTVSS
EVQLLESGGGLVQPPGSLRLSCAASGFTFS	DYNMH	WVRQAPGKGLEWVS	YIGPSGGYTHYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGLFDY	WGRGTLVTVSS
EVQLLESGGGLVQPPGSLRLSCAASGFTFS	DYWMA	WVRQAPGKGLEWVS	SIGPSGGFTVYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGLFDY	WGRGTLVTVSS

Mutants VH-CDR1	LV-FR1	LV-CDR1	LV-FR2	LV-CDR2	LV-FR3	LV-CDR3	LV-FR4	LC
539B-M0067-F06-A	QDIQMTQSPSSLSASVGD RVTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0067-F06-G	QDIQMTQSPSSLSASVGD RVTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0067-F06-V	QDIQMTQSPSSLSASVGD RVTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS

These heavy chain mutant sequences are in the same order as the light chain designations provided above

Mutants Leader	HV-FR1	HV-CDR1	HV-FR2	HV-CDR2	HV-FR3	HV-CDR3	HV-FR4
MKKLLFAIPLVV PFVAQPAMA	EVQLLESGGGLVQPGGSL RLSCAASGFTFS	WYNMA	WVRQAPGKGLEWVS	RISPSGGDTGYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGGLFDY	WGRGTLVTVSS
MKKLLFAIPLVV PFVAQPAMA	EVQLLESGGGLVQPGGSL RLSCAASGFTFS	WYNMG	WVRQAPGKGLEWVS	RISPSGGDTGYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGGLFDY	WGRGTLVTVSS
MKKLLFAIPLVV PFVAQPAMA	EVQLLESGGGLVQPGGSL RLSCAASGFTFS	WYNMV	WVRQAPGKGLEWVS	RISPSGGDTGYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGGLFDY	WGRGTLVTVSS

LV-AA
QDIQMTQSPSSLSASVGDRVTITCRANQSIYTYLNWYQQKPGKAPELLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAGIFGQGTKLEIK
QDIQMTQSPSSLSASVGDRVTITCRANQSIYTYLNWYQQKPGKAPELLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAGIFGQGTKLEIK
QDIQMTQSPSSLSASVGDRVTITCRANQSIYTYLNWYQQKPGKAPELLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAGIFGQGTKLEIK
QDIQMTQSPSSLSASVGDRVTITCRANQSIYTYLNWYQQKPGKAPELLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAGIFGQGTKLEIK
QDIQMTQSPSSLSASVGDRVTITCRANQSIYTYLNWYQQKPGKAPELLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAGIFGQGTKLEIK
QDIQMTQSPSSLSASVGDRVTITCRANQSIYTYLNWYQQKPGKAPELLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAGIFGQGTKLEIK
QDIQMTQSPSSLSASVGDRVTITCRANQSIYTYLNWYQQKPGKAPELLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAGIFGQGTKLEIK
QDIQMTQSPSSLSASVGDRVTITCRANQSIYTYLNWYQQKPGKAPELLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAGIFGQGTKLEIK
QDIQMTQSPSSLSASVGDRVTITCRANQSIYTYLNWYQQKPGKAPELLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAGIFGQGTKLEIK
QDIQMTQSPSSLSASVGDRVTITCRANQSIYTYLNWYQQKPGKAPELLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAGIFGQGTKLEIK
QDIQMTQSPSSLSASVGDRVTITCRANQSIYTYLNWYQQKPGKAPELLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAGIFGQGTKLEIK
QDIQMTQSPSSLSASVGDRVTITCRANQSIYTYLNWYQQKPGKAPELLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAGIFGQGTKLEIK
QDIQMTQSPSSLSASVGDRVTITCRANQSIYTYLNWYQQKPGKAPELLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAGIFGQGTKLEIK

HV-AA
EVQLLESGGGLVQPGGSLRLSCAASGFTFSQYWMGWVRQAPKGLEWVSSI SPGGMTMYADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSQYWMGWVRQAPKGLEWVSSI SPGGMTLYADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSQYWMGWVRQAPKGLEWVSSI SPGGYTFYADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSQYWMGWVRQAPKGLEWVSSI SPGGYTFYADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS

EVQLLESGGGLVQPPGGLRLSCAASGFTFSYWM ~~SWVRQAPGKGL~~ EWVSGISPSGGITFYADSVKGRFTISRDN ~~SKNTLYLQMN~~ SLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPPGGLRLSCAASGFTFSWY ~~WMVVRQAPGKGL~~ EWVSSIGPSGGDTYYADSVKGRFTISRDN ~~SKNTLYLQMN~~ SLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPPGGLRLSCAASGFTFSWY ~~NMHVVRQAPGKGL~~ EWVSGISPSGGNTMYADSVKGRFTISRDN ~~SKNTLYLQMN~~ SLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPPGGLRLSCAASGFTFSWYGM ~~GWVRQAPGKGL~~ EWVSVIVSSGGFTQYADSVKGRFTISRDN ~~SKNTLYLQMN~~ SLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPPGGLRLSCAASGFTFSY ~~YGMGWVRQAPGKGL~~ EWVSVISSSGGFTFYADSVKGRFTISRDN ~~SKNTLYLQMN~~ SLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPPGGLRLSCAASGFTFSQY ~~WMSWVRQAPGKGL~~ EWVSSISPSGGETFYADSVKGRFTISRDN ~~SKNTLYLQMN~~ SLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPPGGLRLSCAASGFTFSWY ~~NMHVVRQAPGKGL~~ EWVSGIVSSGGTTIYADSVKGRFTISRDN ~~SKNTLYLQMN~~ SLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPPGGLRLSCAASGFTFSRY ~~NMHVVRQAPGKGL~~ EWVSGIVPSGGTTHYADSVKGRFTISRDN ~~SKNTLYLQMN~~ SLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPPGGLRLSCAASGFTFSVY ~~GMSWVRQAPGKGL~~ EWVSRIVPSGGRTGYADSVKGRFTISRDN ~~SKNTLYLQMN~~ SLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPPGGLRLSCAASGFTFSEY ~~WMAWVRQAPGKGL~~ EWVSSISPSGGHTFYADSVKGRFTISRDN ~~SKNTLYLQMN~~ SLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPPGGLRLSCAASGFTFSWY ~~NMSWVRQAPGKGL~~ EWVSRISPSGGDTGYADSVKGRFTISRDN ~~SKNTLYLQMN~~ SLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPPGGLRLSCAASGFTFSEY ~~WMGWVRQAPGKGL~~ EWVSIYPSSGNTIYADSVKGRFTISRDN ~~SKNTLYLQMN~~ SLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPPGGLRLSCAASGFTFSY ~~NMSWVRQAPGKGL~~ EWVSGISPSGGPTGYADSVKGRFTISRDN ~~SKNTLYLQMN~~ SLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPPGGLRLSCAASGFTFSY ~~NMHVVRQAPGKGL~~ EWVSGIGPSGGTLYADSVKGRFTISRDN ~~SKNTLYLQMN~~ SLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPPGGLRLSCAASGFTFSLY ~~HMHVVRQAPGKGL~~ EWVSGIGPSGGWTIYADSVKGRFTISRDN ~~SKNTLYLQMN~~ SLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPPGGLRLSCAASGFTFSEY ~~NMHVVRQAPGKGL~~ EWVSGISPSGGMTHYADSVKGRFTISRDN ~~SKNTLYLQMN~~ SLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPPGGLRLSCAASGFTFSEY ~~WMTWVRQAPGKGL~~ EWVSGISPSGGMTFYADSVKGRFTISRDN ~~SKNTLYLQMN~~ SLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPPGGLRLSCAASGFTFSHY ~~NMHVVRQAPGKGL~~ EWVSGISPSGGMTMYADSVKGRFTISRDN ~~SKNTLYLQMN~~ SLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPPGGLRLSCAASGFTFSQY ~~NMHVVRQAPGKGL~~ EWVSGIGPSGGITFYADSVKGRFTISRDN ~~SKNTLYLQMN~~ SLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPPGGLRLSCAASGFTFSY ~~WMHVVRQAPGKGL~~ EWVSGIGPSGGPTFYADSIKGRFTISRDN ~~SKNTLYLQMN~~ SLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPPGGLRLSCAASGFTFSAY ~~GMSWVRQAPGKGL~~ EWVSRISPSGGITGYADSVKGRFTISRDN ~~SKNTLYLQMN~~ SLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPPGGLRLSCAASGFTFSWY ~~YMGWVRQAPGKGL~~ EWVSSISPSGGWTRYADSVKGRFTISRDN ~~SKNTLYLQMN~~ SLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPPGGLRLSCAASGFTFSFY ~~WMDWVRQAPGKGL~~ EWVSSISPSGGTTIYADSVKGRFTISRDN ~~SKNTLYLQMN~~ SLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPPGGLRLSCAASGFTFSDY ~~NMHVVRQAPGKGL~~ EWVSYIGPSGGYTHYADSVKGRFTISRDN ~~SKNTLYLQMN~~ SLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPPGGLRLSCAASGFTFSWY ~~WMVVRQAPGKGL~~ EWVSVIVPSGGFTIYADSVKGRFTISRDN ~~SKNTLYLQMN~~ SLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPPGGLRLSCAASGFTFSRY ~~NMHVVRQAPGKGL~~ EWVSYISSSGGTTIYADSVKGRFTISRDN ~~SKNTLYLQMN~~ SLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPPGGLRLSCAASGFTFSHY ~~NMQWVRQAPGKGL~~ EWVSGIVPSGGITMYADSVKGRFTISRDN ~~SKNTLYLQMN~~ SLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPPGGLRLSCAASGFTFSDY ~~NMHVVRQAPGKGL~~ EWVSYIGPSGGYTHYADSVKGRFTISRDN ~~SKNTLYLQMN~~ SLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPPGGLRLSCAASGFTFSDY ~~WMAWVRQAPGKGL~~ EWVSSIGPSGGFTVYADSVKGRFTISRDN ~~SKNTLYLQMN~~ SLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS

Cycle 2 Inhibitors-Light Chain Variable Region Sequences

Initial Name	LV-FR1	LV-CDR1	LV-FR2	LV-CDR2	LV-FR3	LV-CDR3	LV-FR4
539B-M0105-C05	QDIQMTQSPSSLSASVGDRVITITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGGTDFTLTISSLQPEDEFATYYC	QQAGI	FGQGTKLEIK
539B-M0105-E11	QDIQMTQSPSSLSASVGDRVITITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGGTDFTLTISSLQPEDEFATYYC	QQAGI	FGQGTKLEIK
539B-M0105-F08	QDIQMTQSPSSLSASVGDRVITITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGGTDFTLTISSLQPEDEFATYYC	QQAGI	FGQGTKLEIK
539B-M0107-A12	QDIQMTQSPSSLSASVGDRVITITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGGTDFTLTISSLQPEDEFATYYC	QQAGI	FGQGTKLEIK
539B-M0108-A02	QDIQMTQSPSSLSASVGDRVITITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGGTDFTLTISSLQPEDEFATYYC	QQAGI	FGQGTKLEIK
539B-M0109-G11	QDIQMTQSPSSLSASVGDRVITITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGGTDFTLTISSLQPEDEFATYYC	QQAGI	FGQGTKLEIK
539B-M0110-G05	QDIQMTQSPSSLSASVGDRVITITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGGTDFTLTISSLQPEDEFATYYC	QQAGI	FGQGTKLEIK
539B-M0129-B11	QDIQMTQSPSSLSASVGDRVITITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGGTDFTLTISSLQPEDEFATYYC	QQAGI	FGQGTKLEIK
539B-M0130-A01	QDIQMTQSPSSLSASVGDRVITITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGGTDFTLTISSLQPEDEFATYYC	QQAGI	FGQGTKLEIK
539B-M0130-C12	QDIQMTQSPSSLSASVGDRVITITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGGTDFTLTISSLQPEDEFATYYC	QQAGI	FGQGTKLEIK
539B-M0130-F06	QDIQMTQSPSSLSASVGDRVITITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGGTDFTLTISSLQPEDEFATYYC	QQAGI	FGQGTKLEIK
539B-M0130-H04	QDIQMTQSPSSLSASVGDRVITITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGGTDFTLTISSLQPEDEFATYYC	QQAGI	FGQGTKLEIK
539B-M0131-A06	QDIQMTQSPSSLSASVGDRVITITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGGTDFTLTISSLQPEDEFATYYC	QQAGI	FGQGTKLEIK
539B-M0131-D03	QDIQMTQSPSSLSASVGDRVITITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGGTDFTLTISSLQPEDEFATYYC	QQAGI	FGQGTKLEIK
539B-M0132-A04	QDIQMTQSPSSLSASVGDRVITITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGGTDFTLTISSLQPEDEFATYYC	QQAGI	FGQGTKLEIK
539B-M0133-B08	QDIQMTQSPSSLSASVGDRVITITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGGTDFTLTISSLQPEDEFATYYC	QQAGI	FGQGTKLEIK
539B-M0133-E05	QDIQMTQSPSSLSASVGDRVITITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGGTDFTLTISSLQPEDEFATYYC	QQAGI	FGQGTKLEIK
539B-M0121-E07	QDIQMTQSPSSLSASVGDRVITITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGGTDFTLTISSLQPEDEFATYYC	QQAGI	FGQGTKLEIK
539B-M0118-F11	QDIQMTQSPSSLSASVGDRVITITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGGTDFTLTISSLQPEDEFATYYC	QQAGI	FGQGTKLEIK
539B-M0125-G07	QDIQMTQSPSSLSASVGDRVITITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGGTDFTLTISSLQPEDEFATYYC	QQAGI	FGQGTKLEIK

539B-M0124-E07	QDIQMTQSPSSLSASVGDRVITIC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGGTDFTLTISSLQPEDEFATYYC	QQAGI	FGQGTKLEIK
539B-M0119-D01	QDIQMTQSPSSLSASVGDRVITIC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGGTDFTLTISSLQPEDEFATYYC	QQAGI	FGQGTKLEIK
539B-M0119-A02	QDIQMTQSPSSLSASVGDRVITIC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGGTDFTLTISSLQPEDEFATYYC	QQAGI	FGQGTKLEIK
539B-M0122-C06	QDIQMTQSPSSLSASVGDRVITIC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGGTDFTLTISSLQPEDEFATYYC	QQAGI	FGQGTKLEIK
539B-M0123-G07	QDIQMTQSPSSLSASVGDRVITIC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGGTDFTLTISSLQPEDEFATYYC	QQAGI	FGQGTKLEIK

Cycle 2 Inhibitors-Heavy Chain Variable Sequences (These are in the same order as the Cycle 2 Light Chain Inhibitors provided above)

HV-FR1	HV-CDR1	HV-FR2	HV-CDR2	HV-FR3	HV-CDR3	HV-FR4
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	PYWMH	WVRQAPGKGLEWVS	GISSSGGDTLYADSVKG	RFTISRDN SKNTLYLQMNGLRAEDTAVYYCAR	DIRGAYSSGLFFS	WGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	QYFMH	WVRQAPGKGLEWVS	GIYPSGGDTFYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR	DIRGAYSSGVFDY	WGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	PYWMH	WVRQAPGKGLEWVS	GISSSGGDTLYADSVKG	RFTISRDN SKNTLYLQMNGLRAEDTAVYYCAR	DIRGAYSSGLFFS	WGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	DYNMH	WVRQAPGKGLEWVS	YIGPSGGYTHYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR	DIRGAYASGLFDY	WGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYWMH	WVRQAPGKGLEWVS	GIYSSGGDTIYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAK	DIRGPHSSGLFDY	WGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	EYNMH	WVRQAPGKGLEWVS	GIVPSGGLTHYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAK	DIRGAYSSGLFDY	WGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	EYNMH	WVRQAPGKGLEWVS	GIGPSGGPTMYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAK	DIRGAYSSGLFDY	WGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	PYWMH	WVRQAPGKGLEWVS	GIGPSGGPTFYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR	DIMGAYASGLFHN	WGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	EYNMH	WVRQAPGKGLEWVS	GIVPSGGLTHYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAK	DIRGAYSSGLFDH	WGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	EYNMH	WVRQAPGKGLEWVS	GIVPSGGLTHYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR	DIRGAYSAGIFDY	WGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	PYWMH	WVRQAPGKGLEWVS	GISPSGGETIYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR	DIMGAYSAGHFEY	WGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	PYWMH	WVRQAPGKGLEWVS	GISPSGGHTMYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAK	DIRGAYSSGLFDF	WGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYWMH	WVRQAPGKGLEWVS	GISPSGGMTMYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR	DIVGPYSAGLFDY	WGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYWMH	WVRQAPGKGLEWVS	GISPSGGYTMYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAK	DISGAYSSGLFTF	WGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	PYWMH	WVRQAPGKGLEWVS	GISPSGGNTLYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR	DIRGAYSSGLFYD	WGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYWMH	WVRQAPGKGLEWVS	GISPSGGSTFYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR	DFSGAYSAGLFAY	WGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	YYNMH	WVRQAPGKGLEWVS	GIGPSGGTLYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR	DLSGEYASGLFGY	WGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYGMH	WVRQAPGKGLEWVS	GIVSSGGETFYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAK	DIRGVFLSGLFDH	WGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	YYNMH	WVRQAPGKGLEWVS	GISPSGGTTFYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR	DITGAYSAGLFDL	WGRGTLVTVSS

QDIQMTQSPSSLASVGDRVTITCRANQSIYTYLNWYQQKPGKAPELLIYAASSLQSGVPSRFSGSGGTFTLTISSLQPEDFATYYCQQAQAGIFGQGTKLEIK
QDIQMTQSPSSLASVGDRVTITCRANQSIYTYLNWYQQKPGKAPELLIYAASSLQSGVPSRFSGSGGTFTLTISSLQPEDFATYYCQQAQAGIFGQGTKLEIK
QDIQMTQSPSSLASVGDRVTITCRANQSIYTYLNWYQQKPGKAPELLIYAASSLQSGVPSRFSGSGGTFTLTISSLQPEDFATYYCQQAQAGIFGQGTKLEIK

Variable Heavy Chain Amino Acid Sequences (These are in the same order as the Cycle 2 Light Chain Sequences)

HV-AA	
EVQLLESGGGLVQPGGSLRLSCAASGFTTSPYWMHWVRQAPGKGLEWVSGISSSGGDTLYADSVKGRFTISRDN SKNTLYLQMNGLRAEDTAVYYCARDIRGAYSSGLFFSWGRGTLTVTVSS	
EVQLLESGGGLVQPGGSLRLSCAASGFTTSPYFMHWVRQAPGKGLEWVSGIYPSGGDTFYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIRGAYSSGVFDYWGRGTLTVTVSS	
EVQLLESGGGLVQPGGSLRLSCAASGFTTSPYWMHWVRQAPGKGLEWVSGISSSGGDTLYADSVKGRFTISRDN SKNTLYLQMNGLRAEDTAVYYCARDIRGAYSSGLFFSWGRGTLTVTVSS	
EVQLLESGGGLVQPGGSLRLSCAASGFTTSDYNMHWVRQAPGKLEWVSYIGPSGGYTHYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIRGAYASGLFDYWGRGTLTVTVSS	
EVQLLESGGGLVQPGGSLRLSCAASGFTTSPYWMHWVRQAPGKLEWVSGIYSSGGDTIYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDIRGPHSSGLFDYWGRGTLTVTVSS	
EVQLLESGGGLVQPGGSLRLSCAASGFTTSEYNMHWVRQAPGKLEWVSGIYPSGGLTHYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLTVTVSS	
EVQLLESGGGLVQPGGSLRLSCAASGFTTSEYNMHWVRQAPGKLEWVSGIGIPSGGPTMYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLTVTVSS	
EVQLLESGGGLVQPGGSLRLSCAASGFTTSPYWMHWVRQAPGKLEWVSGIGIPSGGPTFYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIMGAYASGLFHNWGRGTLTVTVSS	
EVQLLESGGGLVQPGGSLRLSCAASGFTTSEYNMHWVRQAPGKLEWVSGIYPSGGLTHYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDIRGAYSSGLFDHWGRGTLTVTVSS	
EVQLLESGGGLVQPGGSLRLSCAASGFTTSEYNMHWVRQAPGKLEWVSGIYPSGGLTHYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIRGAYSAGIFDYWGRGTLTVTVSS	
EVQLLESGGGLVQPGGSLRLSCAASGFTTSPYWMHWVRQAPGKLEWVSGISPSGGETIYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIWGAYSAGHFEYWGRGTLTVTVSS	
EVQLLESGGGLVQPGGSLRLSCAASGFTTSPYWMHWVRQAPGKLEWVSGISPSGGHTMYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDIRGAYSSGLFDWFWGRGTLTVTVSS	
EVQLLESGGGLVQPGGSLRLSCAASGFTTSPYWMHWVRQAPGKLEWVSGISPSGGMTMYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIVGPYSAGLFDYWGRGTLTVTVSS	
EVQLLESGGGLVQPGGSLRLSCAASGFTTSPYWMHWVRQAPGKLEWVSGISPSGGYTMYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDISGAYSSGLFTFWGRGTLTVTVSS	
EVQLLESGGGLVQPGGSLRLSCAASGFTTSPYWMHWVRQAPGKLEWVSGISPSGGNTLYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIRGAYSSGLFYDWGRGTLTVTVSS	
EVQLLESGGGLVQPGGSLRLSCAASGFTTSPYWMHWVRQAPGKLEWVSGISPSGGSTFYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDFSGAYSAGLFAYWGRGTLTVTVSS	
EVQLLESGGGLVQPGGSLRLSCAASGFTTSPYGMHWVRQAPGKLEWVSGIVSSGGETFYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDIRGVFLSGLFDHWGRGTLTVTVSS	
EVQLLESGGGLVQPGGSLRLSCAASGFTTSPYNNMHWVRQAPGKLEWVSGISPSGGTTFYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDITGAYSAGLFDLWGRGTLTVTVSS	
EVQLLESGGGLVQPGGSLRLSCAASGFTTSPYNNMHWVRQAPGKLEWVSGISPSGGNTMYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIWGAYASGLFDYWGRGTLTVTVSS	
EVQLLESGGGLVQPGGSLRLSCAASGFTTSPYWMHWVRQAPGKLEWVSGISPSGGWTFYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIRGAYSSGMFDFWGRGTLTVTVSS	

EVQLLESGGGLVQPGGSLRLSCAASGFTFSPYWMHWVRQAPGKGLEWVSGIGSPGGPTFYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDIRGAYSGGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSAYWMHWVRQAPGKGLEWVSGISPGGLTFYADSVKGRFTISRDD SKNTLYLQMNSLGAEATAVYYCARDIRGAYSSGHFDYWGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSWYWMHWVRQAPGKGLEWVSGISPGGPTMYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDIRGPYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSPYWMHWVRQAPGKGLEWVSGIGSPGGLTFYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDMRGAYASGLFDYWGRGTLVTVSS

Light Chain Variable Region Sequences

539B-M0122 - H05_VL + 539B-M0131-A6 VH	QDIQMTQSPSSLASVGDRVITTC	RASQNI NYLN	WYQQRP GKAPKLLIY	AASN LQT	GVPSRFSGSGSGTD FIF TISSLQPEDIA YYC	QQAGI	FGQGT KLEIK	RTVAAPS
539B-M0131-A06-GA-D-VL	QDIQMTQSPSSLASVGDRVITTC	RADQSI TYLN	WYQQRP GKAPKLLIY	AASS LQS	GVPSRFSGSGSGTD FTL TISSLQPEDFA YYC	QQAGI	FGQGT KLEIK	RTVAAPS
539B-M0131-A06-GA-E-VL	QDIQMTQSPSSLASVGDRVITTC	RAEQSI TYLN	WYQQRP GKAPKLLIY	AASS LQS	GVPSRFSGSGSGTD FTL TISSLQPEDFA YYC	QQAGI	FGQGT KLEIK	RTVAAPS
539B-M0131-A06-GA-T-VL	QDIQMTQSPSSLASVGDRVITTC	RATQSI TYLN	WYQQRP GKAPKLLIY	AASS LQS	GVPSRFSGSGSGTD FTL TISSLQPEDFA YYC	QQAGI	FGQGT KLEIK	RTVAAPS
539B-M0131-A06-GA-V-VL	QDIQMTQSPSSLASVGDRVITTC	RAVQSI TYLN	WYQQRP GKAPKLLIY	AASS LQS	GVPSRFSGSGSGTD FTL TISSLQPEDFA YYC	QQAGI	FGQGT KLEIK	RTVAAPS

Heavy Chain Sequences (in the same order as above)

EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYWMH	WVRQAP GKGLEWVS	GISPSG GMTMYADSVKG	RFTISR DNSKNTLYLQMN SLRAEDTAVYYCAR	DIVGP YSAGLFDY	WGRGT LVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYWMH	WVRQAP GKGLEWVS	GISPSG GMTMYADSVKG	RFTISR DNSKNTLYLQMN SLRAEDTAVYYCAR	DIVGP YSAGLFDY	WGRGT LVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYWMH	WVRQAP GKGLEWVS	GISPSG GMTMYADSVKG	RFTISR DNSKNTLYLQMN SLRAEDTAVYYCAR	DIVGP YSAGLFDY	WGRGT LVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYWMH	WVRQAP GKGLEWVS	GISPSG GMTMYADSVKG	RFTISR DNSKNTLYLQMN SLRAEDTAVYYCAR	DIVGP YSAGLFDY	WGRGT LVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYWMH	WVRQAP GKGLEWVS	GISPSG GMTMYADSVKG	RFTISR DNSKNTLYLQMN SLRAEDTAVYYCAR	DIVGP YSAGLFDY	WGRGT LVTVSS

Cycle 3 Inhibitors-Light Chains

Initial Name	LV-FR1	LV-CDR1	LV-FR2	LV-CDR2	LV-FR3	LV-CDR3	LV-FR4	L-Constant
539B-M0134-A02	QDIQMTQSPSSLASVGDRVTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0134-A05	QDIQMTQSPSSLASVGDRVTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0134-A07	QDIQMTQSPSSLASVGDRVTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0134-A09	QDIQMTQSPSSLASVGDRVTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0134-A10	QDIQMTQSPSSLASVGDRVTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0134-A11	QDIQMTQSPSSLASVGDRVTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0134-B01	QDIQMTQSPSSLASVGDRVTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0134-B04	QDIQMTQSPSSLASVGDRVTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0134-B08	QDIQMTQSPSSLASVGDRVTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0134-B11	QDIQMTQSPSSLASVGDRVTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0134-C01	QDIQMTQSPSSLASVGDRVTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0134-C02	QDIQMTQSPSSLASVGDRVTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0134-C06	QDIQMTQSPSSLASVGDRVTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0134-C09	QDIQMTQSPSSLASVGDRVTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0134-C10	QDIQMTQSPSSLASVGDRVTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0134-C11	QDIQMTQSPSSLASVGDRVTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0134-C12	QDIQMTQSPSSLASVGDRVTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0134-D02	QDIQMTQSPSSLASVGDRVTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0134-D03	QDIQMTQSPSSLASVGDRVTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0134-E04	QDIQMTQSPSSLASVGDRVTITC	RANQSIYTYLN	WYQQKPGKAPELLIY	AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS

[illegible]

M0135-G11							
539B-M0135-H03	QDIQMTQSPSSLSASVGDRVTITC	RANQSIYTYLN	WYQQKPGKAPPELLIY	AASSLQS	GVPSRFSGSGGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK RTVAAPS
539B-M0135-H10	QDIQMTQSPSSLSASVGDRVTITC	RANQSIYTYLN	WYQQKPGKAPPELLIY	AASSLQS	GVPSRFSGSGGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK RTVAAPS

Cycle 3 Heavy Chain Variable Regions (in the same order as the light chains provided above)

HV-FR1	HV-CDR1	HV-FR2	HV-CDR2	HV-FR3	HV-CDR3
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	PYWMH	WVRQAPGKGLEWVS	GISPSGGETIYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR	DIWGAYASGLFDY
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYWMV	WVRQAPGKGLEWVS	SIGPSGGDTIYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR	DIRGAYSSGLFYD
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	EYWMA	WVRQAPGKGLEWVS	SISPSGGHTFYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR	DMRGAYASGLFDY
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	PYWMH	WVRQAPGKGLEWVS	GIGPSGGPTFYADSIKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR	DIWGAYASGLFDY
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	PYWMH	WVRQAPGKGLEWVS	GIGPSGGPTFYADSIKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAK	DIRGPYSSGLFDY
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYWMH	WVRQAPGKGLEWVS	GIVSSGGTTIYADSVKG	RFTISRDD SKNTLYLQMNSLGAEATAVYYCAR	DIRGAYSSGHFDY
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	PYWMH	WVRQAPGKGLEWVS	GISPSGGNTLYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAK	DISGAYSSGLFTF
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYWMV	WVRQAPGKGLEWVS	SIVPSGGFTIYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAK	DIRGAYSSGLFDY
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYWMH	WVRQAPGKGLEWVS	GISPSGGPTMYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAK	DIRGPYSSGLFDY
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	PYWMH	WVRQAPGKGLEWVS	GIGPSGGLTFYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR	DIRGAYSSGMFDF
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	HYWMQ	WVRQAPGKGLEWVS	GIVPSGGLTMYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAK	DISGAYSSGLFTF
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYWMG	WVRQAPGKGLEWVS	SISPSGGYTFYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR	DMRGAYASGLFDY
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	PYWMH	WVRQAPGKGLEWVS	GIGPSGGLTFYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAK	DIRGAYSSGLFDF
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	EYWMT	WVRQAPGKGLEWVS	GISPSGGMTFYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR	DMRGAYASGLFDY
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYWMH	WVRQAPGKGLEWVS	GIVSSGGTTIYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAK	DIRGPYSSGLFDY
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	PYNMH	WVRQAPGKGLEWVS	GISPSGGNTMYADSVKG	RFTISRDD SKNTLYLQMNSLGAEATAVYYCAR	DIRGAYSSGHFDY
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYWMG	WVRQAPGKGLEWVS	SISPSGGYTFYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAK	DIRGAYSSGLFDY
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	EYWMT	WVRQAPGKGLEWVS	GISPSGGMTFYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAK	DIRGAYSSGLFDY
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYWMV	WVRQAPGKGLEWVS	SIVPSGGFTIYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR	DLSGEYASGLFGY
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYNMS	WVRQAPGKGLEWVS	RISPSGGDTGYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAK	DIRGAYSGGLFDY
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	EYWMT	WVRQAPGKGLEWVS	GISPSGGMTFYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR	DIRGAYSSGMFDF
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYWMV	WVRQAPGKGLEWVS	SIGPSGGDTIYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR	DLSGEYASGLFGY
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYWMV	WVRQAPGKGLEWVS	SIVPSGGFTIYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAK	DISGAYSSGLFTF
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYWMH	WVRQAPGKGLEWVS	GIVSSGGTTIYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAK	DIRGAYSSGLFDH

EVQLLESGGGLVQPGGSLRLSCAASGFTFS	AYWMH	WVRQAPGKGLEWVS	GISPSGGLTFYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAR	DIWGAYASGLFDY
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYWMV	WVRQAPGKGLEWVS	SIGPSGGDTYYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAR	DIWGAYSAGHFEY
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYWMH	WVRQAPGKGLEWVS	GIVSSGGTTIYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAR	DIWGAYSAGHFEY
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYWMH	WVRQAPGKGLEWVS	GIVSSGGTTIYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAR	DIRGAYSSGGLFDY
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	PYWM S	WVRQAPGKGLEWVS	GISPSGGITFYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAR	DL SGEYASGLFGY
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	YYGMG	WVRQAPGKGLEWVS	VISSSGGTFYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DISGAYSSGLFTF
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYWMH	WVRQAPGKGLEWVS	GIVSSGGTTIYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGGLFDF
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYWMG	WVRQAPGKGLEWVS	SISPSGGYTFYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAR	DL SGEYASGLFGY
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	PYWMH	WVRQAPGKGLEWVS	GISPSGGNTLYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGGLFDY
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYWMH	WVRQAPGKGLEWVS	GIVSSGGTTIYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAR	DFSGAYSAGLFAY
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	PYWMH	WVRQAPGKGLEWVS	GIGPSGGPTFYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGGLFDY
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	EYWMA	WVRQAPGKGLEWVS	SISPSGGHTFYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGPYSSGGLFDY
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYWMV	WVRQAPGKGLEWVS	SIGPSGGDTYYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGGLFDY
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	PYWMH	WVRQAPGKGLEWVS	GIGPSGGLTFYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGGLFDH
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	HYWMQ	WVRQAPGKGLEWVS	GIVPSGGLTMYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAR	DIMGAYASGLFHN
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	EYWMT	WVRQAPGKGLEWVS	GISPSGGMTFYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGGLFDF
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	PYWM S	WVRQAPGKGLEWVS	GISPSGGITFYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAR	DIWGAYSAGHFEY
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYWMH	WVRQAPGKGLEWVS	GIVSSGGTTIYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAR	DL SGEYASGLFGY
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYWMV	WVRQAPGKGLEWVS	SIGPSGGDTYYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAR	DMRGAYASGLFDY
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYNM S	WVRQAPGKGLEWVS	RISPSGGDTGYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSSGGLFDH
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	PYWMH	WVRQAPGKGLEWVS	GIGPSGGPTFYADSIKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAK	DIRGAYSGGGLFDY

Cycle 3 Light Chain Amino Acid Sequences (provided in the same order as the Cycle 3 Light Chains provided above)

LV-AA
QDIQMTQSPSSLSASVGDRVTITCRANQSIYTYLNWYQQKPKGKAPPELLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAGIFGQGTKLEIK
QDIQMTQSPSSLSASVGDRVTITCRANQSIYTYLNWYQQKPKGKAPPELLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAGIFGQGTKLEIK
QDIQMTQSPSSLSASVGDRVTITCRANQSIYTYLNWYQQKPKGKAPPELLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAGIFGQGTKLEIK
QDIQMTQSPSSLSASVGDRVTITCRANQSIYTYLNWYQQKPKGKAPPELLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAGIFGQGTKLEIK
QDIQMTQSPSSLSASVGDRVTITCRANQSIYTYLNWYQQKPKGKAPPELLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAGIFGQGTKLEIK
QDIQMTQSPSSLSASVGDRVTITCRANQSIYTYLNWYQQKPKGKAPPELLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAGIFGQGTKLEIK
QDIQMTQSPSSLSASVGDRVTITCRANQSIYTYLNWYQQKPKGKAPPELLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAGIFGQGTKLEIK

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QDIQMTQSPSSLASVGDRVTITCRANQSIYTYLNWYQQKPGKAPELLIYAASSLQSGVPSRFSGSGTDFTLTISSLQPEDFATYYCQQAAGIFGQGTKLEIK
QDIQMTQSPSSLASVGDRVTITCRANQSIYTYLNWYQQKPGKAPELLIYAASSLQSGVPSRFSGSGTDFTLTISSLQPEDFATYYCQQAAGIFGQGTKLEIK
QDIQMTQSPSSLASVGDRVTITCRANQSIYTYLNWYQQKPGKAPELLIYAASSLQSGVPSRFSGSGTDFTLTISSLQPEDFATYYCQQAAGIFGQGTKLEIK
QDIQMTQSPSSLASVGDRVTITCRANQSIYTYLNWYQQKPGKAPELLIYAASSLQSGVPSRFSGSGTDFTLTISSLQPEDFATYYCQQAAGIFGQGTKLEIK
QDIQMTQSPSSLASVGDRVTITCRANQSIYTYLNWYQQKPGKAPELLIYAASSLQSGVPSRFSGSGTDFTLTISSLQPEDFATYYCQQAAGIFGQGTKLEIK
QDIQMTQSPSSLASVGDRVTITCRANQSIYTYLNWYQQKPGKAPELLIYAASSLQSGVPSRFSGSGTDFTLTISSLQPEDFATYYCQQAAGIFGQGTKLEIK
QDIQMTQSPSSLASVGDRVTITCRANQSIYTYLNWYQQKPGKAPELLIYAASSLQSGVPSRFSGSGTDFTLTISSLQPEDFATYYCQQAAGIFGQGTKLEIK

Cycle 3Heavy Chain Amino Acid Sequences (provided in the same order as the Cycle 3 Light Chains provided above)

HV-AA
EVQLLESGGGLVQPGGSLRLSCAASGFTFSPYWMHWVRQAPGKGLEWVSGISPSGGETIYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIWGAYASGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSWYWMVVRQAPGKGLEWVSSIGPSGGDTIYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSEYWMVVRQAPGKGLEWVSSISPSGGHTFYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDMRGAYASGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSPYWMHWVRQAPGKGLEWVSGIGPSGGPTFYADSIKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIWGAYASGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSPYWMHWVRQAPGKGLEWVSGIGPSGGPTFYADSIKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDIRGPYS SGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSWYWMHWVRQAPGKGLEWVSGIVSSGGTTIYADSVKGRFTISRDD SKNTLYLQMNSLGAEATAVYYCARDIRGAYSSGHFDYWGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSPYWMHWVRQAPGKGLEWVSGISPSGGNTLIYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDISGAYSSGLFTFWGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSPYWMVVRQAPGKGLEWVSSIVPSGGFTIYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSWYWMHWVRQAPGKGLEWVSGISPSGGPTMYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDIRGPYS SGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSPYWMHWVRQAPGKGLEWVSGIGPSGGLTIFYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIRGAYSSGMFDFWGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYWMQWVRQAPGKGLEWVSGIVPSGGLTIMYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDISGAYSSGLFTFWGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSWYWMGWVRQAPGKGLEWVSSISPSGGYTFYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDMRGAYASGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSPYWMHWVRQAPGKGLEWVSGIGPSGGLTIFYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDIRGAYSSGLFDWFWGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSEYWMTWVRQAPGKGLEWVSGISPSGGMTFYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDMRGAYASGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSWYWMHWVRQAPGKGLEWVSGIVSSGGTTIYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDIRGPYS SGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSPYNMHWVRQAPGKGLEWVSGISPSGGNTMYADSVKGRFTISRDD SKNTLYLQMNSLGAEATAVYYCARDIRGAYSSGHFDYWGRGTLVTSL
EVQLLESGGGLVQPGGSLRLSCAASGFTFSWYWMGWVRQAPGKGLEWVSSISPSGGYTFYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSEYWMTWVRQAPGKGLEWVSGISPSGGMTFYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSWYWMVVRQAPGKGLEWVSSIVPSGGFTIYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDLSGEYASGLFGYWGRTLVTVSS

EVQLLESGGGLVQPPGGSLRLSCAASGFTFSWYNMSWVRQAPGKGLEWVSRI SPSGD TGYADSVKGRFTISRDN SKNT LYLQMN SLRAED TAVYYCAKDIRGAYSGGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPPGGSLRLSCAASGFTFSEYWMTWVRQAPGKGLEWVSGISPSGGMTFYADSVKGRFTISRDN SKNT LYLQMN SLRAED TAVYYCARDIRGAYSSGMFD FWGRG TLVTVSS
EVQLLESGGGLVQPPGGSLRLSCAASGFTFSWYMWVVRQAPGKGLEWVSSIGPSGGDTYYADSVKGRFTISRDN SKNT LYLQMN SLRAED TAVYYCARDLSGEYASGLFGYWGRTLVTVSS
EVQLLESGGGLVQPPGGSLRLSCAASGFTFSWYMWVVRQAPGKGLEWVSSIVPSGGFTIYADSVKGRFTISRDN SKNT LYLQMN SLRAED TAVYYCAKDISGAYSSGLFTFWGRGTLVTVSS
EVQLLESGGGLVQPPGGSLRLSCAASGFTFSWYWMHWVRQAPGKGLEWVSGGVTIYADSVKGRFTISRDN SKNT LYLQMN SLRAED TAVYYCAKDIRGAYSSGLFDHWGRGTLVTVSS
EVQLLESGGGLVQPPGGSLRLSCAASGFTFSAYWMHWVRQAPGKGLEWVSGISPSGGITFYADSVKGRFTISRDN SKNT LYLQMN SLRAED TAVYYCARDIWGAYASGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPPGGSLRLSCAASGFTFSWYMWVVRQAPGKGLEWVSSIGPSGGDTYYADSVKGRFTISRDN SKNT LYLQMN SLRAED TAVYYCARDIWGAYSAGHFEYWGRGTLVTVSS
EVQLLESGGGLVQPPGGSLRLSCAASGFTFSWYWMHWVRQAPGKGLEWVSGGVTIYADSVKGRFTISRDN SKNT LYLQMN SLRAED TAVYYCARDIWGAYSAGHFEYWGRGTLVTVSS
EVQLLESGGGLVQPPGGSLRLSCAASGFTFSWYWMHWVRQAPGKGLEWVSGGVTIYADSVKGRFTISRDN SKNT LYLQMN SLRAED TAVYYCARDIRGAYSSGLFYDWGRGTLVTVSS
EVQLLESGGGLVQPPGGSLRLSCAASGFTFSPYWMSWVRQAPGKGLEWVSGISPSGGITFYADSVKGRFTISRDN SKNT LYLQMN SLRAED TAVYYCARDLSGEYASGLFGYWGRTLVTVSS
EVQLLESGGGLVQPPGGSLRLSCAASGFTFSYYGMGWVRQAPGKGLEWVSVSSSGGFTFYADSVKGRFTISRDN SKNT LYLQMN SLRAED TAVYYCAKDISGAYSSGLFTFWGRGTLVTVSS
EVQLLESGGGLVQPPGGSLRLSCAASGFTFSWYWMHWVRQAPGKGLEWVSGGVTIYADSVKGRFTISRDN SKNT LYLQMN SLRAED TAVYYCAKDIRGAYSSGLFD FWGRG TLVTVSS
EVQLLESGGGLVQPPGGSLRLSCAASGFTFSWYWMGWVRQAPGKGLEWVSSISPSGGYTFYADSVKGRFTISRDN SKNT LYLQMN SLRAED TAVYYCARDLSGEYASGLFGYWGRTLVTVSS
EVQLLESGGGLVQPPGGSLRLSCAASGFTFSPYWMHWVRQAPGKGLEWVSGISPSGGNTLYADSVKGRFTISRDN SKNT LYLQMN SLRAED TAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPPGGSLRLSCAASGFTFSWYWMHWVRQAPGKGLEWVSGGVTIYADSVKGRFTISRDN SKNT LYLQMN SLRAED TAVYYCARD FSGAYSAG LFAYWGRGTLVTVSS
EVQLLESGGGLVQPPGGSLRLSCAASGFTFSPYWMHWVRQAPGKGLEWVSGIGPSGGPTFYADSVKGRFTISRDN SKNT LYLQMN SLRAED TAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPPGGSLRLSCAASGFTFSEYWMAWVRQAPGKGLEWVSSISPSGGHTFYADSVKGRFTISRDN SKNT LYLQMN SLRAED TAVYYCAKDIRGPYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPPGGSLRLSCAASGFTFSWYMWVVRQAPGKGLEWVSSIGPSGGDTYYADSVKGRFTISRDN SKNT LYLQMN SLRAED TAVYYCAKDIRGAYSSGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPPGGSLRLSCAASGFTFSPYWMHWVRQAPGKGLEWVSGIGPSGGITFYADSVKGRFTISRDN SKNT LYLQMN SLRAED TAVYYCAKDIRGAYSSGLFD FWGRG TLVTVSS
EVQLLESGGGLVQPPGGSLRLSCAASGFTFSEYWMTWVRQAPGKGLEWVSGISPSGGMTFYADSVKGRFTISRDN SKNT LYLQMN SLRAED TAVYYCARDIWGAYSAGHFEYWGRGTLVTVSS
EVQLLESGGGLVQPPGGSLRLSCAASGFTFSPYWMSWVRQAPGKGLEWVSGGVTIYADSVKGRFTISRDN SKNT LYLQMN SLRAED TAVYYCARDLSGEYASGLFGYWGRTLVTVSS
EVQLLESGGGLVQPPGGSLRLSCAASGFTFSWYMWVVRQAPGKGLEWVSSIGPSGGDTYYADSVKGRFTISRDN SKNT LYLQMN SLRAED TAVYYCARDMRGAYASGLFDYWGRGTLVTVSS
EVQLLESGGGLVQPPGGSLRLSCAASGFTFSWYNMSWVRQAPGKGLEWVSRISPSGGDTGYADSVKGRFTISRDN SKNT LYLQMN SLRAED TAVYYCAKDIRGAYSSGLFDHWGRGTLVTVSS
EVQLLESGGGLVQPPGGSLRLSCAASGFTFSPYWMHWVRQAPGKGLEWVSGIGPSGGPTFYADSIKGRFTISRDN SKNT LYLQMN SLRAED TAVYYCAKDIRGAYSGGLFDYWGRGTLVTVSS

1. MMP12 binders

Initial Name: L-Variable (AA):

539A-M0013-A02 QDIQMTQSPGTLSSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARESGSGGTFTLTISSPLEPEDFAVYYCQQRSNWPITFGQGRLEIK

539A-M0013-A03	QDIQMTQSPSSVSASVGDRVITITCRASQSISSWLAWYQQKPKGAPKLLISTASNLQSGVPSRFSGSGTDFTLTISSLQPEDFATYYCQQVSNFPITFGQGRLEIK
539A-M0013-A11	QDIQMTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRRATGIPARFSGSGGTDFTLTISLLEPEDFAVYYCQHNEGWPWTFGQGTKVEVK
539A-M0013-B07	QDIQMTQSPSSLSASVGDRVITITCQASQDISNYLNWYQQKPKGAPKLLIYAASKLEDGVPSRFSGSGTDFTLTIRSLQPEDFASYFCQQSYSSPGITFGPGTKVEIK
539A-M0013-B08	QDIQMTQSPSSFSASTGDRVITITCRASQGISSYLAWYQQKPKGAPKLLIYAASTLQSGVPSRFSGSGGTHYTLTINSLQPEDFATYYCQQAANSFPLTFGGGTKVEIK
539A-M0013-B10	QSVLTQPPSASGTPGQRVITISCSGSSSNIGSNTVNWYQQLPGTAPKLLIYSNNQRPSPGVDRFSGSKSGTSAPIAISGLQFEDEADYYCAVWDDSLNGWVFGGTKLTVL
539A-M0013-D02	QDIQMTQSPGTLISLSPGERAALSCRASQSVSSNYLAWYQQKPGQAPRLLMYGASNRRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGRSPRTFGQGTKLEIK
539A-M0013-D04	QDIQMTQSPGILISLSPGDRATLSCRASQSVTSSSLAWYQQRPGQSPRLLIYGASSRRATGIPDRFSGSGGTDFTLTISRLEPEDFASYCQQYGGSPITFGPGTKVDIK
539A-M0013-D06	QDIQMTQSPSSVSASVGDRVITITCRASQDVGSWLAWYQQKPKGAPKLLIFAASSLESIGIPSRFSGSGGTDFTLTISSLQPEDFATYYCQQANGFPLTFGGGTKVEIK
539A-M0013-D10	QDIQMTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYSSPPITFGQGRLEIK
539A-M0013-E05	QDIQMTQSPATLSLSPGERATLSCRASQSVDHFLAWYQQKPGQAPRLLIYGATNRATGVPARENGTSGTDFTLTISLLEPEDFAVYYCQQRLNWPWTFGQGTKVEIK
539A-M0013-F07	QDIQMTQSPSSLSASVGDRVITITCRANQSIYTYLNWYQQKPKGAPPELLIYAASSLQSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQAAGIFGQGTKLEIK
539A-M0013-G04	QYELTQPPSASGTPGQTVTISCSGSTSNIGSNTVAWYQQVPGTAPKLLIHTNNQRPSPGVSDRFSGSKSVASASLAINGLQSEDEADYYCAGWDDSLNGAVFGGTKVTVL
539A-M0013-H04	QDIQMTQSPSFLSASVGDRVITITCRASQGISSYLAWYQQKPKGAPKLLIYGASTLQSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQSYTTPYTFGQGTKLEIK
539A-M0014-A09	QDIQMTQSPGTLISLSPGERATLSCRASQSVSGSYLAWYQQKPGQAPRLLIYGASSRRATGIPDRFSGSGGTDFTLTITRLEPEDFAVYYCQQYSSPRTFGQGTKVEIK
539A-M0014-B09	QDIQMTQSPSSLSASVGDRVITITCRTGQSFNFWYQQKPGTAPNLLIYLASNQSGVPSRFSGSRSGTDFTLTISSLQPEDSAIYYCQQSHSLPWTFGQGTKVEIK
539A-M0014-D11	QDIQMTQSPGTLISLSPGQRATLSCRASQTVNSNYIAWYQQRPGQAPRLLIYAASSRRATGIPDRFSGSGGTDFTLTIRSRLEPEDFAVYYCQKYGRSPQTFGQGTKVEIK
539A-M0015-G04	QSAALTQPPSTSGTPGQRVITISCSGSGSNIGSNPNWYQQLPGAAPKLLIYSNDRPSGVPDRFSGSKSGTSAISLISGLQSEDEADYYCAAWDYSLNGPWVFGGTKLTVL
539A-M0016-A02	QDIQMTQSPATLSLSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYDASNRRATGIPARFSGSGGTDFTLTISLLEPEDFAVYYCQQRSNWPPPLTFGGGTKVEIK
539A-M0016-A04	QDIQMTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRRATGIPARFSGSGGTDFTLTISLLEPEDFAVYYCQQRSNWPPPLTFGGGTKVEIK
539A-M0016-C03	QDIQMTQSPGTLISLSPGERATLSCRASQSVSSNYLAWYQQKPGQAPRLLIYGASSRRATGISDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGTSPETFGGGTKVEIK
539A-M0016-C10	QDIQMTQSPSSLSASVGDRVITITCRASQGISNYLAWYQQKPKGVKPKLLIYAASTLQSGVPSRFSGSGGTDFTLTISSLQPEDVATYYCQKYNSAPFTFGPGTKVDIK
539A-M0016-D07	QYELTQPPSVSVSPGQTASITCSGDKLGDKYASWYQQKPGQSPVLVYHDTRRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDDITAVVFGGTKLTVL
539A-M0016-F03	QSELTQPRSVSGSPGQSVTISCTGTSNDVGEYNYVSWYQQHPGKAPKVMIIYDVTRRPSGVPDRFSGSKSGNTASLTISGLQADDEAHYYCCSYAGRYTYVFGSGTNTVTVL
539A-M0016-H09	QDIQMTQSPGTLISLSSGERATLSCRASQSVSSNYLAWYQQKRGQAPRLLIYGASSRRATGVPGRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGSSPRTFGQGTKLEIK
539A-M0018-A05	QDIQMTQSPLSLPVTPGEPASISCRSSQSLLSHNGYNLDWYLOKPGQSPQLLIYLGSNRASGVPDRFSGSGGTDFTLKISRVEADVGVIYCMQALQTPYTFGQGTKLEIK
539A-M0018-D01	QDIQMTQSPSSLSASVGDRVITITCRASQSIISIYNWYQQKAGKAPKLLIYAASNLIQSGVPSRFSGSGGTDFTLTISSLQPEDFATYYFCQQSYLPPPLTFGGGTTVEIK
539A-M0019-A10	QDIQMTQSPSSLSASVGDRVITIACRASRGITTAIGWYQQKSGTTPKLLIYDASYLDSGVPSRFSGSGGTDFTLTINSVQPEDFATYYCQQFMTYPQGISFGQGRLEIK
539A-M0019-C07	QSELTQPASVSGSPGQSITISCTGTSSDIGDYVSWYQQYPGKAPKLMIIYHVSNNRPSGVSTRFSGSKSANTASLTISGLQAEDEADYYCSSYTSSTSYVFGTGTKTVTVL
539A-M0019-G07	QDIQMTQSPSSLSASVGDRVITITCRASQSIISTKLNWYQQKPKGAPNLLIYDTSTLQSGVPSRFSGSGGTDFTLTISSLQLEDFASYCQQTYGALTWTFGQGTKVEIK
539A-M0019-G10	QDIQMTQSPGTLISLSPGERATLSCRASQSVSSSYAAWYQKPGQAPRLLIYGVSRRRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQFGSSPRTFGQGTKVEIK
539A-M0020-C08	QDIQMTQSPDLSASVGDRVITITCRASQSISSYLNWYQQKPKGAPKLLIYAASSLQSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQSYSSPGITFGPGTKVEIK
539A-M0020-H02	QDIQMTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYSSSIALTFGGGTKVEIK

539A-M0021-B03	QDIQMTQSPSSLSASVGDVRTITICRASQSISSGLNWYQQKPGKAPKLLIYAASILQSGVPSRFSGSGTDFTLTIISSLQPEDFATYYCQQNYDLFGGLTFGPGTKVDVK
539A-M0021-D06	QDIQMTQSPSSLSASVGDVRTITICRTSQDFSNLAWYQQRPGKAPKLLIYAASTLQSGVPSRFSGSGTDFTLTIISSLQPEDVATYYCQRYDNGPLFGPGTKVHVK
539A-M0021-E12	QDIQMTQSPGTLSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSGTEFTLTIISSLQSEDFAVYYCQLYKTFGGGTKVEIK
539A-M0021-G07	QDIQMTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGSSPRTFGQGTKLEIK
539A-M0022-A02	QDIQMTQSPSSLSASVGDVRTITICRASQSISSYLNWYQQKPGKAPKLLIYAASSLIQIGVPSRFSGSGTDFTLTIISSLQPEDFATYYCQQSYITPLTFGPGTKVDIK
539A-M0023-B11	QDIQMTQSPSSLSASVGDVRTITICRANQIGISNYLAWFQQKPGKAPKSLIYAASSLQSGVPSKFSGSGTDFTLTIISSLQPEDSATYYCQQYNSFPLTFGGGTKVEIK
539A-M0023-D03	QDIQMTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASYRATGIPARFGSGSGTDFTLTIISSLEPEDFALYYCQQRSDWPRTFGQGTKLEIK
539A-M0023-D05	QSAALTQPASVSGSPGQSIITISCTGTSSDVGGYVSWYQQHHPGKAPKLLIYDVSNRP SGVSNRFSGSKSGNTASLTISGLQAEDEADYYCSSYTSSSTLADVFGGTKLTVL
539A-M0023-E09	QSELTQPPSVSGSPRQSVTISCTGTTSDIGGYNHVSWYQHHHPGKAPQLLIYDVTRRPSGVPDRFSASKSGNTASLTISGLQAEDEAVYYCSSYGSYFHFVFGTGTQVTVL
539A-M0023-H01	QDIQMTQSPGTLSPGETATLSCWASQSVAWYQQKPGQPPRLLIYDVSTRATGIPDRFSGSGSGTGSTLTISRLEPEDFAVYFCQQYGYSPLSFDDGGTKVEIKRTVAAP
539A-M0024-C02	QSELTQDPAVSVALGQTVRITCRGDRLRTYYSSWYQQKPRQAPVLMFGRNNRPSGIPDRFSGSTSGGTASLTITATQADDEADYFCSSRDGSGNFLFGGGTKLTVL
539A-M0025-F02	QDIQMTQSPLSLSASVGDVRTITICRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIISSLQPEDFATYYCQQSYSTPYTFGQGTKLEIK
539A-M0025-G01	QSELTQPASVSGSPGQSVTISCSGISYDLDYIYVSWYQQHPDKAPQLLLYDVVDKRP SGISDRFSGSKSGDTASLTISGLRTDDEAEYYCSSFTRTTTVVFGTGTQVTVL
539A-M0025-H03	QDIQMTQSPSSLSASVGDVRTITICRASQSISSYLNWYQQKPGKAPKLLIYAASKLEDGVPSRFSGSGTGTDFTLTIRSLQPEDFASYFCQQSYSSPGITTFGPGTKVEIK
539A-M0025-H11	QDIQMTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDIAVYYCQQYGSSAWTFGQGTKVEIK
539A-M0026-A01	QDIQMTQSPSSLSASVGDVITIICRASQININIYLNWYQQKPGKAPKLLISAASSLQSGVPSRFSGSGSGTDFTLTITDLQPEDLATYYCQQYTSA PPPWTFGPGTKVDIK
539A-M0026-A05	QDIQMTQSPATLSLSPGERATLSCRASQSVSYRLAWYQQKPGQAPRLLIYGASSRVHGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGGSP TTFGGGTKVEIK
539A-M0026-A09	QDIQMTQSPSLPVLGQPASISCRSSQSLVYINGNTYLNWFQRPQGQSPRRLIYNVSNRDSGVPERFSGSGSGTDFTLKISRVEADVGVIYCMQTHWPPAFGQGTKVEIK
539A-M0026-A10	QDIQMTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPMYTFGQGTKLEIK
539A-M0026-B11	QDIQMTQSPSSLSASVGDRTVITICRASQSIDTYLNWYQQKPGKAPKLLIYAASKLEDGVPSRFSGSGTGTDFTLTIRSLQPEDFASYFCQQSYSSPGITTFGPGTKVEIK
539A-M0026-C03	QSAALTQPASVSGSPGQSIITISCTGTSTDVGGYKYVSWYQQHHPGKAPKLLIYEVSNRP SGVSNRFSGSKSGNTASLTISGLQAEDEADYYCSSYTSSTTVVFGGTKLTVL
539A-M0026-C07	QSELTQPPSASGTPGQRVTISCSGSSSNIGTNTVNWYQQLPGMAPKVVM SANNERPSGVPDRFSGSKTGTSASLAI SGLQSEDEADYYCAAWDENLSGPVFGTGTQVTVL
539A-M0026-E01	QDIQMTQSPATLSLSPGERATLSCRASQNVYSRLAWYQQKPGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFALYYCQQYGSSPRTFGQGTKLEIR
539A-M0026-E11	QDIQMTQSPGTLSPGERATLSCRASQTISSNQLAWYQQQKPGQAPRLLVYGAFSTATGIPDRFIGGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGGGTKVEIK
539A-M0026-F03	QDIQMTQSPGTLSPGESATLSCRASHSVDRLYLAWYQQKPGQAPRLLIYGTSSRATGIPDRVSGSGSGTDFTLTISRLEREDSAVYYCQHYGSLWTFGQGTKVEIK
539A-M0026-F04	QDIQMTQSPSSLSASVGDVRTITICRASQRIASYNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTVSSLQPEDFATYYCQQSYSAPI TTFGGGTKVEIK
539A-M0026-G12	QDIQMTQSPSSLSASVGDVRTITICRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIISSLQPEDFATYYCQSGLTFGGGTKVEIK
539A-M0026-H05	QDIQMTQSPSSLSASVGDVRTITICRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIISSLQPEDFATYYCQQSYSTPYTFGQGTKLEIK
539A-M0027-A08	QSVLTQPASVSGSPGQSIITISCTGTSTDVGGYVSWYQKHHPGKAPKLLIYDVSNRP SGVSNRFSGSKSGNTASLTISGLQAEDEADYYCSSYTNITTVVFGGTKLTVL
539A-M0027-B03	QDIQMTQSPSSLSASVGDVRTITICRASQGI RNDLGWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGFGTDFTLTIISSLQPEDFATYYCLQDYRYPLTFGGGTKVEIK
539A-M0027-B08	QDIQMTQSPSSLSASVGDRTVITICRASQSIDTYLNWYQQKPGKAPKLLIYAASKLEDGVPSRFSGSGTGTDFTLTIRSLQPEDFASYFCQQSYSSPGITTFGPGTKVEIK
539A-M0027-C07	QDIQMTQSPSSLSASVGDVRTITICRASQSISSYLNWYQQKPGKAPKLLIYAASKLEDGVPSRFSGSGTGTDFTLTINSLQPEDFATYYCQQSYNTPSFGPGTRVDVK

539A-M0027-G02	QDIQMTQSPATLSASVGDRVITITCRASQRISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGTDFTLTIISSLQPEDFATYYCQQSYSTPRTFGQGTKVEIK
539A-M0027-H04	QDIQMTQSPSSLSASVGDRVITITCRASQDISSWLWYQQKPGKAPKVLIIYAASSLQSGIPSRFSGSGTDFTLTIISSLQPEDFATYYCQQANRFPPLTFGGGTKVEIK
539A-M0028-E09	QDIQMTQSPATLSVSPGERATLSCRASQSVSSSLAWYQQKPGQAPRLLISETSNRATAIPAKFSGSGFGTDFTLTIISSLEPEDSAVYYCQQHVSWPPLTFGGGTKVEIK
539A-M0028-F04	QSALTQPPSVSGAPGQTVTISCTGTSSNIGTGAVHWYQHLPGKAPKPLFSGDDNRPSPGVPDRFSASKSGTSASLAIARLQTEDEADYYCESYDKLGWVFGGGTKLTVL

MMP-12 Binders (these are in the same order as the light chain sequences provided above)

H-Variable (AA):	
EVQLLESGGGLVQPGGSLRLSCAASGFTFSYYKMHWVRQAPGKGLEWVSWIGPSGGITDYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTDDDISDYYGMDVWGQGT	TVT
EVQLLESGGGLVQPGGSLRLSCAASGFTFSWYPMNWVRQAPGKGLEWVSVIWPSSGGETAYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTTGRFYGYRDFDYWGQGT	LV
EVQLLESGGGLVQPGGSLRLSCAASGFTFSWYDMLWVRQAPGKGLEWVSYISPSGGYTLYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTTVPPTYCYSGGSCYRDAFDIWGQGT	MT
EVQLLESGGGLVQPGGSLRLSCAASGFTFSYYPMYWVRQAPGKGLEWVSVIGSSGGNTSYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAGAHYDEWSDYYGPDAFDIWGQGT	MT
EVQLLESGGGLVQPGGSLRLSCAASGFTFSWYLMGWVRQAPGKGLEWVSSIYPSSGITNYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGGGADAFDIWGQGT	MT
EVQLLESGGGLVQPGGSLRLSCAASGFTFSRYHMTWVRQAPGKGLEWVSSI	SPSGGPTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGVRSYYDFWSGYSLSLYYYYYYGM
EVQLLESGGGLVQPGGSLRLSCAASGFTFSGYNMVWVRQAPGKGLEWVSI	VSSGGLTDYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGLYYDYDSSSGYYYGGAFDIWGQGT
EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYQMWVRQAPGKGLEWVSGI	SSSGGATGYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRVPHYDSSGYGGGLVDYWGQGT
EVQLLESGGGLVQPGGSLRLSCAASGFTFSRYLMHWVRQAPGKGLEWVSSI	SSSGGETDYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAHGAPLGDYYYYYGM
EVQLLESGGGLVQPGGSLRLSCAASGFTFSRYGMTWVRQAPGKGLEWVSGI	SPSGGNTWYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTSHDYG
EVQLLESGGGLVQPGGSLRLSCAASGFTFSGYDMKWVRQAPGKGLEWVS	YISSSGGPTVYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATELYDSSGYLSLWGQGT
EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYNMHWVRQAPGKGLEWVS	YIGPSGGYTHYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDIRGAYSSG
EVQLLESGGGLVQPGGSLRLSCAASGFTFSQYPMVWVRQAPGKGLEWVSI	YPSGGYTIYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGGGNF
EVQLLESGGGLVQPGGSLRLSCAASGFTFSWYNMFVRQAPGKGLEWVS	YISPSGGPTDYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCASEYRGNYYGMDV
EVQLLESGGGLVQPGGSLRLSCAASGFTFSMYMMWVRQAPGKGLEWVS	GIYPSGGPTGYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAMYYCASNDYGY
EVQLLESGGGLVQPGGSLRLSCAASGFTFSYYHMHWVRQAPGKGLEWVS	GIGPSGGMTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARFNYY
EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYQMDWVRQAPGKGLEWVS	GISSGGNTQYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCASQDYGR
EVQLLESGGGLVQPGGSLRLSCAASGFTFSVYPMQWVRQAPGKGLEWVS	GISSGGFTMYADSVKGRFTISRDN SKNTLYLQMNSLRAEDMAVYYCARGGDS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSWYEMTWVRQAPGKGLEWVS	YIGPSGGRTVYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCALVSQGE
EVQLLESGGGLVQPGGSLRLSCAASGFTFSYLLMNWVRQAPGKGLEWVSI	GSSGGFTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTATYYCASNDYGY
EVQLLESGGGLVQPGGSLRLSCAASGFTFSRYNMVWVRQAPGKGLEWVSI	SSSGGRTKYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCVTIDLGY
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYDMTWVRQAPGKGLEWVS	GIVSSGGLTAYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKFNA
EVQLLESGGGLVQPGGSLRLSCAASGFTFSYYQMNWVRQAPGKGLEWVS	VISPSGGITIIYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATANGYD
EVQLLESGGGLVQPGGSLRLSCAASGFTFSWYGMTWVRQAPGKGLEWVS	RIYSSGGQTMYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREAG

EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYWMHWVRQAPGKGLEWVSSISSSGGMTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTTADYGYYYGMDVWVGQGTTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSLYWMKWVRQAPGKGLEWVSGISPSGGPTDYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTATYYCATGDTLLWFGE LTDYWGQGTTLTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSKYNMMWVRQAPGKGLEWVSYIWSSGGDTLYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARVGYGGGPLYYYYYMDVWVGKGTTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTTFSFYWMAWVRQAPGKGLEWVSSISGPSGGATDYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARTNYIDRGGSFDIWGQGTMTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTTFSQYDMQWVRQAPGKGLEWVSRIGPSGGNTGYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAMYYCARINVIYDSSGGYYGMDVWVGQGTTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTTFSHYSMSWVRQAPGKGLEWVSVIYPSGGETDYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRDQGV DGYDYFYFYIYGMVWVGQGTTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTTFSWYMMWVRQAPGKGLEWVSSIRPSGGFTKYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAVGWKGISTGLDYIYIYMDVWVGKGTTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTTFSAYEMIWVRQAPGKGLEWVSYIYSSGGWTSYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTATYYCARRGLHYDSSGGYLG DYFDYWGQGTTLTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTTSSSYHMDWVRQAPGKGLEWVSSISSSGGDTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGLNYYDSNDYYEVPYIYIYGMVWVGQGTTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTTSEYAMVWVRQAPGKGLEWVSSIIVPSGGTTQYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARVNVHYDILTGYAYIYIYGMVWVGQGTTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTTFSQYADYVWVRQAPGKGLEWVSSISGSSGGFTQYADYVWVRQAPGKGLEWVSSISGSSGGFTQYADYVWVRQAPGKGLEWVSSISGSSGGFTTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTTFSAYEMIWVRQAPGKGLEWVSYIYSSGGWTSYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTATYYCARRGLHYDSSGGYLG DYFDYWGQGTTLTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTTFSHYTMDWVRQAPGKGLEWVSSISGPSGGITGYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTATYYCATSSG WYWDYFDYWGQGTTLTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTTFSKYMMHWVRQAPGKGLEWVSWIWPSSGGVTMYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARWGHYGGNDYWGQGTTLTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTTFSFYSMGWVRQAPGKGLEWVSSISSSGGYTDYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREFSSWYSYMDVWVGKGTTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTTFSRYHMSWVRQAPGKGLEWVSSIRSSSGSTPYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGPQLSTFDI WGQGTMTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTTFSKYEMIWVRQAPGKGLEWVSSIIVPSGGHTQYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGFYGDYDYIYIYGMVWVGQGTTVTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTTFSWYEMYWVRQAPGKGLEWVSWIGPSGGFTHYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTALYYCATRGYSYDFEGWYFDLWGRGTLTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTTFSQYKMQWVRQAPGKGLEWVSVISSSGGHTAYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARETYIYDSSGGYGGAFDIWGQGTMTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTTFSNYMMLWVRQAPGKGLEWVSSIWSSGGYTEYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGDMTTVVRNAFDI WGQGTMTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTTFSGYGMMWVRQAPGKGLEWVSSISGSSGGFTVYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAMYYCARGYHYDSSGGYIYGF EAFDIWGQGTMTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTTFSGYDMAWVRQAPGKGLEWVSSISGPSGGTMYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAMYYCARRMESYIYD YWGQGTTLTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTTFSYDMRWVRQAPGKGLEWVSSIISPSGGVTTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTTDELSWDGDPYYMDVWVGKGTTVTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTTFSVYDMIWVRQAPGKGLEWVSYIISSSGGGTEYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGGSYYETAFDI WGQGTMTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTTFSNYVMSWVRQAPGKGLEWVSSISGSSGGETAYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATVYSYD NSGRLLYSFYSFYSWGQGTTLTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTTFSYNNMMWVRQAPGKGLEWVSSIISSSGGGTDYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRIGQWSSGGYIYFDYWGQGTTLTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTTFSYIYMMWVRQAPGKGLEWVSSISGSSGGDTLYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARVIDSWATAFDI WGQGTMTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTTSEYQMGWVRQAPGKGLEWVSSIIVPSGGLTKYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGSGYKDSHF DYWGQGTTLTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTTFSAYEMIWVRQAPGKGLEWVSYIYSSGGWTSYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTATYYCARRGLHYDSSGGYLG DYFDYWGQGTTLTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTTFSIYEMEWVRQAPGKGLEWVSIVPSGGGTDYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTATYYCARVRWDDFWTGYIYGMVWVGQGTTVTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTTFSNYAMQWVRQAPGKGLEWVSSIWPSGGLTDYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREGISYDAFDI WGQGTMTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTTFSQYTMWVRQAPGKGLEWVSGIYSSGGGTHYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGGSSWYFGDAFDI WGQGTMTVTVSS

EVQLLESGGGLVQPGGSLRLSCAASGFTFSAYAMYVVRQAPGKGLEWVSGISPSGGGTEYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREAHYYDSSGYYSGAFDIWGQGTMTVTSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSLYYMWVRQAPGKGLEWVSGIYPSGGVTSYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTTANGYYDSSGYYYKDAFDIWGQGTMTVTSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSAYEMRWVRQAPGKGLEWVSRIGPSGGNTQYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTAADYGDYYGMDVWVGQGTTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSMYDMGWVRQAPGKGLEWVSYIGSSGGMTTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARMESYYDSYDIWGQGTTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMMWVRQAPGKGLEWVSYISPSGGTTSYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAHSWGSREDFPWGQGTTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSYYQMMWVRQAPGKGLEWVSSIGPSGLTEYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDGATYYDFWDYWGQGTTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSPYAMYVVRQAPGKGLEWVSSIWPSGGSTNYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARESEIDAFDIWGQGTMTVTSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSAYEMIWVRQAPGKGLEWVSYIYSSGGWTSYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTATYYCARRGLHYDSSGYYLGDYFDYWGQGTTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSWYYMAWVRQAPGKGLEWVSVIGPSGGDTKYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTRVSPLDYYDSSGYYPFYYYYYGMDVWVGQGTTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSAYEMIWVRQAPGKGLEWVSYIYSSGGWTSYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTATYYCARRGLHYDSSGYYLGDYFDYWGQGTTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSFYGMGWVRQAPGKGLEWVSWISSGGDTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDRDNDNDAADYWGQGTTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSLYPMSWVRQAPGKGLEWVSSISSGGHTKYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCALYSYYGMDVWVGQGTTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSVYGMNWVRQAPGKGLEWVSYISPSGGTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARGGYYSNSLDFYYYYYYGMDVWVGQGTTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMQWVRQAPGKGLEWVSYIGPSGGETGYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDLRGNYYDSSGYTDAFDIWGQGTMTVTVSS

2. MMP12 inhibitors	
539A-M0013-D11	QDIQMTQSPSSLSASVGDRIITISCGASQDIDNLYNWYQQRSGKAPKLLIYDAYNLKAGVPSRFRGSRSGTDFFLTISSLQPEDFATYYCQQSYRAPLTFGGGTKVEIK
539A-M0013-G12	QDIQMTQSPSSLSASVGDRTITCQASQDITYNRLHWYQKPGKAPKLLIYDAVNLNRGVPSRFRGSGSGTNYILIIITNLQPEDTATYYCQHSDDLSLAFGGGTKVEIK
539A-M0013-H06	QDIQMTQSPATLSLSPGERATLSCRASHSVDNLAWYQQQPGQAPRLLIYDVSYRATGIPARFSGSGSGTDFTLTISLLEPEDFAVYYCQQRNNWPLSLTFGGGTKVEIK
539A-M0014-C09	QDIQMTQSPATLSLSPGERATLSCGASONIDGYLAWYQQKPGQAPSLIIYDASSRSTGVPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQHYGNSLWTFGGGTKVEIK
539A-M0016-A11	QYELTQPPSASGTPGQRIITISCSGSSSNI GSNPVQWYQQLPGSAPKLLIHTNTHRPSGVDPDRFSGSKSVTSASLAISGLQSEDEAEYYCATWDDSLNGGVFGGGTKLTVL
539A-M0016-H05	QDIQMTQSPSSLSASVRDRVTITCRTSQNINTYLNWYYQAPGRAPKLLIFGVSSLHRGVSSRFRSGSGDGTETFTLTISSLQPEDDIGTYFCQQSYSSPWTFGGQTKVEIK
539A-M0019-C05	QDIQMTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASN RATGIPARFSGSGSGTDFTLTLTISLLEPEDFAVYYCQQRSNWPLTFGGGTKVEIK
539A-M0020-B01	QYELTQPRSVSGSPGQSVTISCTGSSSDVAGFYVSWYQQHPGKAPKLMIRDVNDRPSGVSNRFSGSKSGNTASLTIIAGLQTEDEAVYYCSSTSRSDTRVIFGGGTKLTV
539A-M0022-C07	QYELTQPPSVSVAPGQTATITCEGNNIASKSVHWYQQKPGQAPVLVYDDRRDRPSGISERISGSNSGNTPTLTIFRVEAGDEADYYCQVSDSATDHRVFGGGTKLTVL
539A-M0025-	QDIQMTQSPATLSVSPGERATLSCRASQNVNRNYLAWYQQKPGQAPRLLIYDASKRATGIPARFSGSGSGTDFTLTISGLEPEDFAVYYCQQRSNWPTTFPGTKVDIK
	QDIQMTQSPGTLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGSLLTFGGGTKVEIK

D04	
539A-M0027-E11	QDIQMTQSPDTLSLSPGERGTLSCRASQSLSSYLAWYQKPGQAPRLLIYDASSRATGIPDRFSGSGGTDFTLTIIGRLPEDSAVYICQQYGSFPLTFGGGTKVEIK

2. MMP12 Inhibitors Heavy Chain Sequences (provided in the same roder as the light chains provided above)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYPMMWVRQAPGKGLEWVSGIVPSGGVTIYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYICARVGLASSDYYYYYMDVWGKGTITVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSWHMFVVRQAPGKGLEWVSGIVPSGGVTIYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYICATREGMLYDVWGENYMDVWGKGTITVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSAYEMDWVRQAPGKGLEWVSGIVPSGGVTIYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYICARVGGWELLQDYIIYMDVWGKGTITVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYSMHVVRQAPGKGLEWVSGIVPSGGVTIYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYICARGEYSSSDYYYYYGMDVWGQGTITVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSWVVMVVRQAPGKGLEWVSSIYSSGGPTKYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYICAKEGGVYGGPELYIIYYGMDVWGQGTITVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSEYQMAWVRQAPGKGLEWVSSIYPSGGHTHYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYICAKESYYDFWSGGYFDYWGQGTITVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSWYAMSWVRQAPGKGLEWVSRIVPSGGDTGYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYICATFRGIMYGDYGSYYWYFDLWGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSWYAMVVVRQAPGKGLEWVSYIGSSGGVTGYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYICARQKRDYDSSSGYPTNAEFDWGQGTITVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYVMHVVRQAPGKGLEWVSYIGSSGGETRYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYICARADYGDYDIIYYGMDVWGQGTITVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSIYQMWVVRQAPGKGLEWVSSISSSGFTWYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYICTTEDIGYIIYGMDVWGQGTITVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGMHVVRQAPGKGLEWVSGIVSSGGSTIYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYICTTYDYG DHYGMDVWGQGTITVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYEMEVVRQAPGKGLEWVSSISSSGPTMYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYICARGMYG DYDFYIIYYGMDVWGQGTITVTVSS

1. MMP-12 Inhibitors-Light Chain

Initial Name	LV-FR1	LV-CDR1	LV-FR2	LV-CDR2	LV-FR3	LV-CDR3	LV-FR4	L-Constant
539B-M0035-C05	QSELTQPASVSGSPGQSIITISC	TGTSSDVGGNYLS	WYQQHPGKAPKLMIIY	EVTNRPS	GVSNRFSGSKSGNTASLTISGLQA	SSYTSTTTLL	FGGGTKLTVL	GQPKAAP
539B-M0040-A02	QDIQMTQSPATLSLSPGERATLISC	RASQSVSSSYLA	WYQQKPGQAPRLLIY	GASSRAT	GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC	QQYGS SPLT		RTVAAPS
539B-M0041-G04	QYELTQPASVSGSPGQSIITISC	TGTSSDVGGNYVS	WYQQHPGKAPKLMIIY	EVSNRPS	GVSNRFSGSKSGNTASLTISGLQA	SSYTSSTTLFR	FGGGTKLTVL	GQPKAAP
539B-M0007-	QDIQMTQSPSSLSASVGDRTITC	RASQRIASYIN	WYQQKPGKAPKLLIY	AASSLQS	GVPSRFSGSGSGTDFTLTIVSSSLQP	QQSYSAPLT	FGGGTKVEIK	RTVAAPS

[illegible]

F01									
539B-M0030-A10	QSELTQPASVSGS PGQITISC	TGTSSDVGAYNYVS	WYQQHPGKVPKLLMIY	EVSNRPS		GVSNRFSGSKSGNTASLTISGLQA EDEADYYC	NSYTTSATLV	FGGGTKLTVL	SQPKAAP
539B-M0052-E10	QDIQMTQSPLSLP VTPGEPASISC		WYLQKPGQSPQLLLIY	LGSNRAS		GVPDRFSGSGSGTDFTLKISRVEA EDVGVYYC	MQALQTPLT	FGGGTKVEIK	RTVAAPS
539B-M0040-A03	QYELTQPASVSGS PGQITISC	TGTSSDIGGNFVS	WYQQHPGRAPKLLTIY	EVNNRPS		GVSNRFSGSKSGNTASLTISGLQA EDEADYYC	SSYTPSSTLV	FGTGKVTVL	RQPKANP
539B-M0040-B05	QSVLTQPPSVSVA PGQTARITC	GGNNIGSKTVN	WYQQKTQQAPVLV VH	DDSDRPS		GIPERLSGSNSGNTATLTISRVEA GDEADYYC	QVWDSGTDHYV	FGTGKVTVL	GQPKANP
539B-M0041-G01	QDIQMTQSPSSL ASVGDRVITIC	RASQISYFLN	WYQQKPGKAPKLLLIY	AASTLQG		GVPDRFSGSGSGTDFTLTISSLQP EDFATYYC	QHSYSTPPIT	FGPGTKVDIK	RTVAAPS
539B-M0038-H04	QSELTQPHSVSES PGTTVTISC	TSSSGNIASNYVQ	WYQQRNPNSAPTIVIIY	AYNRRPS		GVPDRFSGSIDSSSNSASLTVSGL KTEDEADYYC	QSYDNINRLWV	FGGGTKLTVL	GQPKAAP
539B-M0032-H09	QDIQMTQSPSTLS ASVGDRVITIC	RASQSISSWIA	WYQQKPGKAPKLLLIY	DASSLES		GVPDRFSGSGSGTEFTLTISSLQP EDIGTYIC	QQYDHLPT	FGGGTKVQVK	RTVAAPS

1. MMP-12 Inhibitors –Heavy Chain Variable Sequences (provided in the same order as the Light Chains provided above)

	HV-FR1	HV-CDR1	HV-FR2	HV-CDR2	HV-FR3	HV-CDR3	HV-FR4
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYPMI	WVRQAPGKGLEWVS	SISSSGAYTHYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAR	EGVDTAMAFGY	WGQGTILVTVSS	
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	DYGMN	WVRQAPGKGLEWVS	SISPSGGDTHYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAR	WEAKVDAFDI	WGQGTITVTVSS	
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	DYPMS	WVRQAPGKGLEWVS	SISSSGGST EYADSVKG	RFNISRDN SKNTLYLQMN SLRAEDTAMYYCAR	HPDGVARFDP	WGQGTILVTVSS	
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	EYAMR	WVRQAPGKGLEWVS	SISPSGGSTWYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAR	RGWAAAGY YYGMDV	WGQGTITVTVSS	
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	EYNMH	WVRQAPGKGLEWVS	SISPSGGNTRYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAR	DGVSKWYYHGIDV	WGQGTITVTVSS	
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	EYNMN	WVRQAPGKGLEWVS	GISSSGGQTM YADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAR	GVAYDSKTPDI	WGRGTMVTVSS	
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	EYPMY	WVRQAPGKGLEWVS	VIYPSGGWTDYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAR	MAVTGGSRFDY	WGQGTILVTVSS	
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	FYAMT	WVRQAPGKGLEWVS	RIVPSGGDTMYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAR	DLGDYDFWSGTL YYGMDV	WGQGTITVTVSS	
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	HYWMH	WVRQAPGKGLEWVS	SISSSGGMTYYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCTT	ADYGYYYGMDV	WGQGTITVTVSS	
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	IYMMG	WVRQAPGKGLEWVS	SISPSGGWTRYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCTT	APYPNWNHYHYFDY	WGQGTILVTVSS	
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	KYPMV	WVRQAPGKGLEWVS	SIGPSGGVTAYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAMYYCAR	HSRDIADVY	WGQGTILVTVSS	

EVQLLESGGGLVQPGGSLRLSCAASGFTFS	MYAMV	WVRQAPGKGLEWVS	SISPSGGLTDYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAN	PWPLTAEELADI	WGQGTMTVTSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	MYPMN	WVRQAPGKGLEWVS	RIVSSGGTTHYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCTT	GDYSWDY	WGQGTTLVTSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	PYDMT	WVRQAPGKGLEWVS	GIVPSGGFTSYADSVKG	RFTISRDN SKNTLYLQMN SLRVEDTAVYYCAR	RGVVGGLDY	WGQGTTLVTSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	PYIMK	WVRQAPGKGLEWVS	YISSGGITMYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAA	ENRVPFDY	WGQGTTLVTSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	PYSMG	WVRQAPGKGLEWVS	GIGPSGGYTTYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAR	HPVGYDAFDI	WGQGTMTVTSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	RYGML	WVRQAPGKGLEWVS	VIYPSGGPTLYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAR	DGVLRGSHIYFDY	WGQGTTLVTSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	RYTMG	WVRQAPGKGLEWVS	RIYSSGGNTVYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAR	TRRDGYNPFDY	WGQGTTLVTSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	RYWMD	WVRQAPGKGLEWVS	GIYPSGGYTLYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAR	HGDYMDV	WGKGTTLVTSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	TYPMS	WVRQAPGKGLEWVS	SISPSGGWTRYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAS	SPYGPDAFDI	WGQGTMTVTSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYKMG	WVRQAPGKGLEWVS	GISSSGGLTFYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAR	VPAYSSGYGGFDY	WGQGTTLVTSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYPMI	WVRQAPGKGLEWVS	SISSSGGYTHYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAR	EGVDTAMAFGY	WGQGTTLVTSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	YYEME	WVRQAPGKGLEWVS	GIYPSGGITTYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAR	VFFYYDSSGYYPYFDY	WGQGTTLVTSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	YYPMA	WVRQAPGKGLEWVS	YISSSGGLTTYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAR	SPTYDFWSGYWAGIFDY	WGQGTTLVTSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	YYPMV	WVRQAPGKGLEWVS	VIYPSGGYTHYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAMYYCAR	VGYDSSGYWGYFDY	WGQGTTLVTSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFV	YHMQ	WVRQAPGKGLEWVS	GISPSGGLTDYADSVKG	RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAH	GTDPLTY	WGQGTTLVTSS

2. MMP-12 Inhibitors-Light Chain Variable region

Initial Name	LV-FR1	LV-CDR1	LV-FR2		LV-CDR2	LV-FR3	LV-CDR3	LV-FR4	L-Constant
539B-M0034-C04	QDIQMTQSPSSLSASVGD RVSITC	RASQNINSYLN	WYQQKVKGAPKLLIF		GAYTLHS	GAPSRFSGSGGTDFTLTISSLQPEDVATYYC	QQTYTSYS	FAQGTKLEIK	AAPSVFI
539B-M0039-F01	QNIQMTQSPSSVSASVGD RVTITC	RASQDINYWLA	WYQQKPGKAPKLLIY		AASSLQS	GVPSRFSGSGGTDFTLTISSLQPEDFATYYC	QRANSFPYT	FGQGTKLEIK	RTVAAPS
539B-M0041-B05	QDIQMTQSPSSLSASVGD RVSITC	RASQNINSYLN	WYQQKVKGAPKLLIF		GAYTLHS	GAPSRFSGSGGTDFTLTISSLQPEDVATYYC	QQTYTSYS	FAQGTKLEIK	AAPSVFI
539B-M0041-G01	QDIQMTQSPSSLSASVGD RVTITC	RASQISISYFLN	WYQQKPGKAPKLLIY		AASTLQG	GVPSRFRSGSGGTDFTLTISSLQPEDFATYYC	QHSYSTPPIT	FGPGTKVDIK	RTVAAPS
539B-M0042-B06	QDIQMTQSPDTLSLSPGE RATLSC	RASQTISSTFLA	WYQQKPGQAPRLLIY		GASTRAA	GIPDRFIGSGSGTDFTLTISSELEPEDSAVYYC	QQYDRSPT	FGGGTKVEIK	RTVAAPS
539B-M0006-B10	QDIQMTQSPGTLSLSPGE RATLSC	RASQSVSSSYLA	WYQQKPGQAPRLLIY		GASSRAT	GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC	QQYGSSPRT	FGQGTKLEIK	RTVAAPS
539B-M0007-H06	QDIQMTQSPGTLSSLGGE RATLSC	RASQSVSSNYLA	WYQQKRGQAPRLLIY		GASSRAT	GVPGRFSGSGSGTDFTLTISRLEPEDFAVYYC	QQYGSSPRT	FGQGTKLEIK	RTVAAPS
539B-M0008-H09	QDIQMTQSPSSLSASVGD RVTITC	RANQSIYTYLN	WYQQKPGKAPELLIY		AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQAGI	FGQGTKLEIK	RTVAAPS
539B-M0009-H08	QVELTPPALSVAPGETA TITC	GGDKIGRKSVN	WYQQKAGQAPVLVIF		YDNDRPS	GITGRFSGSNSGNSATLTISRVEAGDEADFYC	QVWGNDFPL	FGGGTKLTVL	GQPKAAP

539B-M0011-H11	QSALTQPPSVSVAPGQTA RITC	GGNNIGTKSVH	WYQQKSGQAPVLVVY	DNSDRPS	GIPERFSGSNSGNTATLTISRVEAGDEADYYC	QVWDNSIDHVV	FGGGTKLTVL	GQPKAAP
539B-M0015-F02	QDIQMTQSPGTLISLSPGE RATLSC	RASQSVSSSYLA	WYQQKPGQAPRLLIY	GASSRAT	GIPDRFSGSGGTDFTLTISRLEPEDFAVYYC	QQYGSPPIT	FGQGTRLEIK	RTVAAPS
539B-M0016-D01	QSELTQPPSVSVSPGQTA TITC	SGDVSVHKSEC	WYQQRPGQSPVLVIY	QIDKRPS	GVPERFSGSISGTTATLTISGTQATDEADYYC	QGWDSTIYYV	FGTGTKVTVL	SQPKANP

1. MMP-12 Inhibitors Heavy Chain Variable Region Sequences (in the same order as the light chains provided above)

HV-FR1	HV- CDR1	HV-FR2	HV-CDR2	HV-FR3	HV-CDR3	HV-FR4
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	DYNMH	WVRQAPGKGLEWVS	YIGPSGGYTHYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAK	DIRGAYSSGLFDY	WGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	EYPMY	WVRQAPGKGLEWVS	VIYPSGGWTDYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR	MAVTGGSRFDY	WGQGTLLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	RYWMD	WVRQAPGKGLEWVS	GIYPSGGYTLYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR	HGDYMDV	WGKGTTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	EYPMY	WVRQAPGKGLEWVS	VIYPSGGWTDYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR	MAVTGGSRFDY	WGQGTLLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	YYPMA	WVRQAPGKGLEWVS	YISSGGLTTHYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR	SPTYDFWSGYWAGIFDY	WGQGTLLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	FYHME	WVRQAPGKGLEWVS	SISPSGGHTDYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAS	LLSGT	WGQGTLLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	SYGMH	WVRQAPGKGLEWVS	GIVSSGGSTIYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCTT	YDYGdHYGMDV	WGQGTTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	HYWMH	WVRQAPGKGLEWVS	SISSSGGMTYYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCTT	ADYGYYGMDV	WGQGTTVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	DYNMH	WVRQAPGKGLEWVS	YIGPSGGYTHYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAK	DIRGAYSSGLFDY	WGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	MYWMF	WVRQAPGKGLEWVS	SISSSGGHTFYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR	GSYSGYDPPDY	WGRGTLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	WYNMW	WVRQAPGKGLEWVS	YIYPSGGNTGYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAV	FEYSSSGPQGY	WGQGTLLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	RYGMT	WVRQAPGKGLEWVS	GISPSGGNTWYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCTS	HDYGdHYGMDV	WGQGTLLVTVSS
EVQLLESGGGLVQPGGSLRLSCAASGFTFS	EYNMP	WVRQAPGKGLEWVS	YIYSSGGSTEYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDMAVYYCAK	DLWEDSSTWGYGMDV	WGQGTTVTVTVSS

2. MMP-12 Inhibitors Heavy Chain FR4 & Constant Region Sequences (in the same order as the light chains provided above)

HV-FR4
WGRGTLVTVSS
WGQGTLLVTVSS

WGKGTTLVTVSS
WGQGTLLVTVSS
WGQGTLLVTVSS
WGQGTLLVTVSS
WGQGTTLVTVSS
WGQGTTLVTVSS
WGRGTLLVTVSS
WGRGTLLVTVSS
WGQGTLLVTVSS
WGQGTLLVTVSS
WGQGTTLVTVSS

Example 6: Additional MMP-12 Binding Proteins

Twenty-one additional mutants were prepared:

Eighteen mutants of DX-2712 were made by changing residues in the CDR1 and 2 of the HC of DX-2712.

A residue in the light chain of each of DX-2712, M0121-E07, and M0008-H09 (the parental antibody) was glycosylated.

18 mutants of DX-2712:

<u>Clone:</u>	<u>Heavy / Light Chain Mutations</u>
	HC Mutant 539B-X41-B01: LC is 539B-X40-A01 (S25)
539B-X0041-A01	W31D;M56Y;M58H
539B-X0041-B01	W31D;M56Y;M58H;V97R;P99A;A102S
539B-X0041-C01	V97R;P99A;A102S
539B-X0041-E01	P99A
539B-X0041-F01	A102S
539B-X0041-A02	M58H
539B-X0041-B02	V97R
539B-X0041-C02	M56Y
539B-X0041-D02	W31D
<u>Clone:</u>	Light chain Swap: LC is S25N
539B-X0042-C01	X0041-A01
539B-X0042-B02	X0041-B01
539B-X0042-F03	X0041-C01
539B-X0042-G04 = 539B- X0042-B04	X0041-E01
539B-X0042-A05	X0041-F01
539B-X0042-D06	X0041-A02
539B-X0042-C07	X0041-B02
539B-X0042-H08	X0041-C02
539B-X0042-G09	X0041-D02

LC S25N glycosylated variants of DX-2712, M008-H09, M0121-E07:

<u>Clone:</u>	<u>Details</u>
539B-X0041-D01	DX-2712 + sugar
539B-X0041-G01	Parental (M0008-H09) + sugar
539B-X0041-H01	Back-up (M0121-E07) + sugar

22 mutants of DX-2712 plus 3 LC S25N glycosylated variants of DX-2712, M008-H09, M0121-E07:

Isolate	L-Leader	LV-FR1	LV-CDR1	LV-FR2	LV-CDR2	LV-FR3	LV-CDR3	LV-FR4	L-Constant
539B-X0041-A01	GVHS	DIQMTQSPS SLSASVGDR VTITC	RASQSI YTYLN	WYQQKPG KAPKLLI Y	AASS LQS	GVPSRFSGSGS GTDFTLTISL QPEDFATYYC	QQAG I	FGQGT KLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNF YPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC..
539B-X0041-A02	GVHS	DIQMTQSPS SLSASVGDR VTITC	RASQSI YTYLN	WYQQKPG KAPKLLI Y	AASS LQS	GVPSRFSGSGS GTDFTLTISL QPEDFATYYC	QQAG I	FGQGT KLEIK	
539B-X0041-B01	GVHS	DIQMTQSPS SLSASVGDR VTITC	RASQSI YTYLN	WYQQKPG KAPKLLI Y	AASS LQS	GVPSRFSGSGS GTDFTLTISL QPEDFATYYC	QQAG I	FGQGT KLEIK	
539B-X0041-B02	GVHS	DIQMTQSPS SLSASVGDR VTITC	RASQSI YTYLN	WYQQKPG KAPKLLI Y	AASS LQS	GVPSRFSGSGS GTDFTLTISL QPEDFATYYC	QQAG I	FGQGT KLEIK	
539B-X0041-C01	GVHS	DIQMTQSPS SLSASVGDR VTITC	RASQSI YTYLN	WYQQKPG KAPKLLI Y	AASS LQS	GVPSRFSGSGS GTDFTLTISL QPEDFATYYC	QQAG I	FGQGT KLEIK	
539B-X0041-C02	GVHS	DIQMTQSPS SLSASVGDR VTITC	RASQSI YTYLN	WYQQKPG KAPKLLI Y	AASS LQS	GVPSRFSGSGS GTDFTLTISL QPEDFATYYC	QQAG I	FGQGT KLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNF YPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC..
539B-X0041-D01	GVHS	DIQMTQSPS SLSASVGDR VTITC	RANQSI YTYLN	WYQQKPG KAPKLLI Y	AASS LQS	GVPSRFSGSGS GTDFTLTISL QPEDFATYYC	QQAG I	FGQGT KLEIK	
539B-X0041-D02	GVHS	DIQMTQSPS SLSASVGDR VTITC	RASQSI YTYLN	WYQQKPG KAPKLLI Y	AASS LQS	GVPSRFSGSGS GTDFTLTISL QPEDFATYYC	QQAG I	FGQGT KLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNF YPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC..
539B-X0041-E01	GVHS	DIQMTQSPS SLSASVGDR VTITC	RASQSI YTYLN	WYQQKPG KAPKLLI Y	AASS LQS	GVPSRFSGSGS GTDFTLTISL QPEDFATYYC	QQAG I	FGQGT KLEIK	
539B-X0041-F01	GVHS	DIQMTQSPS SLSASVGDR VTITC	RASQSI YTYLN	WYQQKPG KAPKLLI Y	AASS LQS	GVPSRFSGSGS GTDFTLTISL QPEDFATYYC	QQAG I	FGQGT KLEIK	
539B-X0041-G01	GVHS	DIQMTQSPS SLSASVGDR VTITC	RANQSI YTYLN	WYQQKPG KAPKLLI Y	AASS LQS	GVPSRFSGSGS GTDFTLTISL QPEDFATYYC	QQAG I	FGQGT KLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNF YPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC..
539B-X0041-H01	GVHS	DIQMTQSPS SLSASVGDR VTITC	RANQSI YTYLN	WYQQKPG KAPKLLI Y	AASS LQS	GVPSRFSGSGS GTDFTLTISL QPEDFATYYC	QQAG I	FGQGT KLEIK	
539B-	GVHS	DIQMTQSPS	RANQSI	WYQQKPG	AASS	GVPSRFSGSGS	QQAG	FGQGT	RTVAAPS

X0042-A05		SLSASVGDR VTITC	YTYLN	KAPKLLI Y	LQS	GTDFTLTISSL QPEDFATYYC	I	KLEIK	
539B- X0042-B02	GVHS	DIQMTQSPS SLSASVGDR VTITC	RANQSI YTYLN	WYQQKPG KAPKLLI Y	AASS LQS	GVPSRFSGSGS GTDFTLTISSL QPEDFATYYC	QQAG I	FGQGT KLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQESVTEQDSKDZ zYSLSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC..
539B- X0042-B04	GVHS	DIQMTQSPS SLSASVGDR VTITC	RANQSI YTYLN	WYQQKPG KAPKLLI Y	AASS LQS	GVPSRFSGSGS GTDFTLTISSL QPEDFATYYC	QQAG I	FGQGT KLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQESVTEQDSKDZ zYSLSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC..
539B- X0042-C01	GVHS	DIQMTQSPS SLSASVGDR VTITC	RANQSI YTYLN	WYQQKPG KAPKLLI Y	AASS LQS	GVPSRFSGSGS GTDFTLTISSL QPEDFATYYC	QQAG I	FGQGT KLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQESVTEQDSKDZ zYSLSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC..
539B- X0042-C07	GVHS	DIQMTQSPS SLSASVGDR VTITC	RANQSI YTYLN	WYQQKPG KAPKLLI Y	AASS LQS	GVPSRFSGSGS GTDFTLTISSL QPEDFATYYC	QQAG I	FGQGT KLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQESVTEQDSKDZ zLLFPVQHFPDPVQGRLEAQQVRLRGDPPGPVL PRDQVLQPGRVLM
539B- X0042-D06	GVHS	DIQMTQSPS SLSASVGDR VTITC	RANQSI YTYLN	WYQQKPG KAPKLLI Y	AASS LQS	GVPSRFSGSGS GTDFTLTISSL QPEDFATYYC	QQAG I	FGQGT KLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQESVTEQDSKDZ zYSLSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC..
539B- X0042-F03	GVHS	DIQMTQSPS SLSASVGDR VTITC	RANQSI YTYLN	WYQQKPG KAPKLLI Y	AASS LQS	GVPSRFSGSGS GTDFTLTISSL QPEDFATYYC	QQAG I	FGQGT KLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQESVTEQDSKDZ zYSLSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC..
539B- X0042-G04	GVHS	DIQMTQSPS SLSASVGDR VTITC	RANQSI YTYLN	WYQQKPG KAPKLLI Y	AASS LQS	GVPSRFSGSGS GTDFTLTISSL QPEDFATYYC	QQAG I	FGQGT KLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQESVTEQDSKDZ zYSLSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC..
539B- X0042-G09	GVHS	DIQMTQSPS SLSASVGDR VTITC	RANQSI YTYLN	WYQQKPG KAPKLLI Y	AASS LQS	GVPSRFSGSGS GTDFTLTISSL QPEDFATYYC	QQAG I	FGQGT KLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQESVTEQDSKDZ zYSLSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC..
539B- X0042-H08	GVHS	DIQMTQSPS SLSASVGDR VTITC	RANQSI YTYLN	WYQQKPG KAPKLLI Y	AASS LQS	GVPSRFSGSGS GTDFTLTISSL QPEDFATYYC	QQAG I	FGQGT KLEIK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF YPREAKVQWKVDNALQSGNSQESVTEQDSKDZ zYSLSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSFNRGEC..

1
2
3
4

Isolate	H-Leader	HV-FR1	HV- CDR1	HV-FR2	HV-CDR2	HV-FR3	HV-CDR3	HV-FR4	H-Constant
539B-X0041-A01	MGWSCIILFL VATATGAHS	EVQLLESGGGLVQP	DYWMH	WVRQAPGKG LEWVS	GISPSGGYTH YADSVKG	RFTISRDN SKNTLYL QMNSLRAEDTAVYYC AR	DIVGPYSA GLFDY	WGRGTLVT VSS	ASTKGPSVFP LAPSSKS
		FS							
539B-X0041-A02	MGWSCIILFL VATATGAHS	EVQLLESGGGLVQP	WYWMH	WVRQAPGKG LEWVS	GISPSGGMTM YADSVKG	RFTISRDN SKNTLYL QMNSLRAEDTAVYYC AR	DIVGPYSA GLFDY	WGRGTLVT VSS	ASTKGPSVFP LAPSSKS
		FS							
539B-X0041-B01	MGWSCIILFL VATATGAHS	EVQLLESGGGLVQP	DYWMH	WVRQAPGKG LEWVS	GISPSGGYTH YADSVKG	RFTISRDN SKNTLYL QMNSLRAEDTAVYYC AR	DIRGAYSS GLFDY	WGRGTLVT VSS	ASTKGPSVFP LAPSSKS
		FS							
539B-X0041-B02	MGWSCIILFL VATATGAHS	EVQLLESGGGLVQP	WYWMH	WVRQAPGKG LEWVS	GISPSGGMTM YADSVKG	RFTISRDN SKNTLYL QMNSLRAEDTAVYYC AR	DIRGPYSA GLFDY	WGRGTLVT VSS	ASTKGPSVFP LAPSSKS
		FS							
539B-X0041-C01	MGWSCIILFL VATATGAHS	EVQLLESGGGLVQP	WYWMH	WVRQAPGKG LEWVS	GISPSGGMTM YADSVKG	RFTISRDN SKNTLYL QMNSLRAEDTAVYYC AR	DIRGAYSS GLFDY	WGRGTLVT VSS	ASTKGPSVFP LAPSSKS
		FS							
539B-X0041-C02	MGWSCIILFL VATATGAHS	EVQLLESGGGLVQP	WYWMH	WVRQAPGKG LEWVS	GISPSGGYTM YADSVKG	RFTISRDN SKNTLYL QMNSLRAEDTAVYYC AR	DIVGPYSA GLFDY	WGRGTLVT VSS	ASTKGPSVFP LAPSSKS
		FS							
539B-X0041-D01	MGWSCIILFL VATATGAHS	EVQLLESGGGLVQP	WYWMH	WVRQAPGKG LEWVS	GISPSGGMTM YADSVKG	RFTISRDN SKNTLYL QMNSLRAEDTAVYYC AR	DIVGPYSA GLFDY	WGRGTLVT VSS	ASTKGPSVFP LAPSSKS
		FS							
539B-X0041-D02	MGWSCIILFL VATATGAHS	EVQLLESGGGLVQP	DYWMH	WVRQAPGKG LEWVS	GISPSGGMTM YADSVKG	RFTISRDN SKNTLYL QMNSLRAEDTAVYYC AR	DIVGPYSA GLFDY	WGRGTLVT VSS	ASTKGPSVFP LAPSSKS
		FS							
539B-X0041-E01	MGWSCIILFL VATATGAHS	EVQLLESGGGLVQP	WYWMH	WVRQAPGKG LEWVS	GISPSGGMTM YADSVKG	RFTISRDN SKNTLYL QMNSLRAEDTAVYYC AR	DIVGAYSA GLFDY	WGRGTLVT VSS	ASTKGPSVFP LAPSSKS
		FS							

539B-X0041-F01	MGWSCIILFL VATATGAHS	EVQLLESGGGLVQP GGSRLRSCAASGFT FS	WYWMH	WVRQAPGKG LEWVS	GISPSGGMTM YADSVKG	RFTISRDN SKNTLYL QMNSLRAEDTAVYIC AR	DIVGPYSS GLFDY	WGRGTLVT VSS	ASTKGPSVFP LAPSSKS
539B-X0041-G01	MGWSCIILFL VATATGAHS	EVQLLESGGGLVQP GGSRLRSCAASGFT FS	DYNMH	WVRQAPGKG LEWVS	YIGPSGGYTH YADSVKG	RFTISRDN SKNTLYL QMNSLRAEDTAVYIC AK	DIRGAYSS GLFDY	WGRGTLVT VSS	ASTKGPSVFP LAPSSKS
539B-X0041-H01	MGWSCIILFL VATATGAHS	EVQLLESGGGLVQP GGSRLRSCAASGFT FS	WYGMH	WVRQAPGKG LEWVS	GIVSSGETF YADSVKG	RFTISRDN SKNTLYL QMNSLRAEDTAVYIC AK	DIRGVFLS GLFDH	WGRGTLVT VSS	ASTKGPSVFP LAPSSKS
539B-X0042-A05	MGWSCIILFL VATATGAHS	EVQLLESGGGLVQP GGSRLRSCAASGFT FS	WYWMH	WVRQAPGKG LEWVS	GISPSGGMTM YADSVKG	RFTISRDN SKNTLYL QMNSLRAEDTAVYIC AR	DIVGPYSS GLFDY	WGRGTLVT VSS	ASTKGPSVFP LAPSLQV
539B-X0042-B02	MGWSCIILFL VATATGAHS	EVQLLESGGGLVQP GGSRLRSCAASGFT FS	DYWMH	WVRQAPGKG LEWVS	GISPSGGYTH YADSVKG	RFTISRDN SKNTLYL QMNSLRAEDTAVYIC AR	DIRGAYSS GLFDY	WGRGTLVT VSS	ASTKGPSVFP LAPSSKS
539B-X0042-B04	MGWSCIILFL VATATGAHS	EVQLLESGGGLVQP GGSRLRSCAASGFT FS	WYWMH	WVRQAPGKG LEWVS	GISPSGGMTM YADSVKG	RFTISRDN SKNTLYL QMNSLRAEDTAVYIC AR	DIVGAYSA GLFDY	WGRGTLVT VSS	ASTKGPSVFP LAPSSKS
539B-X0042-C01	MGWSCIILFL VATATGAHS	EVQLLESGGGLVQP GGSRLRSCAASGFT FS	DYWMH	WVRQAPGKG LEWVS	GISPSGGYTH YADSVKG	RFTISRDN SKNTLYL QMNSLRAEDTAVYIC AR	DIVGPYSA GLFDY	WGRGTLVT VSS	ASTKGPSVFP LAPSSKS
539B-X0042-C07	MGWSCIILFL VATATGAHS	EVQLLESGGGLVQP GGSRLRSCAASGFT FS	WYWMH	WVRQAPGKG LEWVS	GISPSGGMTM YADSVKG	RFTISRDN SKNTLYL QMNSLRAEDTAVYIC AR	DIRGPYSA GLFDY	WGRGTLVT VSS	ASTKGPSVFP LAPSSKS
539B-X0042-D06	MGWSCIILFL VATATGAHS	EVQLLESGGGLVQP GGSRLRSCAASGFT FS	WYWMH	WVRQAPGKG LEWVS	GISPSGGMTM YADSVKG	RFTISRDN SKNTLYL QMNSLRAEDTAVYIC AR	DIVGPYSA GLFDY	WGRGTLVT VSS	ASTKGPSVFP LAPSSKS
539B-X0042-F03	MGWSCIILFL VATATGAHS	EVQLLESGGGLVQP GGSRLRSCAASGFT FS	WYWMH	WVRQAPGKG LEWVS	GISPSGGMTM YADSVKG	RFTISRDN SKNTLYL QMNSLRAEDTAVYIC AR	DIRGAYSS GLFDY	WGRGTLVT VSS	ASTKGPSVFP LAPSSKS
539B-X0042-	MGWSCIILFL	EVQLLESGGGLVQP	WYWMH	WVRQAPGKG	GISPSGGMTM	RFTISRDN SKNTLYL	DIVGAYSA	WGRGTLVT	ASTKGPSVFP

G04	VATATGAHS	GGSLRLSCAASGFT FS		LEWVS	YADSVKG	QMNSLRAEDTAVYIC AR	GLFDY	VSS	LAPSSKS
539B-X0042-G09	MGWSCIILFL VATATGAHS	EVQLLESGGGLVQP GGSLRLSCAASGFT FS	DYMMH	WVRQAPGKG LEWVS	GISPSGGMTM YADSVKG	RFTISRDNKNTLYL QMNSLRAEDTAVYIC AR	DIVGPYSA GLFDY	WGRGTLVT VSS	ASTKGPSVFP LAPSSKS
539B-X0042-H08	MGWSCIILFL VATATGAHS	EVQLLESGGGLVQP GGSLRLSCAASGFT FS	WYMMH	WVRQAPGKG LEWVS	GISPSGGYTM YADSVKG	RFTISRDNKNTLYL QMNSLRAEDTAVYIC AR	DIVGPYSA GLFDY	WGRGTLVT VSS	ASTKGPSVFP LAPSSKS

Isolate	LV-AA				HV-AA				
539B-X0041-A01	DIQMTQSPSSLSASVGDRVTITCRASQSIYTYLNWYQQKPGKAPKLLIYA ASSLQSGVPSRFRSGSGGTDTLTITISLQPEDFATYYCQQAGIFGQGTKL EIK	GGSLRLSCAASGFT FS		LEWVS	YADSVKG	QMNSLRAEDTAVYIC AR	GLFDY	VSS	LAPSSKS
539B-X0041-A02	DIQMTQSPSSLSASVGDRVTITCRASQSIYTYLNWYQQKPGKAPKLLIYA ASSLQSGVPSRFRSGSGGTDTLTITISLQPEDFATYYCQQAGIFGQGTKL EIK	GGSLRLSCAASGFT FS		LEWVS	YADSVKG	QMNSLRAEDTAVYIC AR	GLFDY	VSS	LAPSSKS
539B-X0041-B01	DIQMTQSPSSLSASVGDRVTITCRASQSIYTYLNWYQQKPGKAPKLLIYA ASSLQSGVPSRFRSGSGGTDTLTITISLQPEDFATYYCQQAGIFGQGTKL EIK	GGSLRLSCAASGFT FS		LEWVS	YADSVKG	QMNSLRAEDTAVYIC AR	GLFDY	VSS	LAPSSKS
539B-X0041-B02	DIQMTQSPSSLSASVGDRVTITCRASQSIYTYLNWYQQKPGKAPKLLIYA ASSLQSGVPSRFRSGSGGTDTLTITISLQPEDFATYYCQQAGIFGQGTKL EIK	GGSLRLSCAASGFT FS		LEWVS	YADSVKG	QMNSLRAEDTAVYIC AR	GLFDY	VSS	LAPSSKS
539B-X0041-C01	DIQMTQSPSSLSASVGDRVTITCRASQSIYTYLNWYQQKPGKAPKLLIYA ASSLQSGVPSRFRSGSGGTDTLTITISLQPEDFATYYCQQAGIFGQGTKL EIK	GGSLRLSCAASGFT FS		LEWVS	YADSVKG	QMNSLRAEDTAVYIC AR	GLFDY	VSS	LAPSSKS
539B-X0041-C02	DIQMTQSPSSLSASVGDRVTITCRASQSIYTYLNWYQQKPGKAPKLLIYA ASSLQSGVPSRFRSGSGGTDTLTITISLQPEDFATYYCQQAGIFGQGTKL EIK	GGSLRLSCAASGFT FS		LEWVS	YADSVKG	QMNSLRAEDTAVYIC AR	GLFDY	VSS	LAPSSKS
539B-X0041-D01	DIQMTQSPSSLSASVGDRVTITCRANQSIYTYLNWYQQKPGKAPKLLIYA ASSLQSGVPSRFRSGSGGTDTLTITISLQPEDFATYYCQQAGIFGQGTKL	GGSLRLSCAASGFT FS		LEWVS	YADSVKG	QMNSLRAEDTAVYIC AR	GLFDY	VSS	LAPSSKS

	EIK	LVTVSS
539B-X0041-D02	DIQMTQSPSSLSASVGDRTVITICRASQSIYTYLWNWYQQKPGKAPKLLIYA ASSLQSGVPSRFRFSGSGGTDTLTITSSLQPEDFATYYCQQAIFGQGTKL EIK	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYMMHWVRQAPGKGLEWVSGISPSGGMT MYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIVGPPYSAGLFDYWGRGT LVTVSS
539B-X0041-E01	DIQMTQSPSSLSASVGDRTVITICRASQSIYTYLWNWYQQKPGKAPKLLIYA ASSLQSGVPSRFRFSGSGGTDTLTITSSLQPEDFATYYCQQAIFGQGTKL EIK	EVQLLESGGGLVQPGGSLRLSCAASGFTFSWYMMHWVRQAPGKGLEWVSGISPSGGMT MYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIVGAYSAGLFDYWGRGT LVTVSS
539B-X0041-F01	DIQMTQSPSSLSASVGDRTVITICRASQSIYTYLWNWYQQKPGKAPKLLIYA ASSLQSGVPSRFRFSGSGGTDTLTITSSLQPEDFATYYCQQAIFGQGTKL EIK	EVQLLESGGGLVQPGGSLRLSCAASGFTFSWYMMHWVRQAPGKGLEWVSGISPSGGMT MYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIVGPPYSGLFDYWGRGT LVTVSS
539B-X0041-G01	DIQMTQSPSSLSASVGDRTVITICRANQSIYTYLWNWYQQKPGKAPKLLIYA ASSLQSGVPSRFRFSGSGGTDTLTITSSLQPEDFATYYCQQAIFGQGTKL EIK	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYNMHWVRQAPGKGLEWVS YIGPSGGYT HYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDIRGAYSSGLFDYWGRGT LVTVSS
539B-X0041-H01	DIQMTQSPSSLSASVGDRTVITICRANQSIYTYLWNWYQQKPGKAPKLLIYA ASSLQSGVPSRFRFSGSGGTDTLTITSSLQPEDFATYYCQQAIFGQGTKL EIK	EVQLLESGGGLVQPGGSLRLSCAASGFTFSWYGMHWVRQAPGKGLEWVSGIVSSGGET FYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDIRGVFLSGLFDHWGRGT LVTVSS
539B-X0042-A05	DIQMTQSPSSLSASVGDRTVITICRANQSIYTYLWNWYQQKPGKAPKLLIYA ASSLQSGVPSRFRFSGSGGTDTLTITSSLQPEDFATYYCQQAIFGQGTKL EIK	EVQLLESGGGLVQPGGSLRLSCAASGFTFSWYMMHWVRQAPGKGLEWVSGISPSGGMT MYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIVGPPYSGLFDYWGRGT LVTVSS
539B-X0042-B02	DIQMTQSPSSLSASVGDRTVITICRANQSIYTYLWNWYQQKPGKAPKLLIYA ASSLQSGVPSRFRFSGSGGTDTLTITSSLQPEDFATYYCQQAIFGQGTKL EIK	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYMMHWVRQAPGKGLEWVSGISPSGGYT HYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIRGAYSSGLFDYWGRGT LVTVSS
539B-X0042-B04	DIQMTQSPSSLSASVGDRTVITICRANQSIYTYLWNWYQQKPGKAPKLLIYA ASSLQSGVPSRFRFSGSGGTDTLTITSSLQPEDFATYYCQQAIFGQGTKL EIK	EVQLLESGGGLVQPGGSLRLSCAASGFTFSWYMMHWVRQAPGKGLEWVSGISPSGGMT MYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIVGAYSAGLFDYWGRGT LVTVSS
539B-X0042-C01	DIQMTQSPSSLSASVGDRTVITICRANQSIYTYLWNWYQQKPGKAPKLLIYA ASSLQSGVPSRFRFSGSGGTDTLTITSSLQPEDFATYYCQQAIFGQGTKL EIK	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYMMHWVRQAPGKGLEWVSGISPSGGYT HYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIVGPPYSAGLFDYWGRGT LVTVSS
539B-X0042-C07	DIQMTQSPSSLSASVGDRTVITICRANQSIYTYLWNWYQQKPGKAPKLLIYA ASSLQSGVPSRFRFSGSGGTDTLTITSSLQPEDFATYYCQQAIFGQGTKL	EVQLLESGGGLVQPGGSLRLSCAASGFTFSWYMMHWVRQAPGKGLEWVSGISPSGGMT MYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIRGPPYSAGLFDYWGRGT

	EIK	LVTVSS
539B-X0042-D06	DIQMTQSPSSLSASVGDRVTITCRANQSIYTYLNWYQQKPGKAPKLLIYA ASSLQSGVPSRFRSGSGGTDTLTITSSLQPEDFATYYCQQAQAGIFGQGTKL EIK	EVQLLESGGGLVQPGGSLRLSCAASGFTFSWYMMHWVRQAPGKGLEWVSGISPSGGMT MYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIVGPPYSAGLFDYWGRGT LVTVSS
539B-X0042-F03	DIQMTQSPSSLSASVGDRVTITCRANQSIYTYLNWYQQKPGKAPKLLIYA ASSLQSGVPSRFRSGSGGTDTLTITSSLQPEDFATYYCQQAQAGIFGQGTKL EIK	EVQLLESGGGLVQPGGSLRLSCAASGFTFSWYMMHWVRQAPGKGLEWVSGISPSGGMT MYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIRGAYSSGLFDYWGRGT LVTVSS
539B-X0042-G04	DIQMTQSPSSLSASVGDRVTITCRANQSIYTYLNWYQQKPGKAPKLLIYA ASSLQSGVPSRFRSGSGGTDTLTITSSLQPEDFATYYCQQAQAGIFGQGTKL EIK	EVQLLESGGGLVQPGGSLRLSCAASGFTFSWYMMHWVRQAPGKGLEWVSGISPSGGMT MYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIVGAYSAGLFDYWGRGT LVTVSS
539B-X0042-G09	DIQMTQSPSSLSASVGDRVTITCRANQSIYTYLNWYQQKPGKAPKLLIYA ASSLQSGVPSRFRSGSGGTDTLTITSSLQPEDFATYYCQQAQAGIFGQGTKL EIK	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYMMHWVRQAPGKGLEWVSGISPSGGMT MYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIVGPPYSAGLFDYWGRGT LVTVSS
539B-X0042-H08	DIQMTQSPSSLSASVGDRVTITCRANQSIYTYLNWYQQKPGKAPKLLIYA ASSLQSGVPSRFRSGSGGTDTLTITSSLQPEDFATYYCQQAQAGIFGQGTKL EIK	EVQLLESGGGLVQPGGSLRLSCAASGFTFSWYMMHWVRQAPGKGLEWVSGISPSGGYT MYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIVGPPYSAGLFDYWGRGT LVTVSS

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1 Further, 13 variants on 539B-X0041-D02 were prepared.

2 539B-X0041-D02 plus 13 mutants of 539B-X0041-D02:

Isolate	Initial Name	L-Leader	LV-FR1	LV-CDR1	LV-FR2	LV-CDR2	LV-FR3	LV-CDR3	LV-FR4	I-Constant
539B-X0041-D02	539B-X0041-D02	GVHS	DIQMTQSPSSLS ASVGDRVITIC	RASQSIYT YLN	WYQQKPGAPKL LIY	AASSLQS	GVPSRFGSGSGTDFTLTIS SLQPEDFATY YC	QQAGI	FGQGTKLE IK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC..
539B-X0049-A01	X49-A01 - M at H34 (germline) -LEU (L)	GVHS	DIQMTQSPSSLS ASVGDRVITIC	RASQSIYT YLN	WYQQKPGAPKL LIY	AASSLQS	GVPSRFGSGSGTDFTLTIS SLQPEDFATY YC	QQAGI	FGQGTKLE IK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC..
539B-X0049-B01	X49-B01 - M at H34 (germline) -THR (T)	GVHS	DIQMTQSPSSLS ASVGDRVITIC	RASQSIYT YLN	WYQQKPGAPKL LIY	AASSLQS	GVPSRFGSGSGTDFTLTIS SLQPEDFATY YC	QQAGI	FGQGTKLE IK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC..
539B-X0049-C01	X49-C01 - M at H56 -SER (S)	GVHS	DIQMTQSPSSLS ASVGDRVITIC	RASQSIYT YLN	WYQQKPGAPKL LIY	AASSLQS	GVPSRFGSGSGTDFTLTIS SLQPEDFATY YC	QQAGI	FGQGTKLE IK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC..
539B-X0049-D01	X49-D01 - M at H58 -TYR (Y)	GVHS	DIQMTQSPSSLS ASVGDRVITIC	RASQSIYT YLN	WYQQKPGAPKL LIY	AASSLQS	GVPSRFGSGSGTDFTLTIS SLQPEDFATY YC	QQAGI	FGQGTKLE IK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC..
539B-X0049-E01	X49-E01 - M at H56, H58 -SER, TYR (S,Y)	GVHS	DIQMTQSPSSLS ASVGDRVITIC	RASQSIYT YLN	WYQQKPGAPKL LIY	AASSLQS	GVPSRFGSGSGTDFTLTIS SLQPEDFATY YC	QQAGI	FGQGTKLE IK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC..
539B-X0049-F01	X49-F01 - M at H34, H56, H58 -LEU, SER, TYR (L,S,Y)	GVHS	DIQMTQSPSSLS ASVGDRVITIC	RASQSIYT YLN	WYQQKPGAPKL LIY	AASSLQS	GVPSRFGSGSGTDFTLTIS SLQPEDFATY YC	QQAGI	FGQGTKLE IK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC..
539B-X0049-G01	X49-G01 - P at H52a -GLY (G)	GVHS	DIQMTQSPSSLS ASVGDRVITIC	RASQSIYT YLN	WYQQKPGAPKL LIY	AASSLQS	GVPSRFGSGSGTDFTLTIS SLQPEDFATY YC	QQAGI	FGQGTKLE IK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC..
539B-X0049-H01	X49-H01 - P at H52a M at	GVHS	DIQMTQSPSSLS ASVGDRVITIC	RASQSIYT YLN	WYQQKPGAPKL LIY	AASSLQS	GVPSRFGSGSGTDFTLTIS SLQPEDFATY YC	QQAGI	FGQGTKLE IK	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC..

	H34 (germli ne) -LEU (L)						YC					YACEVTHQGLSSPVTKSFNRGEC..
539B- X0049- A02	X49-A02 - P at H52a M at H34 (germli ne) -THR (T)	GVHS	DIQMTQSPSSLS ASVGDRVTTITC	RASQSIYT YLN	WYQQKP GKAPKL LIY	AASSLQS	GVPSRFGSG SGTDFTLTIS SLQPEDFATY YC	QQAGI	FGQGTKLE IK			RTVAAPSVFIFPPSDEQQLKSGTASVVC LNNFYPREAKVQWKVDNALQSGNSQESV TEQDSKDSSTYSLSSTLTLSKADYEKHKV YACEVTHQGLSSPVTKSFNRGEC..
539B- X0049- B02	X49-B02 - P at H52a M at H56 -SER (S)	GVHS	DIQMTQSPSSLS ASVGDRVTTITC	RASQSIYT YLN	WYQQKP GKAPKL LIY	AASSLQS	GVPSRFGSG SGTDFTLTIS SLQPEDFATY YC	QQAGI	FGQGTKLE IK			RTVAAPSVFIFPPSDEQQLKSGTASVVC LNNFYPREAKVQWKVDNALQSGNSQESV TEQDSKDSSTYSLSSTLTLSKADYEKHKV YACEVTHQGLSSPVTKSFNRGEC..
539B- X0049- C02	X49-C02 - P at H52a M at H58 -TYR (Y)	GVHS	DIQMTQSPSSLS ASVGDRVTTITC	RASQSIYT YLN	WYQQKP GKAPKL LIY	AASSLQS	GVPSRFGSG SGTDFTLTIS SLQPEDFATY YC	QQAGI	FGQGTKLE IK			RTVAAPSVFIFPPSDEQQLKSGTASVVC LNNFYPREAKVQWKVDNALQSGNSQESV TEQDSKDSSTYSLSSTLTLSKADYEKHKV YACEVTHQGLSSPVTKSFNRGEC..
539B- X0049- D02	X49-D02 - P at H52a M at H56, H58 -SER, TYR (S, Y)	GVHS	DIQMTQSPSSLS ASVGDRVTTITC	RASQSIYT YLN	WYQQKP GKAPKL LIY	AASSLQS	GVPSRFGSG SGTDFTLTIS SLQPEDFATY YC	QQAGI	FGQGTKLE IK			RTVAAPSVFIFPPSDEQQLKSGTASVVC LNNFYPREAKVQWKVDNALQSGNSQESV TEQDSKDSSTYSLSSTLTLSKADYEKHKV YACEVTHQGLSSPVTKSFNRGEC..
539B- X0049- E02	X49-E02 - P at H52a M at H34, H56, H58 -LEU, SER, TYR (L, S, Y)	GVHS	DIQMTQSPSSLS ASVGDRVTTITC	RASQSIYT YLN	WYQQKP GKAPKL LIY	AASSLQS	GVPSRFGSG SGTDFTLTIS SLQPEDFATY YC	QQAGI	FGQGTKLE IK			RTVAAPSVFIFPPSDEQQLKSGTASVVC LNNFYPREAKVQWKVDNALQSGNSQESV TEQDSKDSSTYSLSSTLTLSKADYEKHKV YACEVTHQGLSSPVTKSFNRGEC..

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Isolate	Initial Name	H-Leader	HV-FR1	HV- CDR1	HV-FR2	HV-CDR2	HV-FR3	HV-CDR3	HV-FR4	H- Constant
539B- X0041- D02	539B- X0041-D02	MGWSCIILFL VATATGAHS	EVQLLESGGGLVQPGGSL RLSCAASGFTFS	DYWM H	WVRQAPG KGLEWVS	GISPSGGM TMYADSVK G	RFTISRDN SKNTLYLQ MNSLRAEDTAVYYCAR	DIVGPYSAGLFD Y	WGRGTLVT VSS	ASTKGPSV FPLAPSSK S
539B- X0049- A01	X49-A01 - M at H34 (germli ne) -LEU (L)	MGWSCIILFL VATATGAHS	EVQLLESGGGLVQPGGSL RLSCAASGFTFS	DYWL H	WVRQAPG KGLEWVS	GISPSGGM TMYADSVK G	RFTISRDN SKNTLYLQ MNSLRAEDTAVYYCAR	DIVGPYSAGLFD Y	WGRGTLVT VSS	ASTKGPSV FPLAPSSK S
539B- X0049- B01	X49-B01 - M at H34 (germli	MGWSCIILFL VATATGAHS	EVQLLESGGGLVQPGGSL RLSCAASGFTFS	DYWT H	WVRQAPG KGLEWVS	GISPSGGM TMYADSVK G	RFTISRDN SKNTLYLQ MNSLRAEDTAVYYCAR	DIVGPYSAGLFD Y	WGRGTLVT VSS	ASTKGPSV FPLAPSSK S

[illegible]

	(S,Y)														
539B-X0049-E02	X49-E02 - P at H52a M at H34, H56, H58 -LEU, SER, TYR (L,S,Y)	MGWSCIILFL VATATGAHS	EVQLLESGGGLVQPGGSL RLSCAASGFTFS	DYWL H	WVRQAPG KGLEWVS	GISGSGGS TYYADSVK G	RFTISRDN SKNTLYLQ MNSLRAEDTAVYYCAR	DIVGPYSAGLFD Y	WGRGTLVT VSS	ASTKGPSV FPLAPSSK S					

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Isolate	Initial Name	LV-AA	HV-AA									
539B-X0041-D02		DIQMTQSPSSLSASVGDRVTITCRASQSIYTYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQAAGIFGQGTKLEIK	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYMHHWVRQAPGKGLEWVSGISPGSGMTMYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIVGPYSAGLFDYWGRGTLVTVSS									
539B-X0049-A01	X49-A01 - M at H34 (germline) -LEU (L)	DIQMTQSPSSLSASVGDRVTITCRASQSIYTYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQAAGIFGQGTKLEIK	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYMHHWVRQAPGKGLEWVSGISPGSGMTMYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIVGPYSAGLFDYWGRGTLVTVSS									
539B-X0049-B01	X49-B01 - M at H34 (germline) -THR (T)	DIQMTQSPSSLSASVGDRVTITCRASQSIYTYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQAAGIFGQGTKLEIK	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYMHHWVRQAPGKGLEWVSGISPGSGMTMYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIVGPYSAGLFDYWGRGTLVTVSS									
539B-X0049-C01	X49-C01 - M at H56 -SER (S)	DIQMTQSPSSLSASVGDRVTITCRASQSIYTYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQAAGIFGQGTKLEIK	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYMHHWVRQAPGKGLEWVSGISPGSGMTMYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIVGPYSAGLFDYWGRGTLVTVSS									
539B-X0049-D01	X49-D01 - M at H58 -TYR (Y)	DIQMTQSPSSLSASVGDRVTITCRASQSIYTYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQAAGIFGQGTKLEIK	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYMHHWVRQAPGKGLEWVSGISPGSGMTMYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIVGPYSAGLFDYWGRGTLVTVSS									
539B-X0049-E01	X49-E01 - M at H56, H58 -SER, TYR (S,Y)	DIQMTQSPSSLSASVGDRVTITCRASQSIYTYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQAAGIFGQGTKLEIK	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYMHHWVRQAPGKGLEWVSGISPGSGMTMYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIVGPYSAGLFDYWGRGTLVTVSS									
539B-X0049-	X49-F01 - M at H34, H56,	DIQMTQSPSSLSASVGDRVTITCRASQSIYTYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGGTD	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYMHHWVRQAPGKGLEWVSGISPGSGMTMYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIVGPYSA									

F01	H58 -LEU, SER, TYR (L,S,Y)	FTLTISSLQPEDFATYYCQQA GIFGQGTKLEIK	GLFDYWGRGTLVTVSS
539B-X0049-G01	X49-G01 - P at H52a -GLY (G)	DIQMTQSPSSLSASVGDRVTITCRASQSIYTYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQA GIFGQGTKLEIK	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSDYMHHWVRQAPGKGLEWVSGISPGGNTMYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIVGPYSAGLFDYWGRGTLVTVSS
539B-X0049-H01	X49-H01 - P at H52a M at H34 (germline) -LEU (L)	DIQMTQSPSSLSASVGDRVTITCRASQSIYTYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQA GIFGQGTKLEIK	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSDYMHHWVRQAPGKGLEWVSGISPGGNTMYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIVGPYSAGLFDYWGRGTLVTVSS
539B-X0049-A02	X49-A02 - P at H52a M at H34 (germline) -THR (T)	DIQMTQSPSSLSASVGDRVTITCRASQSIYTYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQA GIFGQGTKLEIK	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSDYMHHWVRQAPGKGLEWVSGISPGGNTMYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIVGPYSAGLFDYWGRGTLVTVSS
539B-X0049-B02	X49-B02 - P at H52a M at H56 -SER (S)	DIQMTQSPSSLSASVGDRVTITCRASQSIYTYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQA GIFGQGTKLEIK	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSDYMHHWVRQAPGKGLEWVSGISPGGNTMYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIVGPYSAGLFDYWGRGTLVTVSS
539B-X0049-C02	X49-C02 - P at H52a M at H58 -TYR (Y)	DIQMTQSPSSLSASVGDRVTITCRASQSIYTYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQA GIFGQGTKLEIK	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSDYMHHWVRQAPGKGLEWVSGISPGGNTMYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIVGPYSAGLFDYWGRGTLVTVSS
539B-X0049-D02	X49-D02 - P at H52a M at H56, H58 -SER, TYR (S,Y)	DIQMTQSPSSLSASVGDRVTITCRASQSIYTYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQA GIFGQGTKLEIK	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSDYMHHWVRQAPGKGLEWVSGISPGGNTMYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIVGPYSAGLFDYWGRGTLVTVSS
539B-X0049-E02	X49-E02 - P at H52a M at H34, H56, H58 -LEU, SER, TYR (L,S,Y)	DIQMTQSPSSLSASVGDRVTITCRASQSIYTYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQA GIFGQGTKLEIK	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSDYMHHWVRQAPGKGLEWVSGISPGGNTMYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDIVGPYSAGLFDYWGRGTLVTVSS

WHAT IS CLAIMED IS:

1. An isolated Matrix Metalloproteinase-12 (MMP-12) binding protein, wherein the protein comprises at least one immunoglobulin variable region.
2. The protein of claim 1, wherein the protein binds human MMP-12.
3. The protein of claim 1, wherein the protein inhibits the catalytic activity of MMP-12.
4. The protein of claim 1, wherein the protein comprises an antibody.
5. The protein of claim 1, wherein the protein guides a nano-particle or toxin to a cell expressing MMP-12 on the cell surface.
6. The protein of claim 1, wherein the protein causes effector functions to kill the cell which expresses MMP-12.
7. The protein of claim 1, wherein comprises a heavy chain (HC) immunoglobulin variable domain sequence and a light chain (LC) immunoglobulin variable domain sequence.
8. The protein of claim 7, wherein the HC and LC variable domain sequences are components of the same polypeptide chain.
9. The protein of claim 7, wherein the HC and LC variable domain sequences are components of different polypeptide chains.
10. The protein of claim 1, wherein the protein binds to human MMP-12 specifically, and not to MMP-12 from another species.

11. The protein of claim 1, wherein the protein binds MMP-12 specifically, and not to another matrix metalloproteinase.

12. The protein of claim 1, wherein the protein comprises one or more of the following characteristics:

- (a) a human CDR or human framework region;
- (b) the HC immunoglobulin variable domain sequence comprises one or more CDRs that are at least 85% identical to a CDR of a HC variable domain described herein;
- (c) the LC immunoglobulin variable domain sequence comprises one or more CDRs that are at least 85% identical to a CDR of a LC variable domain described herein;
- (d) the LC immunoglobulin variable domain sequence is at least 85% identical to a LC variable domain described herein;
- (e) the HC immunoglobulin variable domain sequence is at least 85% identical to a HC variable domain described herein;
- (f) the protein binds an epitope bound by a protein described herein, or an epitope that overlaps with such epitope; and
- (g) a primate CDR or primate framework region.

13. The protein of claim 1, wherein the protein also binds to MMP-16 or MMP-24.

14. The protein of claim 1, wherein the protein comprises an antibody comprising light and heavy chains of an antibody selected from the group of antibodies consisting of: M0134-A02, M134-A05, M134-A07, M134-A09, M134-A10, M134-A11, M0134-B01, M134-B04, M0134-B08, M0134-B11, M0134-C01, M0134-C02, M0134-C06, M0134-C09, M0134-C10, M0134-C11, M0134-C12, M0134-D02, M0134-DO3, M0134-E04, M0134-E07, M0134-E08, M134-E11, M0134-F01, M0134-F05, M0134-G02, M0134-G04, M0134-G07, M0135-A03, M0135-A05, M0135-A06, M0135-A07, M0135-B02, M0135-B08, M0135-C01, M0135-C11, M0135-E03, M0135-F03, M0135-F11, M0135-G02, M0135-G03, M0135-G07, M0135-G11, M0135-H03, M0135-H10, M0105-C05, M0105-E11, M0105-F08, M0107-A12, M0108-A02, M0109-G11, M0110-G05, M0129-

B11, M0130-A01, M0130-C12, M0130-F06, M0130-H04, M0131-A06, M0131-D03, M0132-A04, M0133-B08, M0133-E05, M0121-E07, M0118-F11, M0125-G07, M0124-E07, M0119-D01, M0119-A02, M0122-C06, M0123-G07, M0063-A02, M0063-A04, M0063-B01, M0063-B11, M0063-C07, M0063-G01, M0065-E12, M0065-G03, M0065-H05, M0067-A02, M0067-B06, M0067-B09, M0067-C10, M0067-F02, M0067-F06, M0069-A04, M0069-A11, M0069-C02, M0069-D10, M0069-G07, M0071-A01, M0071-B07, M0071-D05, M0071-D09, M0071-H03, M0071-H06, M0087-F09, M0088-F07, M0088-G10, M0088-H10, M0089-C01, M0089-F05, M0089-B07, M0089-H11, , M0034-C04, M0039-F01, M0041-B05, M0041-G01, M0042-B06, M0006-B10, M0007-H06, M0008-H09, M0009-H08, M0011-H11, M0015-F02, M0016-D01, M0013-D11, M0013-G12, M0013-H06, M0014-C09, M0014-G11, M0016-A11, M0016-H05, M0019-C05, M0020-B01, M0022-C07, M0025-D04 and M0027-E11.

15. The protein of claim 1, wherein the protein comprises an antibody comprising a heavy chain selected from the group of antibodies consisting of: M0134-A02, M134-A05, M134-A07, M134-A09, M134-A10, M134-A11, M0134-B01, M134-B04, M0134-B08, M0134-B11, M0134-C01, M0134-C02, M0134-C06, M0134-C09, M0134-C10, M0134-C11, M0134-C12, M0134-D02, M0134-D03, M0134-E04, M0134-E07, M0134-E08, M134-E11, M0134-F01, M0134-F05, M0134-G02, M0134-G04, M0134-G07, M0135-A03, M0135-A05, M0135-A06, M0135-A07, M0135-B02, M0135-B08, M0135-C01, M0135-C11, M0135-E03, M0135-F03, M0135-F11, M0135-G02, M0135-G03, M0135-G07, M0135-G11, M0135-H03, M0135-H10, M0105-C05, M0105-E11, M0105-F08, M0107-A12, M0108-A02, M0109-G11, M0110-G05, M0129-B11, M0130-A01, M0130-C12, M0130-F06, M0130-H04, M0131-A06, M0131-D03, M0132-A04, M0133-B08, M0133-E05, M0121-E07, M0118-F11, M0125-G07, M0124-E07, M0119-D01, M0119-A02, M0122-C06, M0123-G07, M0063-A02, M0063-A04, M0063-B01, M0063-B11, M0063-C07, M0063-G01, M0065-E12, M0065-G03, M0065-H05, M0067-A02, M0067-B06, M0067-B09, M0067-C10, M0067-F02, M0067-F06, M0069-A04, M0069-A11, M0069-C02, M0069-D10, M0069-G07, M0071-A01, M0071-B07, M0071-D05, M0071-D09, M0071-H03, M0071-H06, M0087-F09, M0088-F07, M0088-G10, M0088-H10, M0089-C01, M0089-F05, M0089-B07, M0089-H11, , M0034-C04, M0039-F01,

M0041-B05, M0041-G01, M0042-B06, M0006-B10, M0007-H06, M0008-H09, M0009-H08, M0011-H11, M0015-F02, M0016-D01, M0013-D11, M0013-G12, M0013-H06, M0014-C09, M0014-G11, M0016-A11, M0016-H05, M0019-C05, M0020-B01, M0022-C07, M0025-D04 and M0027-E11.

16. The protein of claim 1, wherein the protein comprises an antibody comprising a light chain selected from the group of antibodies consisting of: M0134-A02, M134-A05, M134-A07, M134-A09, M134-A10, M134-A11, M0134-B01, M134-B04, M0134-B08, M0134-B11, M0134-C01, M0134-C02, M0134-C06, M0134-C09, M0134-C10, M0134-C11, M0134-C12, M0134-D02, M0134-D03, M0134-E04, M0134-E07, M0134-E08, M134-E11, M0134-F01, M0134-F05, M0134-G02, M0134-G04, M0134-G07, M0135-A03, M0135-A05, M0135-A06, M0135-A07, M0135-B02, M0135-B08, M0135-C01, M0135-C11, M0135-E03, M0135-F03, M0135-F11, M0135-G02, M0135-G03, M0135-G07, M0135-G11, M0135-H03, M0135-H10, M0105-C05, M0105-E11, M0105-F08, M0107-A12, M0108-A02, M0109-G11, M0110-G05, M0129-B11, M0130-A01, M0130-C12, M0130-F06, M0130-H04, M0131-A06, M0131-D03, M0132-A04, M0133-B08, M0133-E05, M0121-E07, M0118-F11, M0125-G07, M0124-E07, M0119-D01, M0119-A02, M0122-C06, M0123-G07, M0063-A02, M0063-A04, M0063-B01, M0063-B11, M0063-C07, M0063-G01, M0065-E12, M0065-G03, M0065-H05, M0067-A02, M0067-B06, M0067-B09, M0067-C10, M0067-F02, M0067-F06, M0069-A04, M0069-A11, M0069-C02, M0069-D10, M0069-G07, M0071-A01, M0071-B07, M0071-D05, M0071-D09, M0071-H03, M0071-H06, M0087-F09, M0088-F07, M0088-G10, M0088-H10, M0089-C01, M0089-F05, M0089-B07, M0089-H11, , M0034-C04, M0039-F01, M0041-B05, M0041-G01, M0042-B06, M0006-B10, M0007-H06, M0008-H09, M0009-H08, M0011-H11, M0015-F02, M0016-D01, M0013-D11, M0013-G12, M0013-H06, M0014-C09, M0014-G11, M0016-A11, M0016-H05, M0019-C05, M0020-B01, M0022-C07, M0025-D04 and M0027-E11.

17. The protein of claim 1, wherein the protein comprises an antibody comprising one or more heavy chain CDRs selected from the group of antibodies consisting of: M0134-A02, M134-A05, M134-A07, M134-A09, M134-A10, M134-A11, M0134-B01,

M134-B04, M0134-B08, M0134-B11, M0134-C01, M0134-C02, M0134-C06, M0134-C09, M0134-C10, M0134-C11, M0134-C12, M0134-D02, M0134-DO3, M0134-E04, M0134-E07, M0134-E08, M134-E11, M0134-F01, M0134-F05, M0134-G02, M0134-G04, M0134-G07, M0135-A03, M0135-A05, M0135-A06, M0135-A07, M0135-B02, M0135-B08, M0135-C01, M0135-C11, M0135-E03, M0135-F03, M0135-F11, M0135-G02, M0135-G03, M0135-G07, M0135-G11, M0135-H03, M0135-H10, M0105-C05, M0105-E11, M0105-F08, M0107-A12, M0108-A02, M0109-G11, M0110-G05, M0129-B11, M0130-A01, M0130-C12, M0130-F06, M0130-H04, M0131-A06, M0131-D03, M0132-A04, M0133-B08, M0133-E05, M0121-E07, M0118-F11, M0125-G07, M0124-E07, M0119-D01, M0119-A02, M0122-C06, M0123-G07, M0063-A02, M0063-A04, M0063-B01, M0063-B11, M0063-C07, M0063-G01, M0065-E12, M0065-G03, M0065-H05, M0067-A02, M0067-B06, M0067-B09, M0067-C10, M0067-F02, M0067-F06, M0069-A04, M0069-A11, M0069-C02, M0069-D10, M0069-G07, M0071-A01, M0071-B07, M0071-D05, M0071-D09, M0071-H03, M0071-H06, M0087-F09, M0088-F07, M0088-G10, M0088-H10, M0089-C01, M0089-F05, M0089-B07, M0089-H11, , M0034-C04, M0039-F01, M0041-B05, M0041-G01, M0042-B06, M0006-B10, M0007-H06, M0008-H09, M0009-H08, M0011-H11, M0015-F02, M0016-D01, M0013-D11, M0013-G12, M0013-H06, M0014-C09, M0014-G11, M0016-A11, M0016-H05, M0019-C05, M0020-B01, M0022-C07, M0025-D04 and M0027-E11.

18. The protein of claim 1, wherein the protein comprises an antibody comprising one or more light chain CDRs selected from the group of antibodies consisting of:

M0134-A02, M134-A05, M134-A07, M134-A09, M134-A10, M134-A11, M0134-B01, M134-B04, M0134-B08, M0134-B11, M0134-C01, M0134-C02, M0134-C06, M0134-C09, M0134-C10, M0134-C11, M0134-C12, M0134-D02, M0134-DO3, M0134-E04, M0134-E07, M0134-E08, M134-E11, M0134-F01, M0134-F05, M0134-G02, M0134-G04, M0134-G07, M0135-A03, M0135-A05, M0135-A06, M0135-A07, M0135-B02, M0135-B08, M0135-C01, M0135-C11, M0135-E03, M0135-F03, M0135-F11, M0135-G02, M0135-G03, M0135-G07, M0135-G11, M0135-H03, M0135-H10, M0105-C05, M0105-E11, M0105-F08, M0107-A12, M0108-A02, M0109-G11, M0110-G05, M0129-B11, M0130-A01, M0130-C12, M0130-F06, M0130-H04, M0131-A06, M0131-D03,

M0132-A04, M0133-B08, M0133-E05, M0121-E07, M0118-F11, M0125-G07, M0124-E07, M0119-D01, M0119-A02, M0122-C06, M0123-G07, M0063-A02, M0063-A04, M0063-B01, M0063-B11, M0063-C07, M0063-G01, M0065-E12, M0065-G03, M0065-H05, M0067-A02, M0067-B06, M0067-B09, M0067-C10, M0067-F02, M0067-F06, M0069-A04, M0069-A11, M0069-C02, M0069-D10, M0069-G07, M0071-A01, M0071-B07, M0071-D05, M0071-D09, M0071-H03, M0071-H06, M0087-F09, M0088-F07, M0088-G10, M0088-H10, M0089-C01, M0089-F05, M0089-B07, M0089-H11, , M0034-C04, M0039-F01, M0041-B05, M0041-G01, M0042-B06, M0006-B10, M0007-H06, M0008-H09, M0009-H08, M0011-H11, M0015-F02, M0016-D01, M0013-D11, M0013-G12, M0013-H06, M0014-C09, M0014-G11, M0016-A11, M0016-H05, M0019-C05, M0020-B01, M0022-C07, M0025-D04 and M0027-E11.

19. The protein of claim 1, wherein the protein comprises the light and heavy chains of antibody M0008-H09, M0131-A06 or M0121-E07.

20. The protein of claim 1, wherein the protein comprises the light and heavy chain CDRs of antibody M0008-H09, M0131-A06 or M0121-E07.

21. The protein of claim 1, wherein the protein comprises the light and heavy chains of antibody DX-2712.

22. The protein of claim 1, wherein the protein comprises the light and heavy chain CDRs of antibody DX-2712.

23. The protein of claim 1, wherein the protein comprises the light and heavy chains of antibody 539B-X0041-D02.

24. The protein of claim 1, wherein the protein comprises the light and heavy chain CDRs of antibody 539B-X0041-D02.

25. The protein of claim 1, wherein the protein is a human or humanized antibody or is non-immunogenic in a human.

26. A method of inhibiting an interaction between MMP-12 and an MMP-12 substrate, the method comprising: contacting an MMP-12 binding protein of claim 1 with MMP-12, wherein the binding protein binds to MMP-12 and thereby prevents the binding of the MMP-12 substrate to MMP-12.

27. An MMP-12 binding protein-drug conjugate, wherein the conjugate comprises a MMP-12 binding protein of claim 1 and a drug.

28. The conjugate of claim 27, wherein the drug is a cytotoxic or cytostatic agent.

29. The conjugate of claim 28, wherein the drug is a cytotoxic agent and is selected from the group consisting of an auristatin, a DNA minor groove binding agent, a DNA minor groove alkylating agent, an enediyne, a lexitropsin, a duocarmycin, a taxane, a puromycin, a dolastatin, a podophyllotoxin, a baccatin derivative, a cryptophysin, a combretastatin, a maytansinoid, and a vinca alkaloid.

30. The conjugate of claim 28, wherein the drug is a cytotoxic agent and is an antitubulin agent.

31. The conjugate of claim 27, wherein the MMP-12 binding protein is conjugated to the drug via a linker.

32. A pharmaceutical composition comprising an MMP-12 binding protein of claim 1 and a pharmaceutically acceptable carrier.

33. A method of detecting an MMP-12 in a sample, the method comprising: contacting the sample with an MMP-12 binding protein of claim 1; and detecting an interaction between the protein and the MMP-12, if present.

34. The method of claim 33, wherein the protein includes a detectable label.

35. A method of modulating MMP-12 activity, the method comprising:
contacting an MMP-12 with an MMP-12 binding protein of claim 1, thereby
modulating MMP-12 activity.

36. A method for modulating metastatic activity in a subject, the method
comprising:
administering, to a subject, an MMP-12 binding protein of claim 1 in an amount
effective to modulate metastatic activity.

37. A method of treating cancer, the method comprising:
administering, to a subject, an MMP-12 binding protein of claim 1 in an amount
sufficient to treat a cancer in the subject.

38. The method of claim 37 further comprising providing to the subject a second
therapy that is an anti-cancer therapy.

39. A method of treating inflammation, the method comprising:
administering, to a subject, an MMP-12 binding protein of claim 1 in an amount
sufficient to treat inflammation in the subject.

40. The method of claim 39 further comprising providing to the subject a second
therapy that is a therapy for inflammation.

41. A method of treating a disease associated with inflammation of the lung, the
method comprising:
administering, to a subject, an MMP-12 binding protein of claim 1 in an amount
sufficient to treat a disease associated with inflammation of the lung in the subject.

42. The method of claim 41 further comprising providing to the subject a second therapy that is a therapy for inflammation.

43. A method of treating cardiovascular disease, the method comprising:
administering, to a subject, an MMP-12 binding protein of claim 1 in an amount sufficient to treat cardiovascular disease in the subject.

44. The method of claim 43 further comprising providing to the subject a second therapy that is a therapy for cardiovascular disease.

45. A method of treating a stroke or aneurysm, the method comprising:
administering, to a subject, an MMP-12 binding protein of claim 1 in an amount sufficient to treat a stroke or aneurysm in the subject.

46. The method of claim 45 further comprising providing to the subject a second therapy that is a therapy for a stroke or aneurysm.

47. A method of treating nerve damage, the method comprising:
administering, to a subject, an MMP-12 binding protein of claim 1 in an amount sufficient to treat the nerve damage in the subject.

48. The method of claim 47 further comprising providing to the subject a second therapy that is a therapy for nerve damage.

49. A method of imaging a subject, the method comprising:
administering an MMP-12 binding protein of claim 1 to the subject.

50. The method of claim 49, wherein the MMP-12 binding protein comprises a detectable label.

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PLATE 539B-R0064 □	NAME USED □
539B-M0030-A10 □	A1 □
539B-M0032-H09 □	A4 □
539B-M0038-A03 □	A9 □
539B-M0038-H04 □	A12 □
539B-M0039-B02 □	B1 □
539B-M0040-B05 □	B5 □
539B-M0041-A05 □	B7 □
539A-R0011-B11 □	F1 □
PLATE 539B-R0065 □	□
539B-M0007-A10 □	M7A10 □
539B-M0008-E08 □	M8E8 □

INHIBITION ASSAY OF MMP12 ENZYME

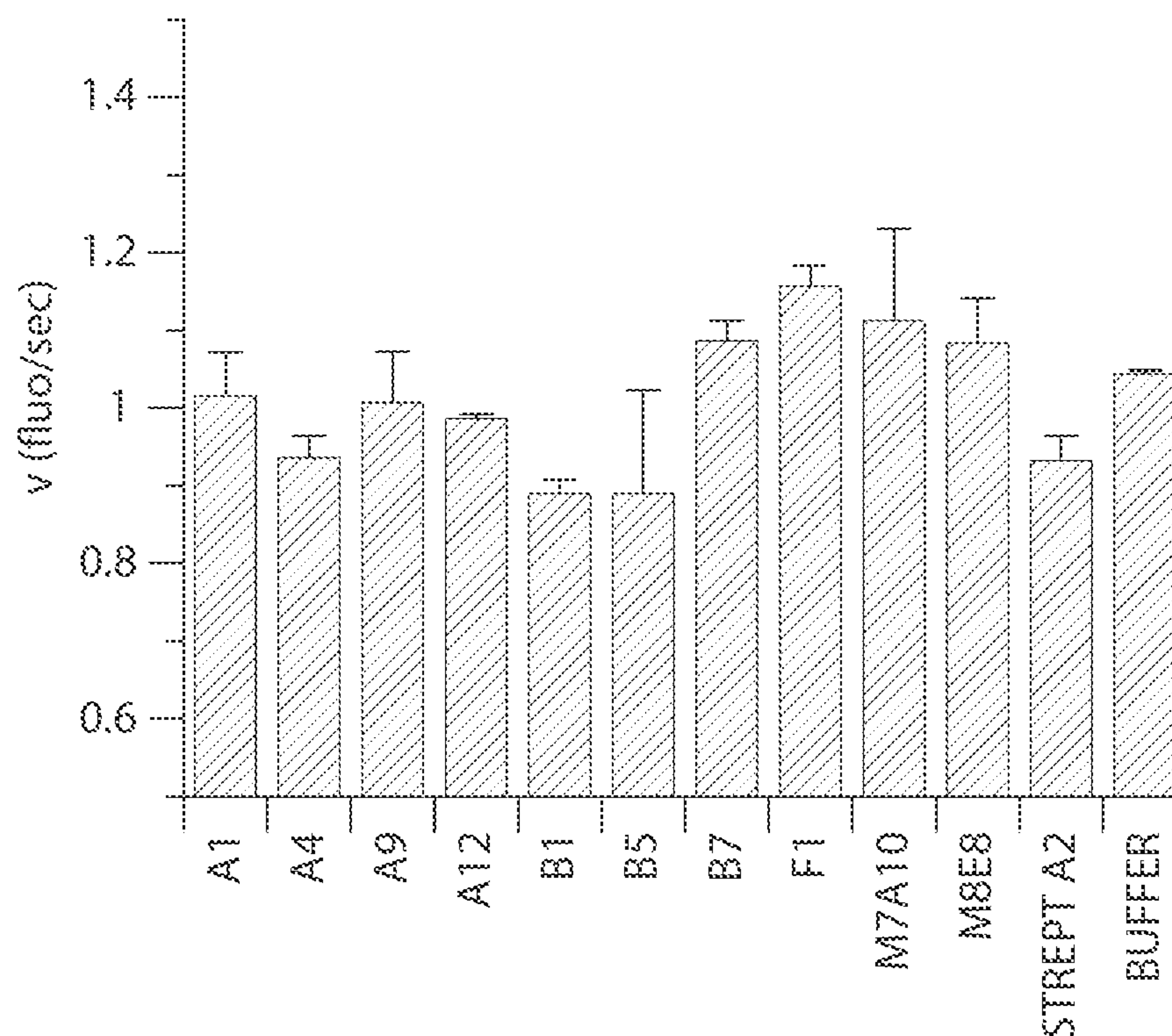


Figure 1

SUBSTITUTE SHEET (RULE 26)

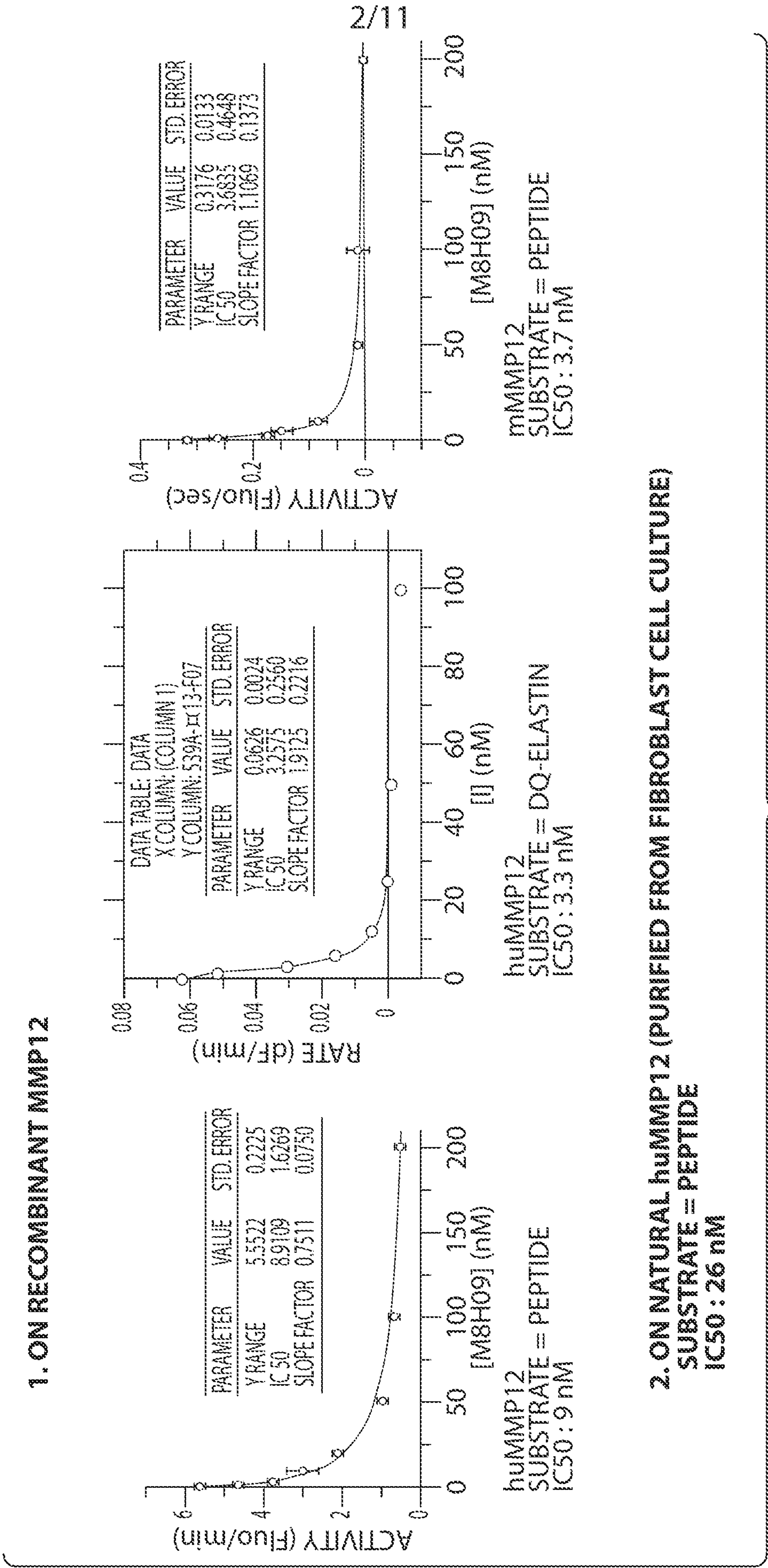
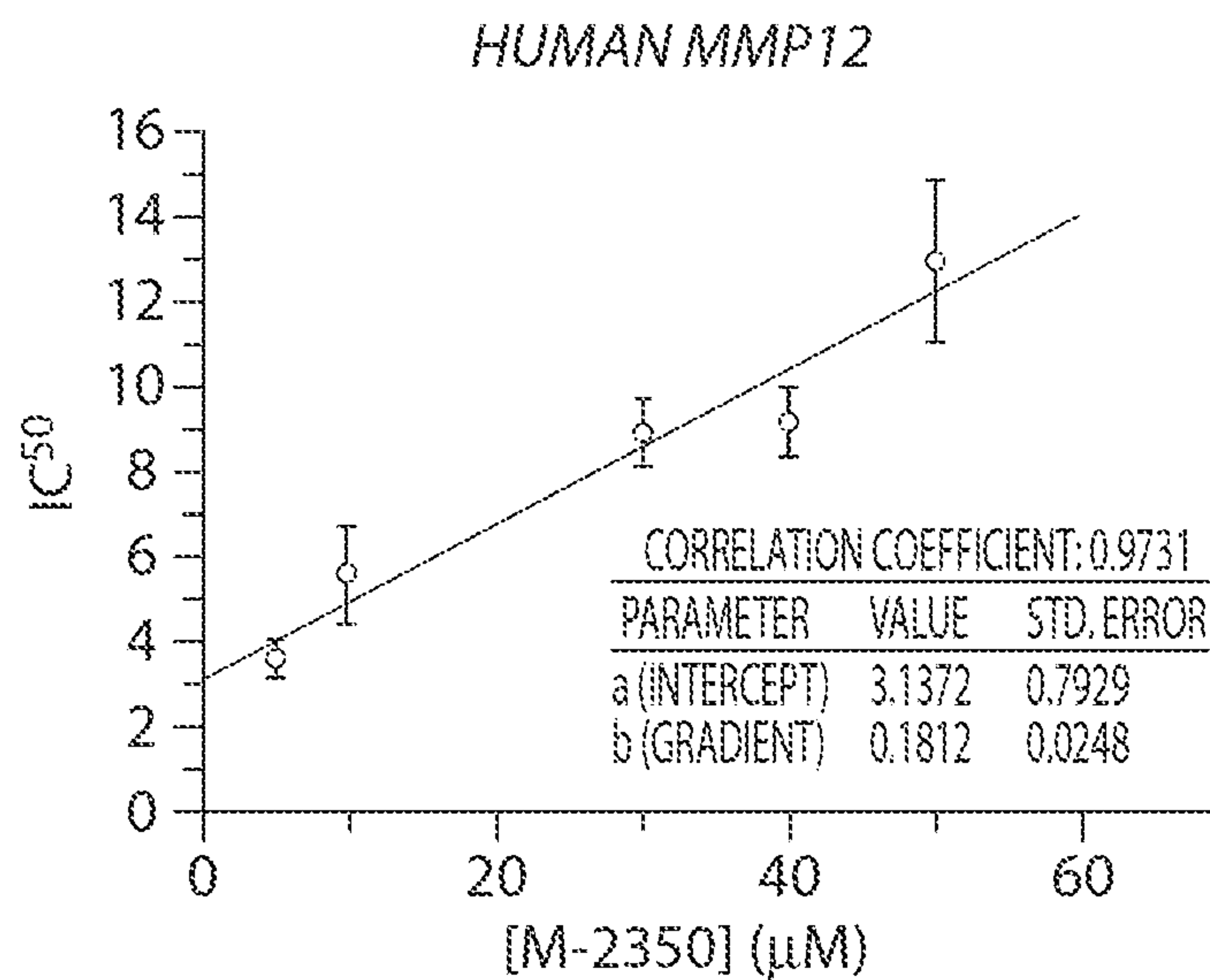


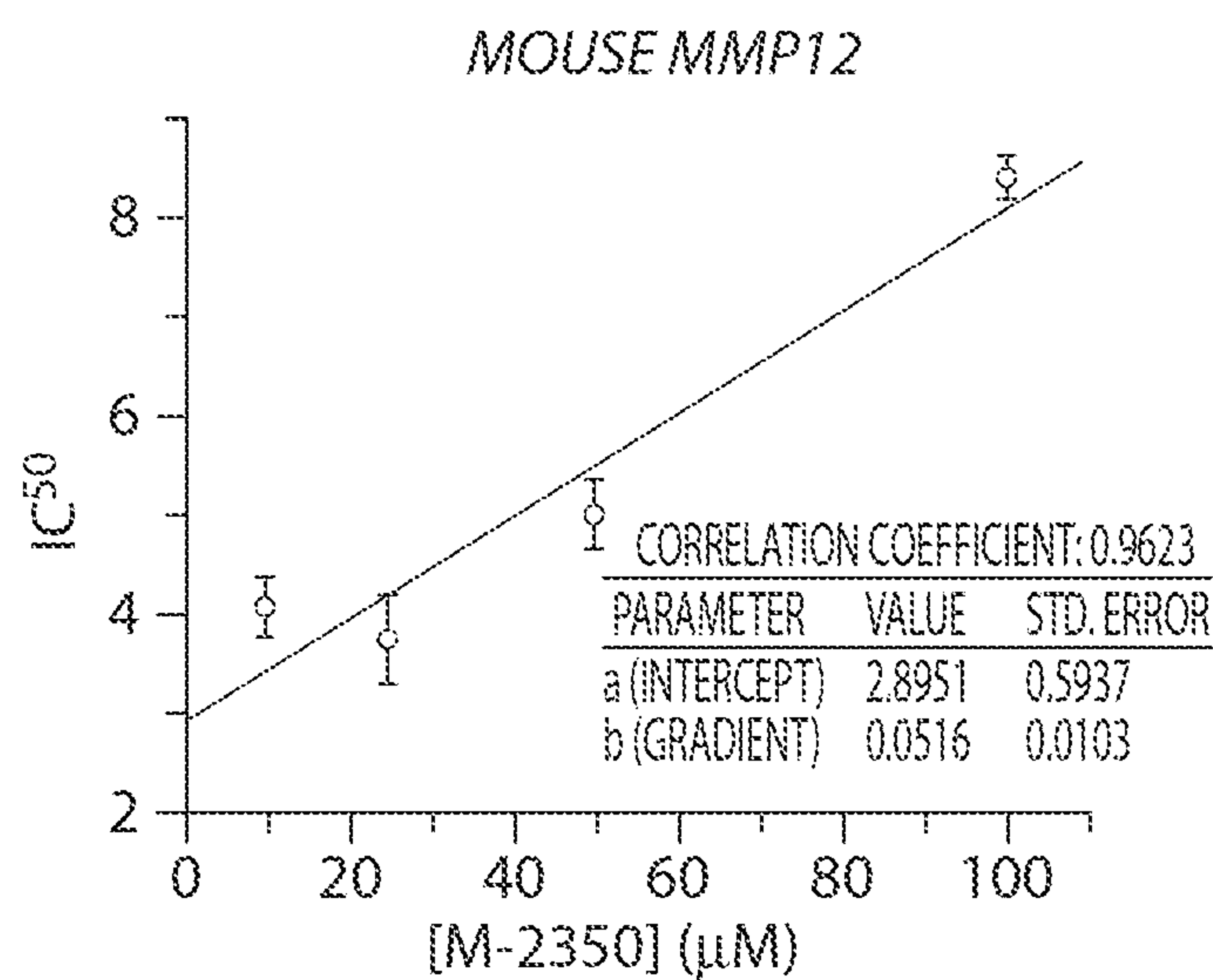
Figure 2

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LINEAR RELATIONSHIP
⇒ COMPETITIVE MODEL
⇒ $K_i = 2.8 \pm 0.8$ nM
 $K_m = 16 \pm 6$ μM

Figure 3A



LINEAR RELATIONSHIP
⇒ COMPETITIVE MODEL
⇒ $K_i = 2.2 \pm 0.6$ nM
 $K_m = 42 \pm 17$ μM

Figure 3B

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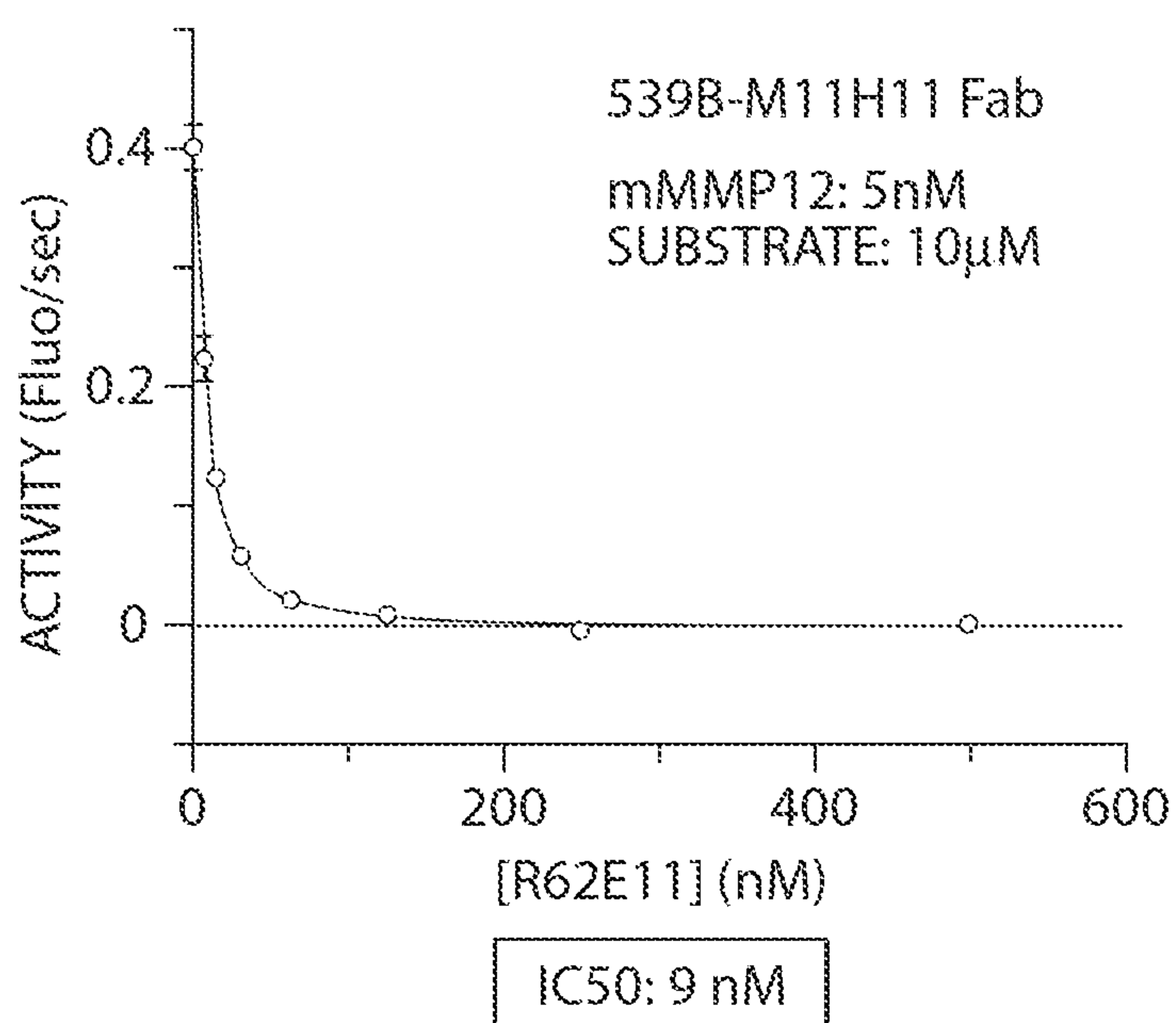
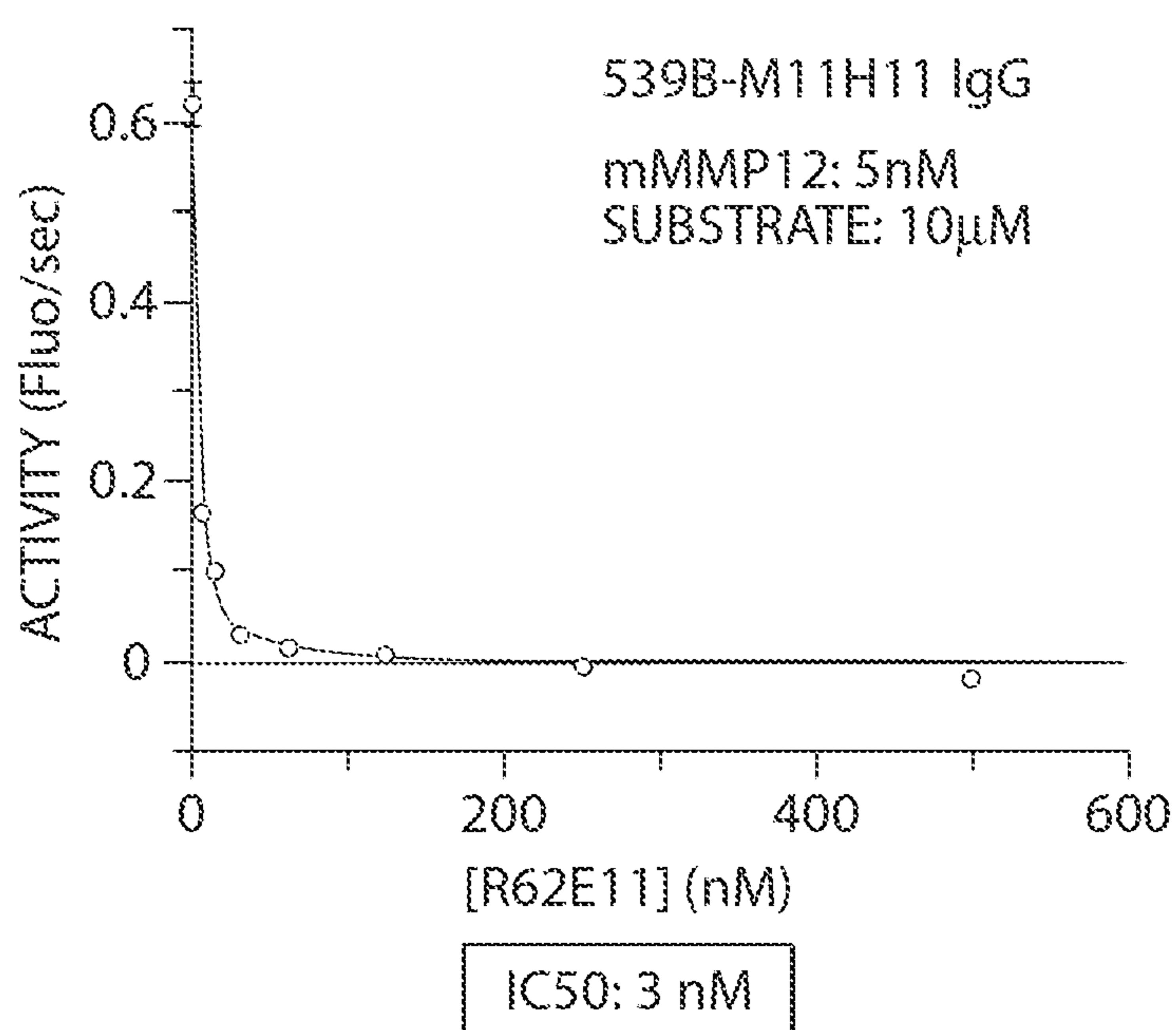


Figure 4A



SUBSTRATE = PEPTIDE (Mca-Pro-Leu-Gly-Leu-Dpa-Ala-Arg-NH₂)
NB: NO INHIBITION OF hMMP12 (500nM)!

Figure 4B

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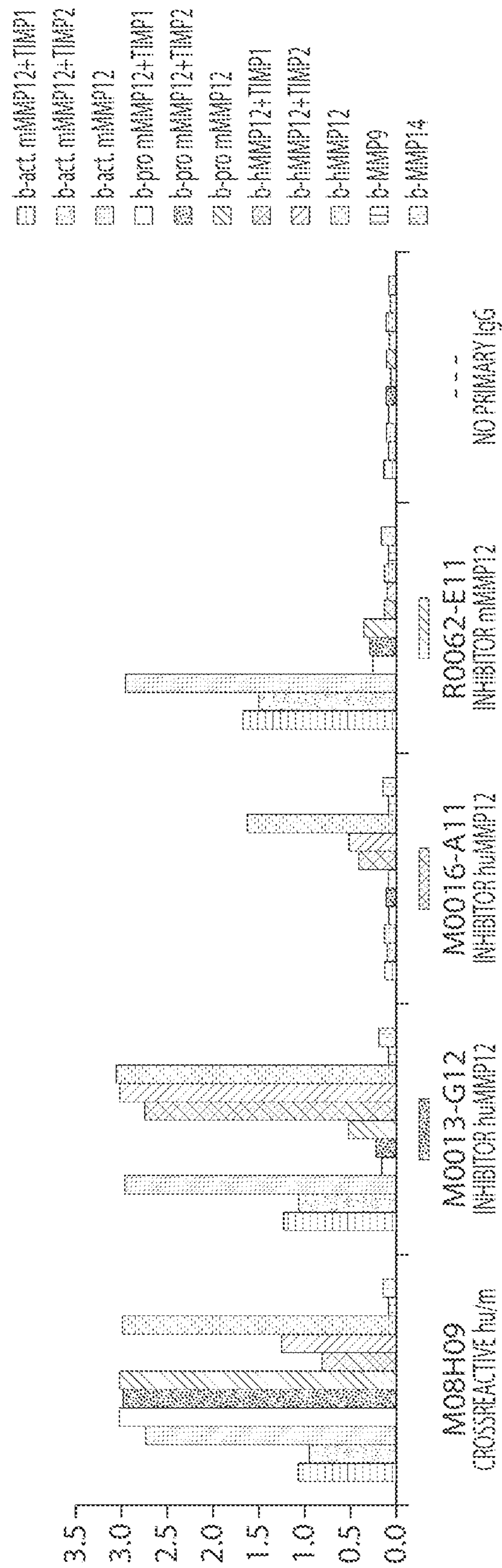
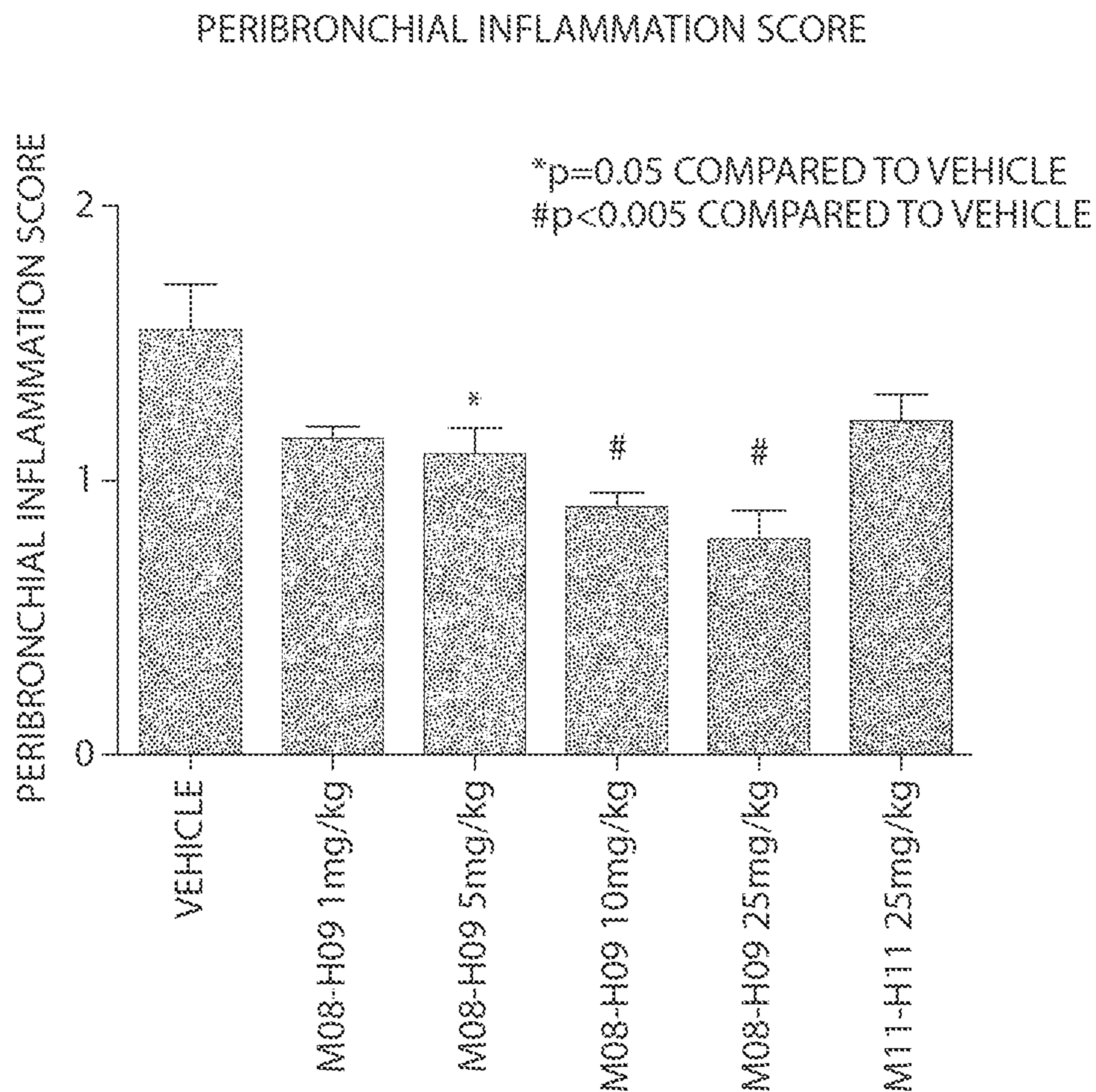


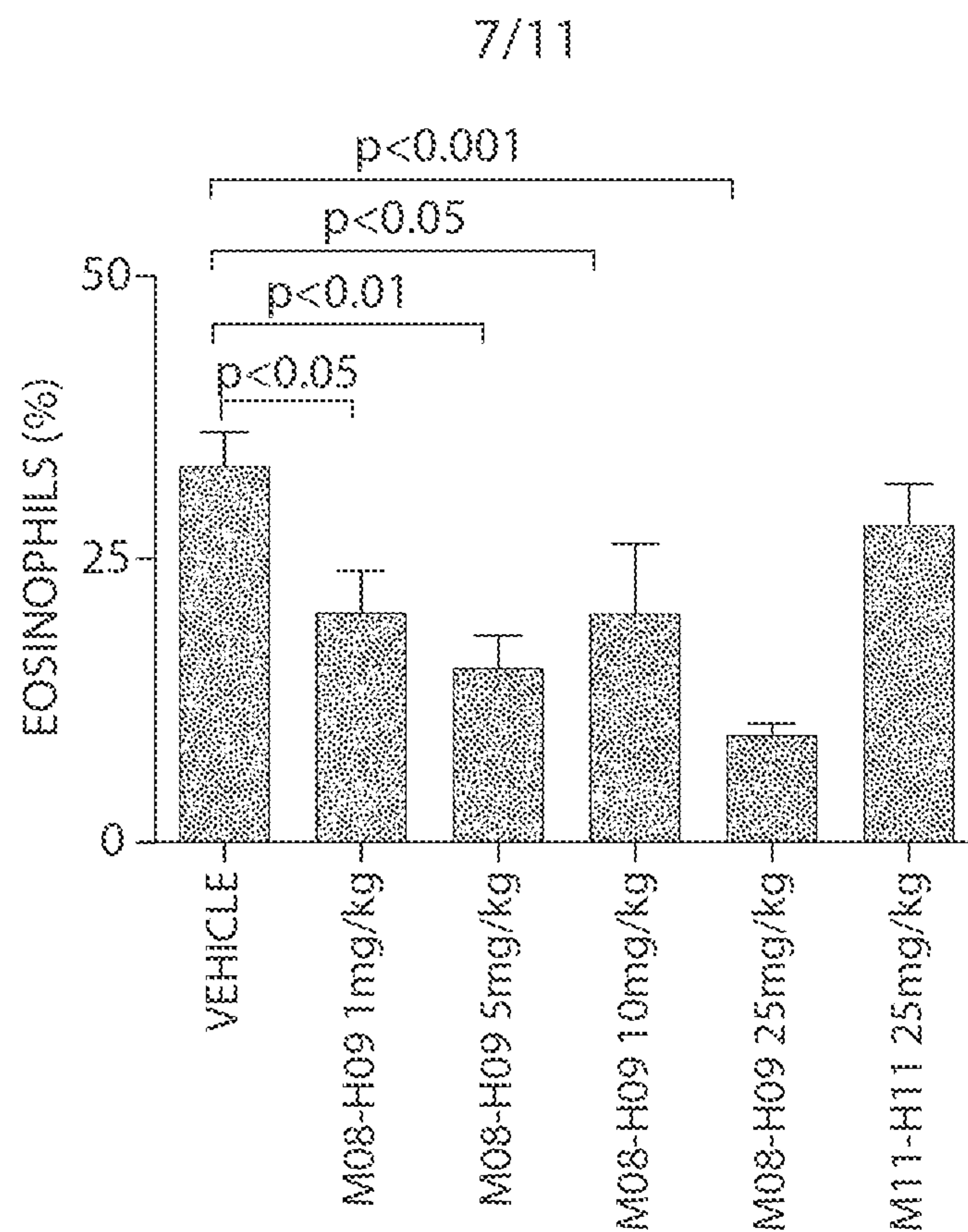
Figure 5

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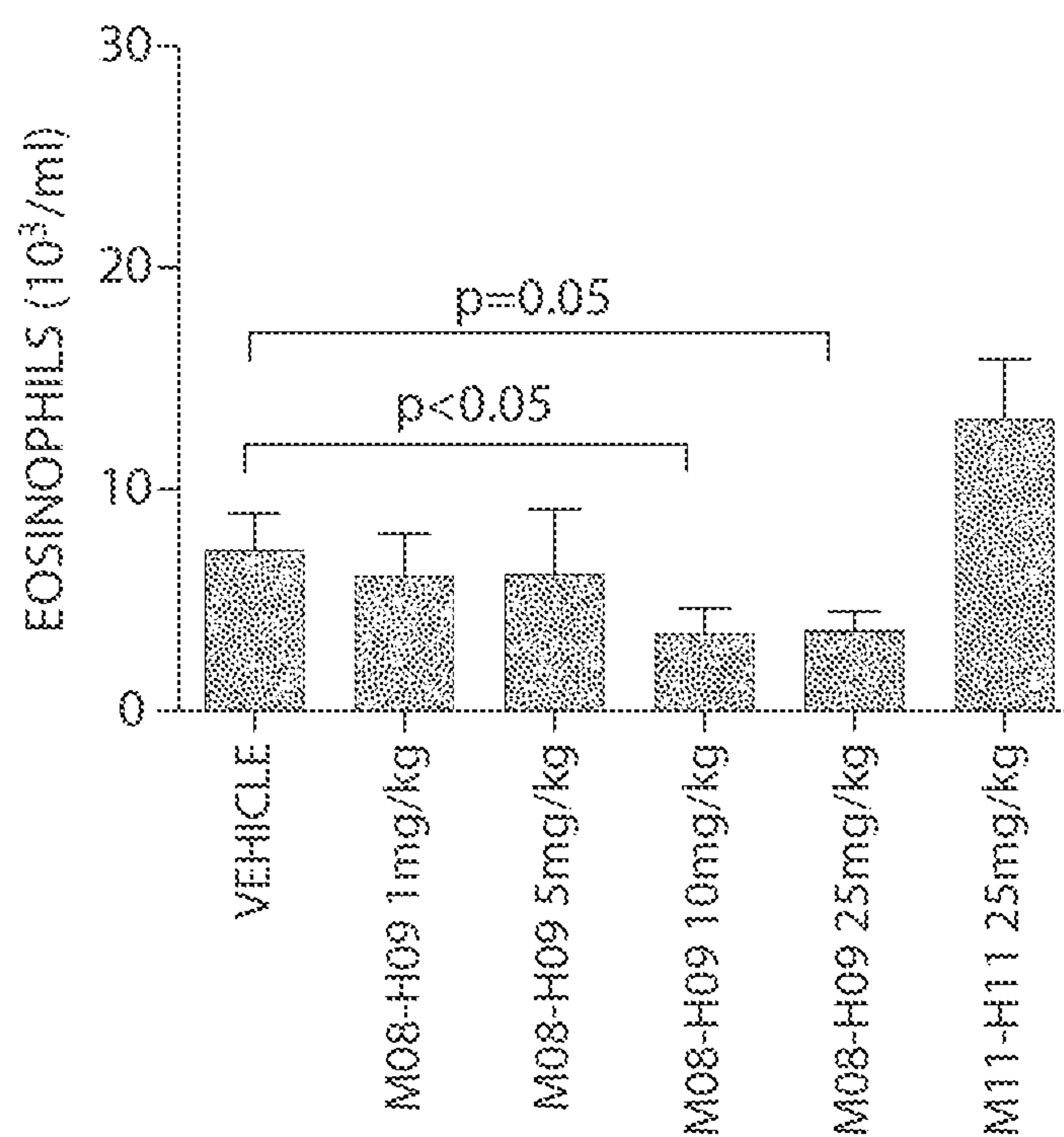
COMMENT: THIS IS THE MOST ENCOURAGING RESULT SHOWING A DOSE-RESPONSE. IN OUR EXPERIENCE, THIS SCORE IS THE MOST RELIABLE PARAMETER RELATED TO BRONCHIAL INFLAMMATION.

Figure 6



COMMENT: EOSINOPHIL PERCENTAGES IN BAL ARE DECREASED FOR EACH TESTED M08-H09

Figure 7A



COMMENT: EOSINOPHIL COUNTS (ABSOLUTE VALUE) ARE DECREASED WITH M08-H09 10 AND 25 mg/kg.

Figure 7B

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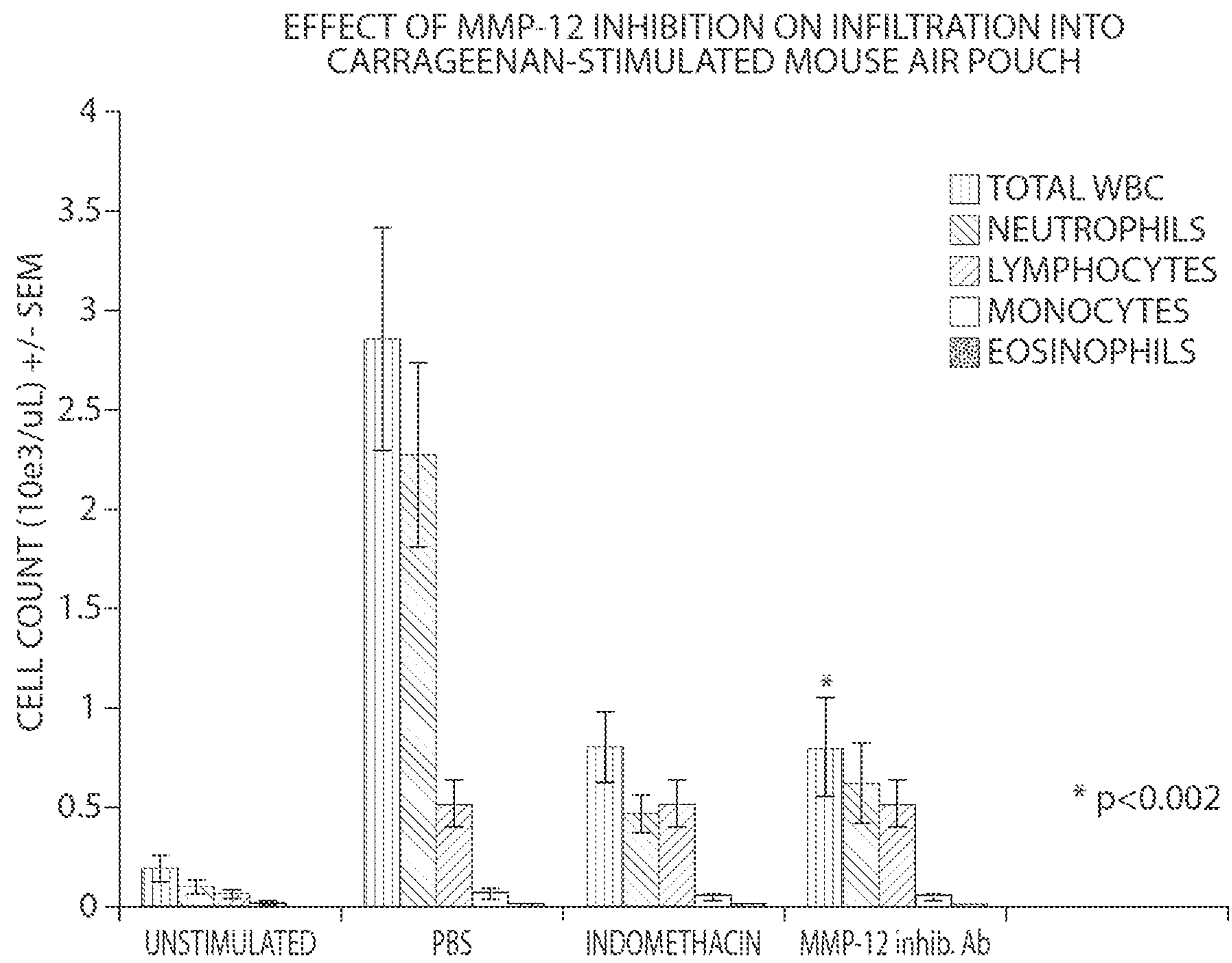
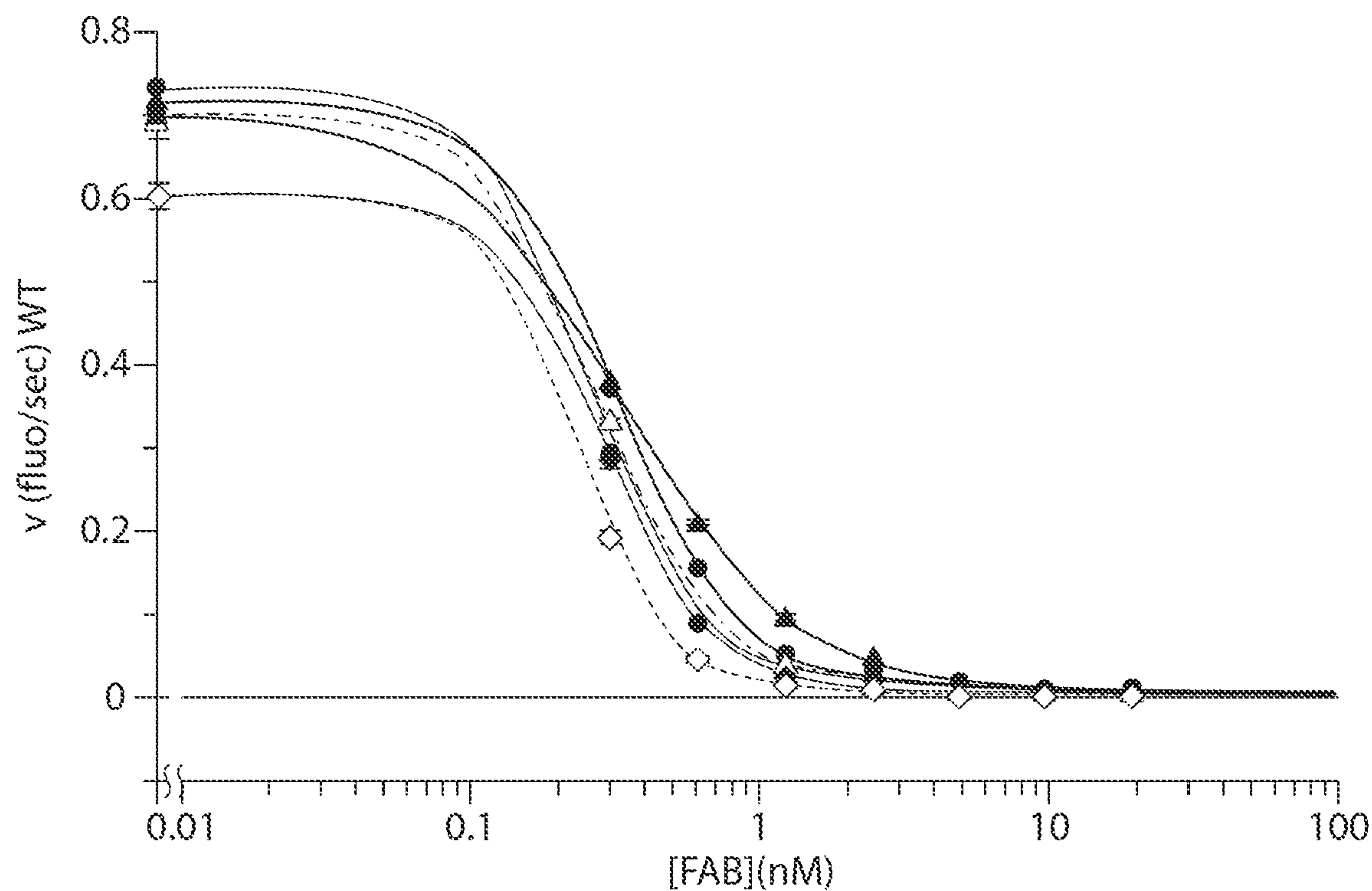


Figure 8

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PARENTAL VL-CDR1: RANQSIYTYLN

SUBSTITUTED AMINO-ACID

● $v(\text{fluor/sec}) \text{ WT}$	▲ $v(\text{fluor/sec}) \text{ V}$
— $\text{IC}_{50} = 0.321 \text{ nM}$	— $\text{IC}_{50} = 0.343 \text{ nM}$
● $v(\text{fluor/sec}) \text{ D}$	◆ $v(\text{Fluor/sec}) \text{ T}$
— $\text{IC}_{50} = 0.261 \text{ nM}$	— $\text{IC}_{50} = 0.294 \text{ nM}$
△ $v(\text{fluor/sec}) \text{ E}$	◇ $v(\text{Fluor/sec}) \text{ S}$
- - - $\text{IC}_{50} = 0.297 \text{ nM}$	- - - $\text{IC}_{50} = 0.233 \text{ nM}$

- SUCCESSFUL WITH ALL FAB MUTANTS (IDENTICAL IC_{50} COMPARED TO LEAD WITH PARENTAL VL)
- VL WITH GERMLINE RESIDUE (S) IS CHOSEN TO REPLACE PARENTAL VL (N)
- CROSSREACTIVITY TO MOUSE MMP12 VERIFIED AND IDENTICAL TO LEAD WITH PARENTAL VL
- CROSSREACTIVITY TO A PANEL OF MMPs VERIFIED : NO CROSSREACTIVITY
- LEAD NAME: 539B-M131A06-GA-S

Figure 9

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NAME	SEQUENCE																												AFF. MAT. CYCLE	HUMAN MMP12								
	HC-CDR1				HC-CDR2												HC-CDR3													IC50	Kd (nM)	OFF RATE						
M08-H09	D	Y	N	M	H	Y	I	G	P	S	G	G	Y	T	H	Y	A	D	S	V	K	G	D	I	R	G	A	Y	S	S	G	L	E	D	Y	14	18	9.54E-03
M63-B01	W	Y	M	M	G	S	I	S	P	S	G	G	Y	T	F	Y	A	D	S	V	K	G	D	I	R	G	A	Y	S	S	G	L	F	D	Y	0.7	0.17	8.80E-05
M63-B11	P	Y	W	M	H	G	I	G	P	S	G	G	L	T	F	Y	A	D	S	V	K	G	D	I	R	G	A	Y	S	S	G	L	F	D	Y	0.7	0.12	5.88E-05
M63-C07	P	Y	W	M	S	G	I	S	P	S	G	G	I	T	F	Y	A	D	S	V	K	G	D	I	R	G	A	Y	S	S	G	L	F	D	Y	1	23	6.20E-03
M63-G01	W	Y	W	M	V	S	I	G	P	S	G	G	D	T	F	Y	A	D	S	V	K	G	D	I	R	G	A	Y	S	S	G	L	F	D	Y	0.8	1.6	1.01E-03
M065-H05	Y	Y	G	M	G	V	I	S	S	S	G	G	F	T	F	Y	A	D	S	V	K	G	D	I	R	G	A	Y	S	S	G	L	F	D	Y	0.7	2.2	1.59E-03
M067-B06	W	Y	W	M	H	G	I	V	S	S	G	G	T	T	I	Y	A	D	S	V	K	G	D	I	R	G	A	Y	S	S	G	L	F	D	Y	0.7	0.62	3.56E-04
M067-F06	W	Y	N	M	S	R	I	S	P	S	G	G	D	T	G	Y	A	D	S	V	K	G	D	I	R	G	A	Y	S	S	G	L	F	D	Y	0.7	0.2	8.58E-05
M069-C02	Y	Y	N	M	H	G	I	G	P	S	G	G	G	T	L	Y	A	D	S	V	K	G	D	I	R	G	A	Y	S	S	G	L	F	D	Y	1.6	7	2.89E-03
M071-A01	E	Y	W	M	Y	G	I	S	P	S	G	G	M	T	F	Y	A	D	S	V	K	G	D	I	R	G	A	Y	S	S	G	L	F	D	Y	0.3	1.1	3.30E-04
M071-H03	P	Y	W	M	H	G	I	G	P	S	G	G	P	T	F	Y	A	D	S	I	K	G	D	I	R	G	A	Y	S	S	G	L	F	D	Y	0.2	1	8.21E-04
M069-D10	L	Y	H	M	H	G	I	G	P	S	G	G	W	T	I	Y	A	D	S	V	K	G	D	I	R	G	A	Y	S	S	G	L	F	D	Y	23	5.7	3.72E-03
M071-D09	P	Y	W	M	H	G	I	S	S	S	G	G	D	T	L	Y	A	D	S	V	K	G	D	I	R	G	A	Y	S	S	G	L	F	D	Y	24	4.2	2.40E-03
M065-E12	W	Y	N	M	H	G	I	S	P	S	G	G	N	T	S	Y	A	D	S	V	K	G	D	I	R	G	A	Y	S	S	G	L	F	D	Y	1.4	1.1	8.63E-04
M088-H10	W	Y	W	M	V	S	I	V	P	S	G	G	F	T	I	Y	A	D	S	V	K	G	D	I	R	G	A	Y	S	S	G	L	F	D	Y	0.6		
M107-A12	D	Y	N	M	H	Y	I	G	P	S	G	G	Y	T	H	Y	A	D	S	V	K	G	D	I	R	G	A	Y	A	S	G	L	F	D	Y	2.34	1.8	1.31E-03
M108-A02	W	Y	W	M	H	G	I	Y	S	S	G	G	D	T	I	Y	A	D	S	V	K	G	D	I	R	G	P	H	S	S	G	L	F	D	Y	2.21	ND	4.63E-03
M109-G11	E	Y	N	M	H	G	I	V	P	S	G	G	L	T	H	Y	A	D	S	V	K	G	D	I	R	G	A	Y	S	S	G	L	F	D	Y	6.22	7.5	3.90E-03
M131-A06	W	Y	W	M	H	G	I	S	P	S	G	G	M	T	M	Y	A	D	S	V	K	G	D	I	V	G	P	Y	S	A	G	L	F	D	Y	0.299	0.18	1.91E-04
M121-E07	W	Y	G	M	H	G	I	V	S	S	G	G	E	T	F	Y	A	D	S	V	K	G	D	I	R	G	V	F	L	S	G	L	F	D	H	0.006	0.197	1.41E-04
M118-F11	Y	Y	N	M	H	G	I	S	P	S	G	G	T	T	F	Y	A	D	S	V	K	G	D	I	T	G	A	Y	S	A	G	L	F	D	L	0.914	1.17	4.13E-04
M130-C12	E	Y	N	M	H	G	I	V	P	S	G	G	L	T	H	Y	A	D	S	V	K	G	D	I	R	G	A	Y	S	A	G	L	F	D	Y	0.688		

HC-CDR1 AA CHANGE COMPARED TO PARENTALHC-CDR2 AA CHANGE COMPARED TO PARENTALHC-CDR3 AA CHANGE COMPARED TO PARENTAL

Figure 10A

MOUSE MMP12			ESTIMATE Kd IMPROVEMENT ON huMMP-12	ESTIMATE OFF-RATE IMPROVEMENT ON mMMP-12
IC50	Kd (nM)	OFF RATE		
<10		4.00E-03		
>10		2.50E-03	100	1.5
>10		3.11E-03	150	1
<10		2.00E-03	8	2
>10		6.54E-03	10	
ND	ND	ND	8	
<10		3.05E-03	30	1
<10		2.50E-04	30	16
~10		4.54E-03	2.5	1
>10		1.54E-02	18	
<10	ND	ND	18	
	3.4	1.69E-03	3	2
	1.3	6.06E-04	4.5	7
	1.7	8.49E-04	18	5
>20	34.4	6.62E-03	23 (IC50)	1
	0.9	3.29E-04	10	12
	ND	2.42E-03	10	1.5
	1	5.40E-04	2	7
	7.27E-11	4.84E-05	100	82
	1.81E-10	1.15E-04	100	35
	7.27E-10	1.93E-04	20	20
			20 (IC50)	

Figure 10B

EFFECT OF MMP-12 INHIBITION ON INFILTRATION INTO CARRAGEENAN-STIMULATED MOUSE AIR POUCH

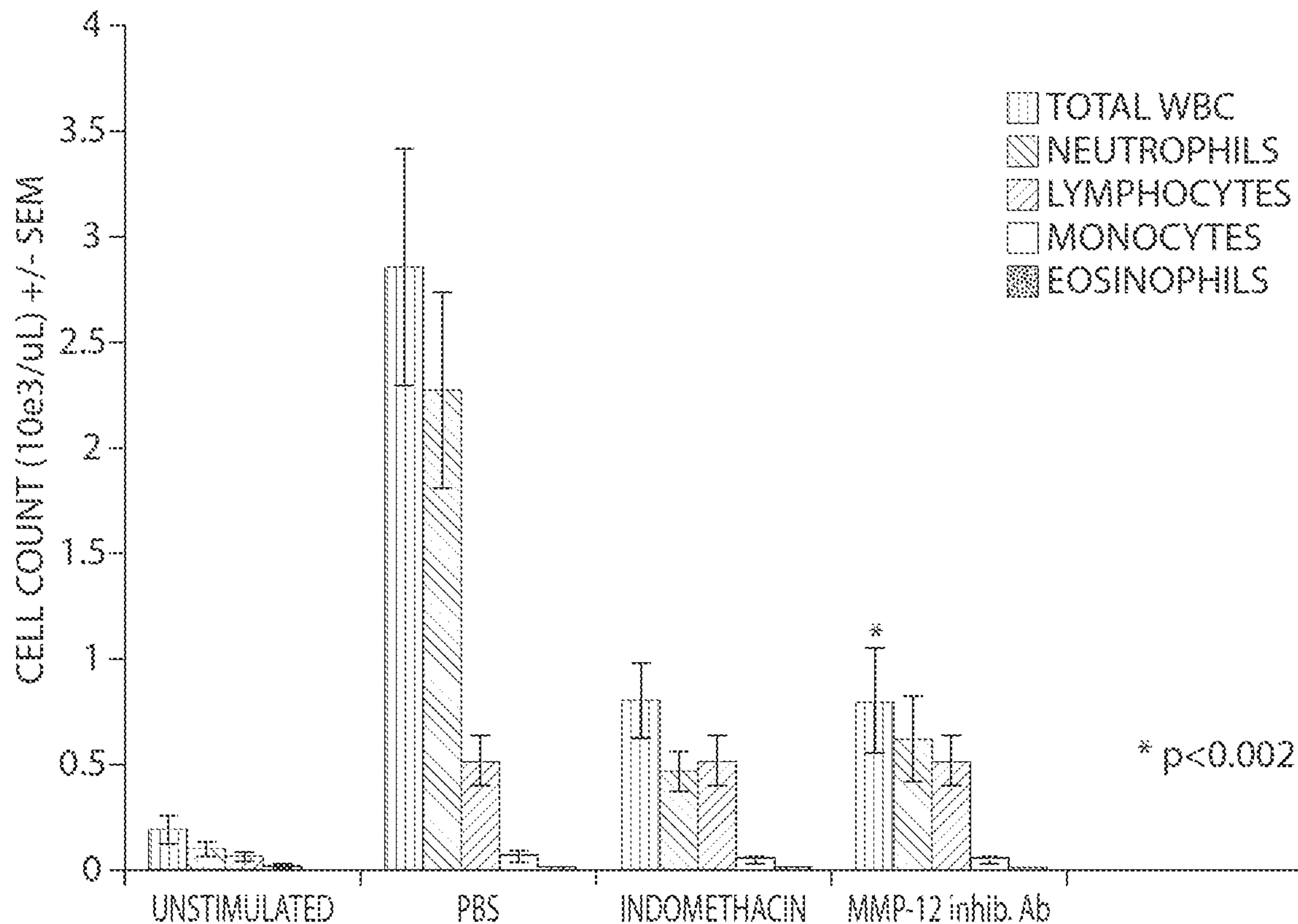


Figure 8