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(54) Title: ANTIBODIES TO MATRIX METALLOPROTEINASE 9

FIGURE 1

Anti-MMP9 humanized heavy chains

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AB0041    QVQLRESGPG LVAPSQSLSI TCTVSGFSLL SYGVHWVRQP PGKGLEWLGV
VH1       QVQLQESGPG LVKPSETLSL TCTVSGFSLL SYGVHWVRQP PGKGLEWLGV
VH2       QVQLQESGPG LVKPSETLSL TCTVSGFSLL SYGVHWVRQP PGKGLEWLGV
VH3       QVQLQESGPG LVKPSETLSL TCTVSGFSLL SYGVHWVRQP PGKGLEWLGV
VH4       QVQLQESGPG LVKPSETLSL TCTVSGFSLL SYGVHWVRQP PGKGLEWLGV

AB0041    IWTGGTTNYN SALMSRLSIS KDDSKSQVFL KMNSLQTDDT AIYYCARYYY
VH1       IWTGGTTNYN SALMSRLTIS KDDSKSTVYL KMNSLKTEDT AIYYCARYYY
VH2       IWTGGTTNYN SALMSRLTIS KDDSKNTVYL KMNSLKTEDT AIYYCARYYY
VH3       IWTGGTTNYN SALMSRFTIS KDDSKNTVYL KMNSLKTEDT AIYYCARYYY
VH4       IWTGGTTNYN SALMSRFTIS KDDSKNTLYL KMNSLKTEDT AIYYCARYYY

AB0041    GMDYWGQGTS VTVSS  (SEQ ID NO:3)
VH1       GMDYWGQGTS VTVSS  (SEQ ID NO:5)
VH2       GMDYWGQGTL VTVSS  (SEQ ID NO:6)
VH3       GMDYWGQGTL VTVSS  (SEQ ID NO:7)
VH4       GMDYWGQGTL VTVSS  (SEQ ID NO:8)
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(57) Abstract: The present disclosure provides compositions and methods of use involving binding proteins, e.g., antibodies and antigen-binding fragments thereof, that bind to the matrix metalloproteinase-9 (MMP9) protein (MMP9 is also known as gelatinase-B), such as where the binding proteins comprise an immunoglobulin (Ig) heavy chain (or functional fragment thereof) and an Ig light chain (or functional fragment thereof).

ANTIBODIES TO MATRIX METALLOPROTEINASE 9

REFERENCE TO SEQUENCE LISTING SUBMITTED VIA EFS-WEB

[0001] The entire content of the following electronic submission of the sequence listing via the USPTO EFS-WEB server, as authorized and set forth in MPEP §1730 II.B.2(a)(C), is incorporated herein by reference in its entirety for all purposes. The sequence listing is identified on the electronically filed text file as follows:

File Name	Date of Creation	Size (bytes)
246102008540Seqlist	February 29, 2012	65,102 bytes

FIELD

[0002] This disclosure is in the field of extracellular enzymes, extracellular matrix enzymes, proteases and immunology.

BACKGROUND

[0003] Matrix metalloproteinases (MMPs) belong to a family of extracellular enzymes involved in forming and remodeling the extracellular matrix. These enzymes contain a conserved catalytic domain in which a zinc atom is coordinated by three histidine residues. Over 20 members of this family are known, organized into a number of groups including collagenases, gelatinases, stromelysins, matrilysins, enamelysins and membrane MMPs.

[0004] MMP2 and MMP9 belong to the gelatinase group of matrix metalloproteinases. Besides containing signal peptide, propeptide, catalytic, zinc-binding and heamopexin-like domains common to most MMPs, the gelatinases also contain a plurality of fibronectin-like domains and an O-glycosylated domain.

[0005] MMPs are associated with a number of diseases. However, available inhibitors of MMPs have been unsuccessful, in part due to toxicity and lack of efficacy. Therefore, there is a need for specific and effective MMP inhibitors.

SUMMARY

[0006] The present disclosure provides compositions and methods of use involving binding proteins, e.g., antibodies and antigen-binding fragments thereof, that bind to matrix metalloproteinase-9 (MMP9) protein (also known as gelatinase-B). The binding proteins typically are antibodies or fragments (e.g., antigen-binding fragments) thereof and typically contain an immunoglobulin (Ig) heavy chain (or functional fragment thereof) and an Ig light chain (or functional fragment thereof). The heavy chain is typically an IgG, typically a human

IgG, such as an IgG1 or IgG4, or other IgG such as an IgG2, or modified version thereof. The light chain typically is a kappa chain.

[0007] Among the MMP9 binding proteins, e.g., antibodies, are those that bind specifically to MMP9 and not to other matrix metalloproteinases. Such MMP9 binding proteins find use in applications in which it is necessary or desirable to obtain specific modulation (*e.g.*, inhibition) of MMP9, e.g., without directly affecting the activity of other matrix metalloproteinases. Thus, in certain embodiments of the present disclosure an anti-MMP9 antibody or fragment thereof is a specific inhibitor of the activity of MMP9. In some aspects, the MMP9 binding proteins disclosed herein will be useful for inhibition of MMP9 while allowing normal function of other, related matrix metalloproteinases.

[0008] The antibodies and fragments can be described with reference to their amino acid sequences or portions thereof, and/or various functions such as binding specificity to MMP9 or particular epitopes thereof or the ability to compete for binding to epitopes on MMP9 with particular antibodies, and/or activity, such as the ability to inhibit MMP9, e.g., non-competitively.

[0009] The antibodies and fragments include those having a heavy chain variable (VH) region having a heavy chain complementary determining region (CDR) with an amino acid sequence of SEQ ID NO: 13, SEQ ID NO: 14, or SEQ ID NO: 15; those having a light chain variable (VL) region having a light chain complementary determining region (CDR) with an amino acid sequence of SEQ ID NO: 16, SEQ ID NO: 17, or SEQ ID NO: 18. Exemplary antibodies and fragments include those having a heavy chain CDR1 with the amino acid sequence of SEQ ID NO: 13, a heavy chain CDR2 with the amino acid sequence of SEQ ID NO: 14, and a heavy chain CDR3 with the amino acid sequence of SEQ ID NO: 15, and those having a heavy chain CDR3 of SEQ ID NO: 15. Exemplary antibodies and fragments further include those with a light chain CDR1 with the amino acid sequence of SEQ ID NO: 16, a light chain CDR2 with the amino acid sequence of SEQ ID NO: 17, and a light chain CDR3 with the amino acid sequence of SEQ ID NO: 18, and those having a light chain CDR3 with the amino acid sequence of SEQ ID NO: 18, as well as those having heavy chain CDRs of SEQ ID NOs: 13, 14, and 15, and light chain CDRs of SEQ ID NOs: 16, 17, and 18.

[0010] Exemplary antibodies and fragments further include those having a heavy chain CDR1 with the amino acid sequence of SEQ ID NO: 34, a heavy chain CDR2 with the amino acid sequence of SEQ ID NO: 35, and a heavy chain CDR3 with the amino acid sequence of SEQ ID NO: 36, those with a heavy chain CDR3 with the amino acid sequence of SEQ ID NO: 36, those with a light chain CDR1 with the amino acid sequence of SEQ ID NO: 37, a light chain CDR2 with the amino acid sequence of SEQ ID NO: 38, and a light chain CDR3 with the

amino acid sequence of SEQ ID NO: 39, those with a light chain CDR3 with the amino acid sequence of SEQ ID NO: 39, as well as those having heavy chain CDRs of SEQ ID NOs: 34, 35, and 36, and light chain CDRs of SEQ ID NOs: 37, 38, and 39.

[0011] Exemplary antibodies and fragments further include those having a light chain CDR1 with the amino acid sequence of SEQ ID NO: 42, a light chain CDR2 with the amino acid sequence of SEQ ID NO: 43, and a light chain CDR3 with the amino acid sequence of SEQ ID NO: 44, and those with a light chain CDR3 with the amino acid sequence of SEQ ID NO: 44.

[0012] The antibodies and fragments further include those having a VH region with an amino acid sequence set forth in SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, or SEQ ID NO: 8, and those having a VL region with an amino acid sequence set forth in SEQ ID NO: 4, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, or SEQ ID NO: 12, as well as antibodies and fragments having a VH region with an amino acid sequence set forth in SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, or SEQ ID NO: 8 and a VL region with an amino acid sequence set forth in SEQ ID NO: 4, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, or SEQ ID NO: 12. In a particular example, the antibodies or fragments have a VH region of SEQ ID NO: 7 and a VL region of SEQ ID NO: 12, or at least at or about 75 %, 80 %, 85 %, 90 %, 91 %, 92 %, 93 %, 94 %, 95 %, 96 %, 97 %, 98 %, 99 % or more sequence identity with such sequences. They further include those having a VH region with an amino acid sequence set forth in SEQ ID NO: 32 or 47, and those with a VL region with an amino acid sequence set forth in SEQ ID NO: 33 or in SEQ ID NO: 41 or in SEQ ID NO: 48, and combinations thereof, and sequence having at least at or about 75 %, 80 %, 85 %, 90 %, 91 %, 92 %, 93 %, 94 %, 95 %, 96 %, 97 %, 98 %, 99 % or more sequence identity with such sequences.

[0013] The antibodies and fragments further include those having a VH region with an amino acid sequence set forth in SEQ ID NO: 1, and/or having a VL region with an amino acid sequence set forth in SEQ ID NO: 2, and/or a VH or VL region having at least at or about 75 %, 80 %, 85 %, 90 %, 91 %, 92 %, 93 %, 94 %, 95 %, 96 %, 97 %, 98 %, 99 % or more sequence identity with such sequences.

[0014] In some cases, the heavy chain is encoded by a polynucleotide having a nucleotide sequence selected from the group consisting of SEQ ID NOs: 19-22 and the light chain is encoded by a polynucleotide having a nucleotide sequence selected from the group consisting of SEQ ID NOs: 23-26.

[0015] In some embodiments, the antibodies or fragments thereof inhibit the enzymatic activity of MMP9, such as by non-competitive inhibition.

[0016] The antibodies and fragments further include those that specifically bind to a given epitope of MMP9. In some cases, the epitope is an epitope specifically bound by any of the above-described antibodies. In one example, the epitope contains an amino acid residue (i.e., one or more amino acid residue(s)) outside of cysteine-switch active pocket of SEQ ID NO: 27. In certain examples, the epitope includes an amino acid residue (i.e., one or more amino acid residue(s)) within a given region of MMP9, for example, where the region is residues 104-202 of SEQ ID NO: 27. In some examples, the epitope includes an amino acid residue (i.e., one or more amino acid residue(s)) within a given region of MMP9, for example, where the region is residues 104-119, residues 159-166, or residues 191-202 of SEQ ID NO: 27. In one example, the epitope includes an amino acid residue (i.e., one or more amino acid residue) within a region of MMP9 that is residues 104-119 of SEQ ID NO: 27, an amino acid residue within a region of MMP9 that is residues 159-166 of SEQ ID NO: 27, and an amino acid residue within a region of MMP9 that is residues 191-202 of SEQ ID NO: 27. In some cases, the epitope includes E111, D113, R162, or I198 of SEQ ID NO: 27. In some cases, it includes R162 of SEQ ID NO: 27. In some cases, it includes E111, D113, R162, and I198 of SEQ ID NO: 27.

[0017] In some cases, the antibody or fragment is human or is humanized.

[0018] In some examples, the antibodies and fragments specifically bind to human MMP9 with a dissociation constant (K_d) equal to or lower than 100 nM, optionally lower than 10 nM, optionally lower than 1 nM, optionally lower than 0.5 nM, optionally lower than 0.1 nM, optionally lower than 0.01 nM, or optionally lower than 0.005 nM, in certain examples, between 0.1 and 0.2 nM, or between 0.1 and 10 pM, e.g., between 0.4 and 9 pm, such as between 0.4 and 8.8 pm, in the form of monoclonal antibody, scFv, Fab, or other form of antibody measured at a temperature of about 4°C, 25°C, 37°C or 42°C.

[0019] Also among the provided antibodies and fragments are those having at least at or about 75 %, 80 %, 85 %, 90 %, 91 %, 92 %, 93 %, 94 %, 95 %, 96 %, 97 %, 98 %, 99 % or more sequence identity with any of the above-described antibodies or containing various portions with at least at or about 75 %, 80 %, 85 %, 90 %, 91 %, 92 %, 93 %, 94 %, 95 %, 96 %, 97 %, 98 %, 99 % or more sequence identity with the respective portions of the antibodies described above, such as having a VH region with such identity with SEQ ID NO: 7 and a VL region with such identity with SEQ ID NO: 12. Also provided are antibodies that compete for binding to MMP9 with any of the above-described antibodies, such as those that compete for binding to MMP9 with an antibody having a VH region with the amino acid sequence set forth in SEQ ID NO: 7 and a VL region with the amino acid sequence set forth in SEQ ID NO: 12.

[0020] Also provided are isolated nucleic acids encoding the antibodies and fragments, such as nucleic acids including a coding sequence for any of the above-described antibodies and

fragments. Among the provided nucleic acids are those containing a nucleotide sequence encoding a heavy chain polypeptide comprising CDRs with the amino acid sequences set forth in SEQ ID NOs: 13-15, and/or a light chain polypeptide comprising CDRs with the amino acid sequences set forth in SEQ ID NOs: 16-18. In one example, the nucleotide sequence encodes the heavy chain polypeptide, which has an amino acid sequence selected from the group consisting of SEQ ID NOS: 1, 3, and 5-8. In another example, the nucleotide sequence encodes the light chain polypeptide, which has an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, and 9-12. In one example, the nucleotide sequence includes a sequence selected from the group consisting of SEQ ID NOs: 19-26, such as SEQ ID NO: 21, SEQ ID NO: 26, or SEQ ID NOs: 21 and 26. Also provided are vectors containing such nucleic acids and cells including the same, such as host cells.

[0021] Also provided are pharmaceutical compositions including the antibodies, fragments, nucleic acids, vectors, and cells. In some examples, the pharmaceutical compositions further include a carrier or excipient, such as a pharmaceutically acceptable or biologically acceptable carrier or excipient. In some cases, the pharmaceutical compositions are used in the provided therapeutic methods and uses.

[0022] Also provided are methods and uses of the antibodies, fragments, nucleic acids, vectors, cells, and compositions, for example in therapeutics, such as inhibiting MMP9 in a subject, and diagnostics, such as for detecting MMP9 in the subject.

[0023] For example, provided are diagnostic and prognostic methods involving detection of MMP9, and agents (such as any of the above-described anti-MMP9 antibodies and other MMP9 binding proteins) for use in such methods. In some cases, the diagnostic method detects MMP9 expression in a test sample from a subject. Such methods can be carried out, for example, by contacting the test sample with an antibody or fragment as described herein (such as any of the above-described antibodies or fragments) and detecting binding of the antibody or fragment to protein in the sample, thereby detecting the presence of MMP9. In some cases, a sample is first obtained or provided. In some examples, the methods include comparing the amount or level of MMP9 detected to a control level or amount, such as by comparing the amount of binding detected in the test sample with an amount of binding of the antibody or fragment to a control sample. In some cases, the methods involve simply comparing a test level and a control level of MMP9. In some cases, a higher test level (as compared to the control level) is indicative of the disease or condition.

[0024] In some cases, the MMP9 detected by the method indicates the presence of a disease or condition in the subject, such as an MMP9-associated disease or condition. In some cases, the methods further include treating the subject or adjusting (i.e., altering or discontinuing)

treatment of the subject based on the results of the method, e.g., based on the levels of MMP9 detected in the sample. Among the biological samples are tissue, cells isolated from such tissues, and the like. In some cases, the methods are performed on liquid samples, such as blood, plasma, serum, whole blood, saliva, urine, or semen. Tissue samples include, for example, formalin-fixed or frozen tissue sections.

[0025] Also provided are methods of inhibiting MMP9 activity in a subject and/or treating a disease or condition in the subject, for example, using an agent that non-competitively inhibits MMP9, and agents (such as any of the above-described anti-MMP9 antibodies and other MMP9 binding proteins) for use in such methods. The methods generally are carried out by administering to the subject an MMP9 binding protein, such as an MMP9-binding antibody or fragment thereof as provided herein, e.g., in an effective amount. The antibody or fragment generally specifically binds to and non-competitively inhibits MMP9, for example, such that MMP9 activity is inhibited in the subject. In some cases, the antibody or fragment is one that binds MMP9 outside of the cysteine-switch active pocket, such as in one of the epitopes described above. In some cases, the antibody or fragment does not substantially bind to an MMP protein other than MMP9 and/or does not substantially bind to MMP2.

[0026] The subject generally is one with a disease or condition, typically one associated with increased or decreased MMP9 expression and/or activity. In certain cases, the subject with a disease or condition associated with increased MMP9 expression and/or activity. In other cases, the subject with a disease or condition associated with decreased MMP9 expression and/or activity.

[0027] Also provided are MMP9 polypeptides, including mutant MMP9 polypeptides, such as those containing residues 111-198 of SEQ ID NO: 27, and those having an amino acid sequence containing residues 111-198 of SEQ ID NO: 27 with an amino acid substitution at residue 111, 113, 162, or 198 of SEQ ID NO 27, or with an amino acid substitution at all such residues.

[0028] Also provided are uses of any of the above-described antibodies, nucleic acids, vectors, cells, and compositions, in the therapeutic and diagnostic methods described above.

BRIEF DESCRIPTION OF THE DRAWINGS

[0029] **Figure 1** shows the amino acid sequence of the heavy chain variable region of a mouse monoclonal anti-MMP9 antibody (AB0041), along with the amino acid sequences of humanized variants of heavy chain (VH1-VH4), aligned to show differences in framework amino acid sequence resulting from humanization. CDRs are shown in italics, and amino acids

that are different in the humanized variants, compared to the parent mouse monoclonal, are underlined.

[0030] **Figure 2** shows the amino acid sequence of the light chain variable region of a mouse monoclonal anti-MMP9 antibody (AB0041), along with the amino acid sequences of humanized variants of this light chain (VH1-VH4), aligned to show differences in framework amino acid sequence resulting from humanization. CDRs are shown in italics, and amino acids that are different in the humanized variants, compared to the parent mouse monoclonal, are underlined.

[0031] **Figure 3** shows a schematic diagram of the MMP9 protein.

[0032] **Figure 4** shows a comparison between the amino acid sequences of the heavy and light chains of antibodies designated AB0041, M4, and M12.

DETAILED DESCRIPTION

[0033] Practice of the present disclosure employs, unless otherwise indicated, standard methods and conventional techniques in the fields of cell biology, toxicology, molecular biology, biochemistry, cell culture, immunology, oncology, recombinant DNA and related fields as are within the skill of the art. Such techniques are described in the literature and thereby available to those of skill in the art. See, for example, Alberts, B. *et al.*, "Molecular Biology of the Cell," 5th edition, Garland Science, New York, NY, 2008; Voet, D. *et al.* "Fundamentals of Biochemistry: Life at the Molecular Level," 3rd edition, John Wiley & Sons, Hoboken, NJ, 2008; Sambrook, J. *et al.*, "Molecular Cloning: A Laboratory Manual," 3rd edition, Cold Spring Harbor Laboratory Press, 2001; Ausubel, F. *et al.*, "Current Protocols in Molecular Biology," John Wiley & Sons, New York, 1987 and periodic updates; Freshney, R.I., "Culture of Animal Cells: A Manual of Basic Technique," 4th edition, John Wiley & Sons, Somerset, NJ, 2000; and the series "Methods in Enzymology," Academic Press, San Diego, CA. See also, for example, "Current Protocols in Immunology," (R. Coico, series editor), Wiley, last updated August 2010.

[0034] Certain MMPs play roles in tumor growth, metastasis, inflammation, autoimmunity, and vascular disease. *See*, for example, Hu *et al.* (2007) *Nature Reviews: Drug Discovery* **6:**480-498. Thus, it is desirable to inhibit the activity of one or more particular MMPs in certain therapeutic settings. While sharing significant homology at a sequence level, the expression and functional roles of the two gelatinases MMP9 and MMP2 vary significantly. MMP9 expression is induced by a number of disease associated cytokines and growth factors. Also, the MMP9 knockout mouse is protected in a variety of disease models, whereas MMP2 is more constitutively expressed and the MMP2 knockout animals tend toward little protection. Some studies have shown that MMP2 knockout mouse exhibited worse disease in challenge models. For some diseases or disorders, the activity of more than one MMPs is inhibited. In clinical

studies, the inhibitors to more than one MMPs have caused adverse effects, such as toxicity or lack of efficacy, that are not desired. It has been shown that the activity of certain MMPs, e.g., MMP2, is often required for normal tissue homeostasis and/or is protective against disease. Certain available MMP inhibitors have caused side effects.

[0035] Among the provided embodiments are agents, including therapeutic reagents, such as antibodies and antigen-binding fragments thereof, that specifically inhibit the catalytic activity of a single MMP or a select plurality of MMPs, such as MMP9 and that do not react with or inhibit certain other MMPs or any other MMPs. Also among the provided embodiments are methods and uses of the same for treatment of various diseases.

MMP9 Binding Proteins

[0036] The present disclosure provides binding proteins, e.g., antibodies and fragments (e.g., antigen-binding fragments) thereof, that bind to the matrix metalloproteinase-9 (MMP9) protein (MMP9 is also known as gelatinase-B), e.g., human MMP9, such as the human MMP9 having an amino acid sequence set forth in SEQ ID NO: 27 or SEQ ID NO: 28. The binding proteins of the present disclosure generally comprise an immunoglobulin (Ig) heavy chain (or functional fragment thereof) and an Ig light chain (or functional fragment thereof).

[0037] The disclosure further provides MMP9 binding proteins that bind specifically to MMP9 and not to other matrix metalloproteinases such as MMP1, MMP2, MMP3, MMP7, MMP9, MMP10, MMP12, and MMP13. Such specific MMP9 binding proteins are thus generally not significantly or detectably crossreactive with non-MMP9 matrix metalloproteinases. MMP9 binding proteins that specifically bind MMP9 find use in applications in which it is necessary or desirable to obtain specific modulation (*e.g.*, inhibition) of MMP9, e.g., without directly affecting the activity of other matrix metalloproteinases.

[0038] In certain embodiments of the present disclosure, an anti-MMP9 antibody is an inhibitor of the activity of MMP9, and can be a specific inhibitor of MMP9. In one embodiment, the MMP9 binding proteins disclosed herein is useful for inhibition of MMP9 while not affecting other matrix metalloproteinases. "An inhibitor of MMP" or "inhibitor of MMP9 activity" can be an antibody or an antigen binding fragment thereof that directly or indirectly inhibits activity of MMP9, including but not limited to enzymatic processing, inhibiting action of MMP9 on it substrate (e.g., by inhibiting substrate binding, substrate cleavage, and the like), and the like.

[0039] The present disclosure also provides MMP9 binding proteins that specifically bind to non-mouse MMP9, such as human MMP9, Cynomolgus monkey MMP9, and rat MMP9.

[0040] The present disclosure also provides MMP9 binding proteins (e.g., anti-MMP9 antibodies and functional fragments thereof) that act as non-competitive inhibitors. A "non-competitive inhibitor" refers to an inhibitor binds at site away from substrate binding site of an enzyme, and thus can bind the enzyme and effect inhibitory activity regardless of whether or not the enzyme is bound to its substrate. The non-competitive or allosteric inhibition is generally independent of substrate association or concentration. Such non-competitive inhibitors can, for example, provide for a level of inhibition that can be substantially independent of substrate concentration.

[0041] MMP9 binding proteins (e.g., antibodies and functional fragments thereof) of the present disclosure include those that bind MMP9, particularly human MMP9, and having a heavy chain polypeptide (or functional fragment thereof) that has at least about 80%, 85%, 90%, 95% or more amino acid sequence identity to a heavy chain polypeptide disclosed herein.

[0042] MMP9 binding proteins (e.g., antibodies and functional fragments thereof) of the present disclosure include those that bind MMP9, particularly human MMP9, and having a light polypeptide (or functional fragment thereof) that has at least about 80%, 85%, 90%, 95% or more amino acid sequence identity to a heavy chain polypeptide disclosed herein.

[0043] MMP9 binding proteins (e.g., antibodies and functional fragments thereof) of the present disclosure include those that bind MMP9, particularly human MMP9, and have a heavy chain polypeptide (or functional fragment thereof) having the complementarity determining regions ("CDRs") of heavy chain polypeptide and the CDRs of a light chain polypeptide (or functional fragment thereof) as disclosed herein.

[0044] "Homology" or "identity" or "similarity" as used herein in the context of nucleic acids and polypeptides refers to the relationship between two polypeptides or two nucleic acid molecules based on an alignment of the amino acid sequences or nucleic acid sequences, respectively. Homology and identity can each be determined by comparing a position in each sequence which may be aligned for purposes of comparison. When an equivalent position in the compared sequences is occupied by the same base or amino acid, then the molecules are identical at that position; when the equivalent site occupied by the same or a similar amino acid residue (e.g., similar in steric and/or electronic nature), then the molecules can be referred to as homologous (similar) at that position. Expression as a percentage of homology/similarity or identity refers to a function of the number of identical or similar amino acids at positions shared by the compared sequences. In comparing two sequences, the absence of residues (amino acids or nucleic acids) or presence of extra residues also decreases the identity and homology/similarity.

[0045] As used herein, "identity" means the percentage of identical nucleotide or amino acid residues at corresponding positions in two or more sequences when the sequences are aligned to maximize sequence matching, i.e., taking into account gaps and insertions. Sequences are generally aligned for maximum correspondence over a designated region, e.g., a region at least about 20, 25, 30, 35, 40, 45, 50, 55, 60, 65 or more amino acids or nucleotides in length, and can be up to the full-length of the reference amino acid or nucleotide. For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are input into a computer program, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. The sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated program parameters.

[0046] Examples of algorithms that are suitable for determining percent sequence identity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al. (1990) J. Mol. Biol. 215: 403-410 and Altschul et al. (1977) Nucleic Acids Res. 25: 3389-3402, respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (www.ncbi.nlm.nih.gov). Further exemplary algorithms include ClustalW (Higgins D., et al. (1994) Nucleic Acids Res 22: 4673-4680), available at www.ebi.ac.uk/Tools/clustalw/index.html.

[0047] Residue positions which are not identical can differ by conservative amino acid substitutions. Conservative amino acid substitutions refer to the interchangeability of residues having similar side chains. For example, a group of amino acids having aliphatic side chains is glycine, alanine, valine, leucine, and isoleucine; a group of amino acids having aliphatic-hydroxyl side chains is serine and threonine; a group of amino acids having amide-containing side chains is asparagine and glutamine; a group of amino acids having aromatic side chains is phenylalanine, tyrosine, and tryptophan; a group of amino acids having basic side chains is lysine, arginine, and histidine; and a group of amino acids having sulfur-containing side chains is cysteine and methionine.

[0048] Sequence identity between two nucleic acids can also be described in terms of hybridization of two molecules to each other under stringent conditions. The hybridization conditions are selected following standard methods in the art (see, for example, Sambrook, et al., Molecular Cloning: A Laboratory Manual, Second Edition, (1989) Cold Spring Harbor, N.Y.). An example of stringent hybridization conditions is hybridization at 50°C or higher and 0.1 × SSC (15 mM sodium chloride/1.5 mM sodium citrate). Another example of stringent hybridization conditions is overnight incubation at 42 °C in a solution: 50 % formamide, 5 ×

SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH7.6), 5 × Denhardt's solution, 10% dextran sulfate, and 20 mg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1 × SSC at about 65 °C. Stringent hybridization conditions are hybridization conditions that are at least as stringent as the above representative conditions, where conditions are considered to be at least as stringent if they are at least about 80% as stringent, typically at least 90% as stringent as the above specific stringent conditions.

[0049] Accordingly, the present disclosure provides, for example, antibodies or antigen binding fragments thereof, comprising a heavy chain variable region polypeptide having at least 80%, 85%, 90%, 95%, or greater amino acid sequence identity to an amino acid sequence of a heavy chain variable region described herein (e.g., SEQ ID NOS:1 or 5-8), and a variable light chain polypeptide having at least 80%, 85%, 90%, 95%, or greater amino acid sequence identity to an amino acid sequence of a light chain polypeptide as set forth herein (e.g., SEQ ID NOS:2 or 9-12).

[0050] Examples of anti-MMP9 antibodies of the present disclosure are described in more detail below.

Antibodies

[0051] The MMP9 binding proteins include antibodies and functional fragments thereof, such as those that specifically bind to MMP9. As used herein, the term "antibody" means an isolated or recombinant polypeptide binding agent that comprises peptide sequences (*e.g.*, variable region sequences) that specifically bind an antigenic epitope. The term is used in its broadest sense and specifically covers monoclonal antibodies (including full-length monoclonal antibodies), polyclonal antibodies, human antibodies, humanized antibodies, chimeric antibodies, nanobodies, diabodies, multispecific antibodies (*e.g.*, bispecific antibodies), and antibody fragments including but not limited to Fv, scFv, Fab, Fab' $F(ab')_2$ and Fab_2, so long as they exhibit the desired biological activity. The term "human antibody" refers to antibodies containing sequences of human origin, except for possible non-human CDR regions, and does not imply that the full structure of an immunoglobulin molecule be present, only that the antibody has minimal immunogenic effect in a human (*i.e.*, does not induce the production of antibodies to itself).

[0052] An "antibody fragment" comprises a portion of a full-length antibody, for example, the antigen binding or variable region of a full-length antibody. Such antibody fragments may also be referred to herein as "functional fragments: or "antigen-binding fragments". Examples of antibody fragments include Fab, Fab', $F(ab')_2$, and Fv fragments; diabodies; linear antibodies (Zapata *et al.* (1995) *Protein Eng.* **8(10):**1057-1062); single-chain antibody molecules; and

multispecific antibodies formed from antibody fragments. Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, each with a single antigen-binding site, and a residual "Fc" fragment, a designation reflecting the ability to crystallize readily. Pepsin treatment yields an $F(ab')_2$ fragment that has two antigen combining sites and is still capable of cross-linking antigen.

[0053] "Fv" is a minimum antibody fragment containing a complete antigen-recognition and -binding site. This region consists of a dimer of one heavy- and one light-chain variable domain in tight, non-covalent association. It is in this configuration that the three complementarity-determining regions (CDRs) of each variable domain interact to define an antigen-binding site on the surface of the V_H-V_L dimer. Collectively, the six CDRs confer antigen-binding specificity to the antibody. However, even a single variable domain (or an isolated V_H or V_L region comprising only three of the six CDRs specific for an antigen) has the ability to recognize and bind antigen, although generally at a lower affinity than does the entire F_v fragment.

[0054] The "F_{ab}" fragment also contains, in addition to heavy and light chain variable regions, the constant domain of the light chain and the first constant domain (CH_1) of the heavy chain. Fab fragments were originally observed following papain digestion of an antibody. Fab' fragments differ from Fab fragments in that F(ab') fragments contain several additional residues at the carboxy terminus of the heavy chain CH_1 domain, including one or more cysteines from the antibody hinge region. $F(ab')_2$ fragments contain two Fab fragments joined, near the hinge region, by disulfide bonds, and were originally observed following pepsin digestion of an antibody. Fab'-SH is the designation herein for Fab' fragments in which the cysteine residue(s) of the constant domains bear a free thiol group. Other chemical couplings of antibody fragments are also known.

[0055] The "light chains" of antibodies (immunoglobulins) from any vertebrate species can be assigned to one of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains. Depending on the amino acid sequence of the constant domain of their heavy chains, immunoglobulins can be assigned to five major classes: IgA, IgD, IgE, IgG, and IgM, and several of these may be further divided into subclasses (isotypes), e.g., IgG1, IgG2, IgG3, IgG4, IgA1, and IgA2.

[0056] "Single-chain Fv" or "sFv" or "scFv" antibody fragments comprise the V_H and V_L domains of antibody, wherein these domains are present in a single polypeptide chain. In some embodiments, the Fv polypeptide further comprises a polypeptide linker between the V_H and V_L domains, which enables the sFv to form the desired structure for antigen binding. For a review of sFv, see Pluckthun, in *The Pharmacology of Monoclonal Antibodies,* vol. 113 (Rosenburg and Moore eds.) Springer-Verlag, New York, pp. 269-315 (1994).

[0057] The term "diabodies" refers to small antibody fragments with two antigen-binding sites, which fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) in the same polypeptide chain (V_H-V_L). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain, thereby creating two antigen-binding sites. Diabodies are additionally described, for example, in EP 404,097; WO 93/11161 and Hollinger *et al.* (1993) *Proc. Natl. Acad. Sci. USA* **90:**6444-6448.

[0058] An "isolated" antibody is one that has been identified and separated and/or recovered from a component of its natural environment. Components of its natural environment may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In some embodiments, an isolated antibody is purified (1) to greater than 95% by weight of antibody as determined by the Lowry method, for example, more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence, *e.g.*, by use of a spinning cup sequenator, or (3) to homogeneity by gel electrophoresis (*e.g.*, SDS-PAGE) under reducing or nonreducing conditions, with detection by Coomassie blue or silver stain. The term "isolated antibody" includes an antibody *in situ* within recombinant cells, since at least one component of the antibody's natural environment will not be present. In certain embodiments, isolated antibody is prepared by at least one purification step.

[0059] As used herein, “immunoreactive” refers to antibodies or fragments thereof that are specific to a sequence of amino acid residues (“binding site” or “epitope”), yet if are cross-reactive to other peptides/proteins, are not toxic at the levels at which they are formulated for administration to human use. "Epitope" refers to that portion of an antigen capable of forming a binding interaction with an antibody or antigen binding fragment thereof. An epitope can be a linear peptide sequence (i.e., “continuous”) or can be composed of noncontiguous amino acid sequences (i.e., “conformational” or “discontinuous”). The term “preferentially binds” means that the binding agent binds to the binding site with greater affinity than it binds unrelated amino acid sequences.

[0060] Anti-MMP9 antibodies can be described in terms of the CDRs of the heavy and light chains. As used herein, the term "CDR" or "complementarity determining region" is intended to mean the non-contiguous antigen combining sites found within the variable region of both heavy and light chain polypeptides. These particular regions have been described by Kabat et al., J. Biol. Chem. 252:6609-6616 (1977); Kabat et al., U.S. Dept. of Health and Human Services, "Sequences of proteins of immunological interest" (1991); by Chothia et al., J. Mol. Biol. 196:901-917 (1987); and MacCallum et al., J. Mol. Biol. 262:732-745 (1996), where the definitions include overlapping or subsets of amino acid residues when compared against each

other. Nevertheless, application of either definition to refer to a CDR of an antibody or grafted antibodies or variants thereof is intended to be within the scope of the term as defined and used herein. The amino acid residues which encompass the CDRs as defined by each of the above cited references are set forth below in Table 1 as a comparison.

Table 1: CDR Definitions

	Kabat[1]	Chothia[2]	MacCallum[3]
V_H CDR1	31-35	26-32	30-35
V_H CDR2	50-65	53-55	47-58
V_H CDR3	95-102	96-101	93-101
V_L CDR1	24-34	26-32	30-36
V_L CDR2	50-56	50-52	46-55
V_L CDR3	89-97	91-96	89-96

[1]Residue numbering follows the nomenclature of Kabat et al., *supra*

[2]Residue numbering follows the nomenclature of Chothia et al., *supra*

[3]Residue numbering follows the nomenclature of MacCallum et al., *supra*

[0061] As used herein, the term "framework" when used in reference to an antibody variable region is intended to mean all amino acid residues outside the CDR regions within the variable region of an antibody. A variable region framework is generally a discontinuous amino acid sequence between about 100-120 amino acids in length but is intended to reference only those amino acids outside of the CDRs. As used herein, the term "framework region" is intended to mean each domain of the framework that is separated by the CDRs.

[0062] In some embodiments, an antibody is a humanized antibody or a human antibody. Humanized antibodies include human immununoglobulins (recipient antibody) in which residues from a complementary-determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. Thus, humanized forms of non-human (*e.g.*, murine) antibodies are chimeric immunoglobulins which contain minimal sequence derived from non-human immunoglobulin. The non-human sequences are located primarily in the variable regions, particularly in the complementarity-determining regions (CDRs). In some embodiments, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues that are found neither in the recipient antibody nor in the imported CDR or framework sequences. In certain embodiments, a humanized antibody comprises substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDRs correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. For the purposes of the present disclosure,

humanized antibodies can also include immunoglobulin fragments, such as Fv, Fab, Fab', $F(ab')_2$ or other antigen-binding subsequences of antibodies.

[0063] The humanized antibody can also comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. See, for example, Jones *et al.* (1986) *Nature* **321:**522-525; Riechmann *et al.* (1988) Nature **332:**323-329; and Presta (1992) *Curr. Op. Struct. Biol.* **2:**593-596.

[0064] Methods for humanizing non-human antibodies are known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source that is non-human. These non-human amino acid residues are often referred to as "import" or “donor” residues, which are typically obtained from an "import" or “donor” variable domain. For example, humanization can be performed essentially according to the method of Winter and co-workers , by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. See, for example, Jones *et al.*, *supra*; Riechmann *et al., supra* and Verhoeyen *et al.* (1988) *Science* **239:**1534-1536. Accordingly, such "humanized" antibodies include chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In certain embodiments, humanized antibodies are human antibodies in which some CDR residues and optionally some framework region residues are substituted by residues from analogous sites in rodent antibodies (*e.g.*, murine monoclonal antibodies).

[0065] Human antibodies can also be produced, for example, by using phage display libraries. Hoogenboom *et al.* (1991) *J. Mol. Biol,* **227:**381; Marks *et al.* (1991) *J. Mol. Biol.* **222:**581. Other methods for preparing human monoclonal antibodies are described by Cole *et al.* (1985) “Monoclonal Antibodies and Cancer Therapy,” Alan R. Liss, p. 77 and Boerner *et al.* (1991) *J. Immunol.* **147:**86-95.

[0066] Human antibodies can be made by introducing human immunoglobulin loci into transgenic animals (*e.g.*, mice) in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon immunological challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks *et al.* (1992) *Bio/Technology* **10:**779-783 (1992); Lonberg *et al.* (1994) *Nature* **368:** 856-859; Morrison (1994) *Nature* **368:**812-813; Fishwald *et al.* (1996) *Nature Biotechnology* **14:**845-851; Neuberger (1996) *Nature Biotechnology* **14:**826; and Lonberg *et al.* (1995) *Intern. Rev. Immunol.* **13:**65-93.

[0067] Antibodies can be affinity matured using known selection and/or mutagenesis methods as described above. In some embodiments, affinity matured antibodies have an affinity which is five times or more, ten times or more, twenty times or more, or thirty times or more than that of the starting antibody (generally murine, rabbit, chicken, humanized or human) from which the matured antibody is prepared.

[0068] An antibody can also be a bispecific antibody. Bispecific antibodies are monoclonal, and may be human or humanized antibodies that have binding specificities for at least two different antigens. In the present case, the two different binding specificities can be directed to two different MMPs, or to two different epitopes on a single MMP (*e.g.*, MMP9).

[0069] An antibody as disclosed herein can also be an immunoconjugate. Such immunoconjugates comprise an antibody (*e.g.*, to MMP9) conjugated to a second molecule, such as a reporter An immunoconjugate can also comprise an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, a toxin (*e.g.*, an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (*i.e.*, a radioconjugate).

[0070] An antibody that "specifically binds to" or is "specific for" a particular polypeptide or an epitope refers to the selective binding of the antibody to the target antigen or epitope; these terms, and methods for determining specific binding, are well understood in the art. An antibody exhibits "specific binding" for a particular target antigen or epitope if it binds with greater affinity, avidity, more readily, and/or with greater duration to that target antigen or epitope than it does with other substances. In some embodiments, the antibody that specifically binds to the polypeptide or epitope is one that that binds to that particular polypeptide or epitope without substantially binding to any other polypeptide or polypeptide epitope.

[0071] In some embodiments, the provided antibodies specifically bind to human MMP9 with a dissociation constant (K_d) equal to or lower than 100 nM, optionally lower than 10 nM, optionally lower than 1 nM, optionally lower than 0.5 nM, optionally lower than 0.1 nM, optionally lower than 0.01 nM, or optionally lower than 0.005 nM, in certain examples, between 0.1 and 0.2 nM, or between 0.1 and 10 pM, e.g., between 0.4 and 9 pm, such as between 0.4 and 8.8 pm, in the form of monoclonal antibody, scFv, Fab, or other form of antibody measured at a temperature of about 4°C, 25°C, 37°C or 42°C.

[0072] In certain embodiments, an antibody of the present disclosure binds to one or more processing sites (*e.g.*, sites of proteolytic cleavage) in MMP9, thereby effectively blocking processing of the proenzyme or preproenzyme to the catalytically active enzyme, and thus reducing the proteolytic activity of the MMP9.

[0073] In certain embodiments, an antibody according to the present disclosure binds to MMP9 with an affinity at least 2 times, at least 5 times, at least 10 times, at least 25 times, at least 50 times, at least 100 times, at least 500 times, or at least 1000 times greater than its binding affinity for another MMP. Binding affinity can be measured by any method known in the art and can be expressed as, for example, on-rate, off-rate, dissociation constant (K_d), equilibrium constant (K_{eq}) or any term in the art.

[0074] In certain embodiments, an antibody according to the present disclosure is one that inhibits the enzymatic (i.e., catalytic) activity of MMP9, such as a non-competitive inhibitor of the catalytic activity of MMP9. In certain embodiments, an antibody according to the present disclosure binds within the catalytic domain of MMP9. In additional embodiments, an antibody according to the present disclosure binds outside the catalytic domain of MMP9.

[0075] Also provided are antibodies or antigen binding fragments thereof that compete with any one or more of the anti-MMP9 antibodies or antigen binding fragments thereof described herein for binding to MMP9. Thus, the present disclosure contemplates anti-MMP9 antibodies, and functional fragments thereof, that compete for binding with, for example, an antibody having a heavy chain polypeptide of any of SEQ ID NOS: 1 or 5-8, a light chain polypeptide of SEQ ID NOS: 2 or 9-12, or combinations thereof. In one embodiment, the anti-MMP9 antibody, or functional fragment thereof, competes for binding to human MMP9 with the antibody described herein as AB0041.

Epitope Binding

[0076] Also provided are antibodies and fragments thereof that bind to the same epitope, e.g., MMP9 epitope as any one or more of the antibodies described herein. Also provided are antibodies and fragments that specifically bind to an epitope of MMP9, where the epitope includes an amino acid residue within a particular region of MMP9 or multiple regions of MMP9. Such regions can include, for example, structural loops and/or other structural domains of MMP9, such as those shown to be important for binding to exemplary antibodies described herein. Typically, the regions are defined according to amino acid residue positions on the full-length MMP9 sequence, e.g., SEQ ID NO: 27. In some examples, the epitope is outside of cysteine-switch active pocket of SEQ ID NO: 27. In some example, the epitope contains an amino acid residue (i.e., one or more amino acid residue(s)) within a region that is residues 104-202 of SEQ ID NO: 27. In one example, the epitope contains an amino acid residue (i.e., one or more amino acid residue(s)) within a region that is residues 104-119, residues 159-166, or residues 191-202 of SEQ ID NO: 27. In some aspects, the epitope includes an amino acid residue (i.e., one or more amino acid residue(s)) within a region of MMP9 that is residues 104-

119 of SEQ ID NO: 27, an an amino acid residue within a region of MMP9 that is residues 159-166 of SEQ ID NO: 27, and an amino acid residue within a region of MMP9 that is residues 191-202 of SEQ ID NO: 27. In some cases, the epitope includes E111, D113, R162, or I198 of SEQ ID NO: 27. In some cases, it includes R162 of SEQ ID NO: 27. In some cases, it includes E111, D113, R162, and I198 of SEQ ID NO: 27.

MMP9 sequence

[0077] The amino acid sequence of human MMP9 protein is as follows:

```
MSLWQPLVLV LLVLGCCFAA PRQRQSTLVL FPGDLRTNLT DRQLAEEYLY  50
RYGYTRVAEM RGESKSLGPA LLLLQKQLSL PETGELDSAT LKAMRTPRCG  100
VPDLGRFQTF EGDLKWHHHN ITYWIQNYSE DLPRAVIDDA FARAFALWSA  150
VTPLTFTRVY SRDADIVIQF GVAEHGDGYP FDGKDGLLAH AFPPGPGIQG  200
DAHFDDDELW SLGKGVVVPT RFGNADGAAC HFPFIFEGRS YSACTTDGRS  250
DGLPWCSTTA NYDTDDRFGF CPSERLYTRD GNADGKPCQF PFIFQGQSYS  300
ACTTDGRSDG YRWCATTANY DRDKLFGFCP TRADSTVMGG NSAGELCVFP  350
FTFLGKEYST CTSEGRGDGR LWCATTSNFD SDKKWGFCPD QGYSLFLVAA  400
HEFGHALGLD HSSVPEALMY PMYRFTEGPP LHKDDVNGIR HLYGPRPEPE  450
PRPPTTTTPQ PTAPPTVCPT GPPTVHPSER PTAGPTGPPS AGPTGPPTAG  500
PSTATTVPLS PVDDACNVNI FDAIAEIGNQ LYLFKDGKYW RFSEGRGSRP  550
QGPFLIADKW PALPRKLDSV FEEPLSKKLF FFSGRQVWVY TGASVLGPRR  600
LDKLGLGADV AQVTGALRSG RGKMLLFSGR RLWRFDVKAQ MVDPRSASEV  650
DRMFPGVPLD THDVFQYREK AYFCQDRFYW RVSSRSELNQ VDQVGYVTYD  700
ILQCPED  (SEQ ID NO:27)
```

[0078] Protein domains are shown schematically in Figure 3 and are indicated below:

Amino Acid #	Feature
1-19	Signal Peptide
38-98	Peptidoglycan Binding Domain
R98/C99	Cysteine-switch active pocket
112-445	Zn dependent metalloproteinase domain
223-271	Fibronectin type II domain (gelatin binding domain)
281-329	Fibronectin type II domain (gelatin binding domain)
340-388	Fibronectin type II domain (gelatin binding domain)
400-411	Zn binding region
521-565	Hemopexin-like domain
567-608	Hemopexin-like domain
613-659	Hemopexin-like domain
661-704	Hemopexin-like domain

[0079] The amino acid sequence of mature full-length human MMP9 (which is the amino acid sequence of the propolypeptide of SEQ ID NO:27 without the signal peptide) is:

APRQRQSTLVL FPGDLRTNLT DRQLAEEYLY RYGYTRVAEM RGESKSLGPA
LLLLQKQLSL PETGELDSAT LKAMRTPRCG VPDLGRFQTF EGDLKWHHHN
ITYWIQNYSE DLPRAVIDDA FARAFALWSA VTPLTFTRVY SRDADIVIQF
GVAEHGDGYP FDGKDGLLAH AFPPGPGIQG DAHFDDDELW SLGKGVVVPT
RFGNADGAAC HFPFIFEGRS YSACTTDGRS DGLPWCSTTA NYDTDDRFGF
CPSERLYTRD GNADGKPCQF PFIFQGQSYS ACTTDGRSDG YRWCATTANY
DRDKLFGFCP TRADSTVMGG NSAGELCVFP FTFLGKEYST CTSEGRGDGR
LWCATTSNFD SDKKWGFCPD QGYSLFLVAA HEFGHALGLD HSSVPEALMY
PMYRFTEGPP LHKDDVNGIR HLYGPRPEPE PRPPTTTTPQ PTAPPTVCPT
GPPTVHPSER PTAGPTGPPS AGPTGPPTAG PSTATTVPLS PVDDACNVNI
FDAIAEIGNQ LYLFKDGKYW RFSEGRGSRP QGPFLIADKW PALPRKLDSV
FEEPLSKKLF FFSGRQVWVY TGASVLGPRR LDKLGLGADV AQVTGALRSG
RGKMLLFSGR RLWRFDVKAQ MVDPRSASEV DRMFPGVPLD THDVFQYREK
AYFCQDRFYW RVSSRSELNQ VDQVGYVTYD ILQCPED (SEQ ID NO:28)

[0080] The amino acid sequence of the signal peptide is MSLWQPLVLV LLVLGCCFA (SEQ ID NO:29).

[0081] Also provided are MMP9 polypeptides, including mutant MMP9 polypeptides. Such peptides are useful, for example, in generating and selecting antibodies and fragments as provided herein. Exemplary polypeptides include those having an amino acid sequence containing residues 104-202 of SEQ ID NO: 27, and those having an amino acid sequence of SEQ ID NO: 27 with an amino acid substitution at residue 111, 113, 162, or 198 of SEQ ID NO 27 or with an amino acid substitution at all such residues. Other exemplary polypeptides include those having an amino acid sequence containing residues 111-198 of SEQ ID NO: 27, and those having an amino acid sequence containing residues 111-198 of SEQ ID NO: 27 with an amino acid substitution at residue 111, 113, 162, or 198 of SEQ ID NO 27 or with an amino acid substitution at all such residues. Such polypeptides find use, for example, in selecting antibodies that bind to epitopes containing such residues and/or for which such residues of MMP9 are important for binding, such as those described herein.

[0082] The present disclosure contemplates MMP9 binding proteins that bind any portion of MMP9, e.g., human MMP9, with MMP9 binding proteins that preferentially bind MMP9 relative to other MMPs being of particular interest.

[0083] Anti-MMP9 antibodies, and functional fragments thereof, can be generated accordingly to methods well known in the art. Exemplary anti-MMP9 antibodies are provided below.

Mouse monoclonal anti-MMP9 antibodies

[0084] A mouse monoclonal antibody to human MMP9 was obtained as described in Example 1. This antibody contains a mouse IgG2b heavy chain and a mouse kappa light chain, and is denoted AB0041.

[0085] The amino acid sequence of the AB0041 heavy chain is as follows:

MAVLVLFLCLVAFPSCVLSQVQLKESGPGLVAPSQSLSITCTVSGFSLLSY
GVHWVRQPPGKGLEWLGVIWTGGTTNYNSALMSRLSISKDDSKSQVFLK
MNSLQTDDTAIYYCARYYYGMDYWGQGTSVTVSS*AKTTPPSVYPLAPGC*
GDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSGLYTMSSSVT
VPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHKCPAPNL
EGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVRISWFVNNVEVHTA
QTQTHREDYNSTIRVVSALPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIK
GLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKD
TAPVLDSDGSYFIYSKLDIKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK
(SEQ ID NO:1)

[0086] The signal sequence is underlined, and the sequence of the IgG2b constant region is presented italics.

[0087] The amino acid sequence of theAB0041 light chain is as follows:

MESQIQVFVFVFLWLSGVDGDIVMTQSHKFMSTSVGDRVSITCKASQDV
RNTVAWYQQKTGQSPKLLIYSSSYRNTGVPDRFTGSGSGTDFTFTISSVQ
AEDLAVYFCQQHYITPYTFGGGTKLEIK*RADAAPTVSIFPPSSEQLTSGGASV*
VCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDE
YERHNSYTCEATHKTSTSPIVKSFNRNEC (SEQ ID NO:2)

[0088] The signal sequence is underlined, and the sequence of the kappa constant region is presented in italics.

[0089] The following amino acid sequence comprises the framework regions and complementarity-determining regions (CDRs) of the variable region of the IgG2b heavy chain of AB0041 (with CDRs underlined):

QVQLKESGPGLVAPSQSLSITCTVSGFSLLSYGVHWVRQPPGKGLEWLGV
IWTGGTTNYNSALMSRLSISKDDSKSQVFLKMNSLQTDDTAIYYCARYY
YGMDYWGQGTSVTVSS (SEQ ID NO:3)

[0090] The following amino acid sequence comprises the framework regions and complementarity-determining regions (CDRs) of the variable region of the kappa light chain of AB0041 (with CDRs underlined):

DIVMTQSHKFMSTSVGDRVSITCKASQDVRNTVAWYQQKTGQSPKLLIY SSSYRNTGVPDRFTGSGSGTDFTFTISSVQAEDLAVYFCQQHYITPYTFGG GTKLEIK (SEQ ID NO:4)

Other exemplary mouse anti-human MMP9 antibodies (e.g., M4 and M12) are described in Example 1B. An exemplary anti-mouse MMP9 antibody (AB0046) is described in Example 1C. Other exemplary mouse anti-human MMP9 antibodies include antibodies comprise the variable regions having the sequence of SEQ ID NO: 3, and the constant regions having 95% similarity as the sequences of the IgG2b constant regions. In addition, the exemplary mouse anti-human MMP9 antibodies include antibodies comprise the variable regions having the sequence of SEQ ID NO: 4, and the constant regions having 95% similarity as the sequences of the IgG2b constant regions. Other exemplary mouse anti-human MMP9 antibodies include antibodies comprise the variable regions having the sequences of SEQ ID NOs: 3 and 4, and the constant regions having 95% similarity as the sequences of the IgG2b constant regions. Such anti-mouse antibodies are suitable for testing and assessing the MMP9-inhibition methods.

Heavy-chain variants

[0091] The amino acid sequences of the variable regions of the AB0041 heavy and light chains were separately modified, by altering framework region sequences in the heavy and light chain variable regions. The effect of these sequence alterations was to deplete the antibody of human T-cell epitopes, thereby reducing or abolishing its immunogenicity in humans.

[0092] Four heavy-chain variants were constructed, in a human IgG4 heavy chain background containing a S241P amino acid change that stabilizes the hinge domain (Angal *et al.* (1993) *Molec. Immunol.* **30:**105-108), and are denoted VH1, VH2, VH3 and VH4. The amino acid sequences of their framework regions and CDRs are as follows:

VH1

QVQLQESGPGLVKPSETLSLTCTVSGFSLLSYGVHWVRQPPGKGLEWLG VIWTGGTTNYNSALMSRLTISKDDSKSTVYLKMNSLKTEDTAIYYCARY YYGMDYWGQGTSVTVSS (SEQ ID NO:5)

VH2

QVQLQESGPGLVKPSETLSLTCTVSGFSLLSYGVHWVRQPPGKGLEWLG
VIWTGGTTNYNSALMSRLTISKDDSKNTVYLKMNSLKTEDTAIYYCARY
YYGMDYWGQGTLVTVSS (SEQ ID NO:6)

VH3

QVQLQESGPGLVKPSETLSLTCTVSGFSLLSYGVHWVRQPPGKGLEWLG
VIWTGGTTNYNSALMSRFTISKDDSKNTVYLKMNSLKTEDTAIYYCARY
YYGMDYWGQGTLVTVSS (SEQ ID NO:7)

VH4

QVQLQESGPGLVKPSETLSLTCTVSGFSLLSYGVHWVRQPPGKGLEWLG
VIWTGGTTNYNSALMSRFTISKDDSKNTLYLKMNSLKTEDTAIYYCARY
YYGMDYWGQGTLVTVSS (SEQ ID NO:8)

[0093] Figure 1 shows an alignment of the amino acid sequences of the variable regions of the humanized heavy chains and indicates the differences in amino acid sequences in the framework regions among the four variants.

Light-chain variants

[0094] Four light-chain variants were constructed, in a human kappa chain background, and are denoted Vk1, Vk2, Vk3 and Vk4. The amino acid sequences of their framework regions and CDRs are as follows:

Vk1

DIVMTQSPSFLSASVGDRVTITCKASQDVRNTVAWYQQKTGKAPKLLIYS
SSYRNTGVPDRFTGSGSGTDFTLTISSLQAEDVAVYFCQQHYITPYTFGGG
TKVEIK (SEQ ID NO:9)

Vk2

DIVMTQSPSSLSASVGDRVTITCKASQDVRNTVAWYQQKPGKAPKLLIYS
SSYRNTGVPDRFTGSGSGTDFTLTISSLQAEDVAVYFCQQHYITPYTFGGG
TKVEIK (SEQ ID NO:10)

Vk3

DIQMTQSPSSLSASVGDRVTITCKASQDVRNTVAWYQQKPGKAPKLLIYS
SSYRNTGVPDRFSGSGSGTDFTLTISSLQAEDVAVYFCQQHYITPYTFGGG
TKVEIK (SEQ ID NO:11)

Vk4

DIQMTQSPSSLSASVGDRVTITCKASQDVRNTVAWYQQKPGKAPKLLIYS
SSYRNTGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQHYITPYTFGG
GTKVEIK (SEQ ID NO:12)

[0095] Figure 2 shows an alignment of the amino acid sequences of the variable regions of the humanized light chains and indicates the differences in amino acid sequences in the framework regions among the four variants.

[0096] The humanized heavy and light chains are combined in all possible pair-wise combinations to generate a number of functional humanized anti-MMP9 antibodies. For example, provided are antibodies with a heavy chain variable (VH) region having the amino acid sequence set forth in any of SEQ ID NOs: 3, 5, 6, 7, and 8; antibodies having a light chain variable (VL) region having the amino acid sequence set forth in any of SEQ ID NOs: 4, 9, 10, 11, and 12; and antibodies with a heavy chain variable (VH) region having the amino acid sequence set forth in any of SEQ ID NOs: 3, 5, 6, 7, and 8 and a light chain variable (VL) region having the amino acid sequence set forth in any of SEQ ID NOs: 4, 9, 10, 11, and 12, as well as antibodies that compete for binding to MMP9 with such antibodies and antibodies having at least at or about 75 %, 80 %, 85 %, 90 %, 91 %, 92 %, 93 %, 94 %, 95 %, 96 %, 97 %, 98 %, 99 % or more sequence identity with such antibodies. In one example, the antibody has a VH region with an amino acid sequence having at least at or about 75 %, 80 %, 85 %, 90 %, 91 %, 92 %, 93 %, 94 %, 95 %, 96 %, 97 %, 98 %, 99 % or more sequence identity with SEQ ID NO: 7 and a VL region with an amino acid sequence having at least at or about 75 %, 80 %, 85 %, 90 %, 91 %, 92 %, 93 %, 94 %, 95 %, 96 %, 97 %, 98 %, 99 % or more sequence identity with SEQ ID NO: 12, or a VH region of SEQ ID NO: 7 and a VL region of SEQ ID NO: 12.

[0097] Additional heavy chain variable region amino acid sequences having 75% or more, 80% or more, 90% or more, 95% or more, or 99% or more homology to the heavy chain variable region sequences disclosed herein are also provided. Furthermore, additional light chain variable region amino acid sequences having 75% or more, 80% or more, 90% or more, 95% or more, or 99% or more homology to the light chain variable region sequences disclosed herein are also provided.

[0098] Additional heavy chain variable region amino acid sequences having 75% or more, 80% or more, 90% or more, 95% or more, or 99% or more sequence identity to the heavy chain variable region sequences disclosed herein are also provided. Furthermore, additional light chain variable region amino acid sequences having 75% or more, 80% or more, 90% or more, 95% or more, or 99% or more sequence identity to the light chain variable region sequences disclosed herein are also provided.

Complementarity-determining regions (CDRs)

[0099] In some embodiments, the CDRs of the heavy chain of exemplary provided anti-MMP9 antibodies as disclosed herein have the following amino acid sequences:

CDR1: GFSLLSYGVH (SEQ ID NO:13)
CDR2: VIWTGGTTNYNSALMS (SEQ ID NO:14)
CDR3: YYYGMDY (SEQ ID NO:15)

[0100] Thus, among the provided anti-MMP9 antibodies are antibodies having a heavy chain CDR1 region with an amino acid sequence as set forth in SEQ ID NO: 13, antibodies having a heavy chain CDR2 region with an amino acid sequence set forth in SEQ ID NO: 14, and antibodies having a heavy chain CDR3 region with an amino acid sequence as set forth in SEQ ID NO: 15, and antibodies that compete for binding with or bind to the same epitope on MMP9 as such antibodies. In some cases, the antibodies contain VH CDRs having the sequences set forth in SEQ ID NO: 13, 14, and 15.

[0101] In some embodiments, the CDRs of the light chain of exemplary anti-MMP9 antibodies as disclosed herein have the following amino acid sequences:

CDR1: KASQDVRNTVA (SEQ ID NO:16)
CDR2: SSSYRNT (SEQ ID NO:17)
CDR3: QQHYITPYT (SEQ ID NO:18)

[0102] Thus, among the provided anti-MMP9 antibodies are antibodies having a light chain CDR1 region with an amino acid sequence as set forth in SEQ ID NO: 16, antibodies having a light chain CDR2 region with an amino acid sequence set forth in SEQ ID NO: 17, and antibodies having a light chain CDR3 region with an amino acid sequence as set forth in SEQ ID NO: 18, and antibodies that compete for binding with or bind to the same epitope on MMP9 as such antibodies. In some cases, the antibodies contain VL CDRs having the sequences set forth in SEQ ID NO: 16, 17, and 18.

Nucleic acids encoding anti-MMP9 antibodies

[0103] The present disclosure provides nucleic acids encoding anti-MMP9 antibodies and functional fragments thereof. Accordingly, the present disclosure provides an isolated polynucleotide (nucleic acid) encoding an antibody or antigen-binding fragment as described herein, vectors containing such polynucleotides, and host cells and expression systems for transcribing and translating such polynucleotides into polypeptides.

[0104] The present disclosure also contemplates constructs in the form of plasmids, vectors, transcription or expression cassettes which comprise at least one polynucleotide as above.

[0105] The present disclosure also provides a recombinant host cell which comprises one or more constructs as above, as well as methods of production of the antibody or antigen-binding fragments thereof described herein which method comprises expression of nucleic acid encoding a heavy chain polypeptide and a light chain polypeptide (in the same or different host cells, and from the same or different constructs) in a recombination host cell. Expression can be achieved by culturing under appropriate conditions recombinant host cells containing the nucleic acid. Following production by expression, an antibody or antigen-binding fragment can be isolated and/or purified using any suitable technique, then used as appropriate.

[0106] Systems for cloning and expression of a polypeptide in a variety of different host cells are well known. Suitable host cells include bacteria, mammalian cells, yeast and baculovirus systems. Mammalian cell lines available in the art for expression of a heterologous polypeptide include Chinese hamster ovary cells, HeLa cells, baby hamster kidney cells, NSO mouse melanoma cells and many others. A common bacterial host is E. coli.

[0107] Suitable vectors can be chosen or constructed, containing appropriate regulatory sequences, including operably linked promoter sequences, terminator sequences, polyadenylation sequences, enhancer sequences, marker genes and/or other sequences as appropriate. Vectors can be plasmids, viral e.g. 'phage, or phagemid, as appropriate. For further details see, for example, Molecular Cloning: a Laboratory Manual: 2nd edition, Sambrook et al., 1989, Cold Spring Harbor Laboratory Press. Many known techniques and protocols for manipulation of nucleic acid, for example in preparation of nucleic acid constructs, mutagenesis, sequencing, introduction of DNA into cells and gene expression, and analysis of proteins, are described in detail in Short Protocols in Molecular Biology, Second Edition, Ausubel et al. eds., John Wiley & Sons, 1992. The disclosures of Sambrook et al. and Ausubel et al. are incorporated herein by reference in their entirety.

[0108] The nucleic acid encoding a polypeptide of interest is integrated into the genome of the host cell or can be maintained as a stable or transient episomal element.

[0109] Any of a wide variety of expression control sequences – sequences that control the expression of a DNA sequence operatively linked to it – can be used in these vectors to express the DNA sequences. For example, a nucleic acid encoding a polypeptide of interest can be operably linked to a promoter, and provided in an expression construct for use in methods of production of recombinant MMP9 proteins or portions thereof.

[0110] Those of skill in the art are aware that nucleic acids encoding the antibody chains disclosed herein can be synthesized using standard knowledge and procedures in molecular biology.

[0111] Examples of nucleotide sequences encoding the heavy and light chain amino acid sequences disclosed herein, are as follows:

VH1: CAGGTGCAGC TGCAGGAATC CGGCCCTGGC CTGGTCAAGC CCTCCGAGAC ACTGTCCCTG ACCTGCACCG TGTCCGGCTT CTCCCTGCTG TCCTACGGCG TGCACTGGGT CCGACAGCCT CCAGGGAAGG GCCTGGAATG GCTGGGCGTG ATCTGGACCG GCGGCACCAC CAACTACAAC TCCGCCCTGA TGTCCCGGCT GACCATCTCC AAGGACGACT CCAAGTCCAC CGTGTACCTG AAGATGAACT CCCTGAAAAC CGAGGACACC GCCATCTACT ACTGCGCCCG GTACTACTAC GGCATGGACT ACTGGGGCCA GGGCACCTCC GTGACCGTGT CCTCA (SEQ ID NO:19)

VH2: CAGGTGCAGC TGCAGGAATC CGGCCCTGGC CTGGTCAAGC CCTCCGAGAC ACTGTCCCTG ACCTGCACCG TGTCCGGCTT CTCCCTGCTG TCCTACGGCG TGCACTGGGT CCGACAGCCT CCAGGCAAAG GCCTGGAATG GCTGGGCGTG ATCTGGACCG GCGGCACCAC CAACTACAAC TCCGCCCTGA TGTCCCGGCT GACCATCTCC AAGGACGACT CCAAGAACAC CGTGTACCTG AAGATGAACT CCCTGAAAAC CGAGGACACC GCCATCTACT ACTGCGCCCG GTACTACTAC GGCATGGACT ACTGGGGCCA GGGCACCCTG GTCACCGTGT CCTCA (SEQ ID NO:20)

VH3: CAGGTGCAGC TGCAGGAATC CGGCCCTGGC CTGGTCAAGC CCTCCGAGAC ACTGTCCCTG ACCTGCACCG TGTCCGGCTT CTCCCTGCTG TCCTACGGCG TGCACTGGGT CCGACAGCCT CCAGGCAAAG GCCTGGAATG GCTGGGCGTG ATCTGGACCG GCGGCACCAC CAACTACAAC TCCGCCCTGA TGTCCCGGTT CACCATCTCC AAGGACGACT CCAAGAACAC CGTGTACCTG AAGATGAACT CCCTGAAAAC CGAGGACACC GCCATCTACT ACTGCGCCCG GTACTACTAC GGCATGGACT ACTGGGGCCA GGGCACCCTG GTCACCGTGT CCTCA (SEQ ID NO:21)

VH4: CAGGTGCAGC TGCAGGAATC CGGCCCTGGC CTGGTCAAGC CCTCCGAGAC ACTGTCCCTG ACCTGCACCG TGTCCGGCTT CTCCCTGCTG TCCTACGGCG TGCACTGGGT CCGACAGCCT CCAGGCAAAG GCCTGGAATG GCTGGGCGTG ATCTGGACCG GCGGCACCAC CAACTACAAC TCCGCCCTGA TGTCCCGGTT CACCATCTCC AAGGACGACT CCAAGAACAC CCTGTACCTG AAGATGAACT CCCTGAAAAC CGAGGACACC GCCATCTACT ACTGCGCCCG GTACTACTAC GGCATGGACT ACTGGGGCCA GGGCACCCTG GTCACCGTGT CCTCA (SEQ ID NO:22)

Vk1: GACATCGTGA TGACCCAGTC CCCCAGCTTC CTGTCCGCCT CCGTGGGCGA CAGAGTGACC ATCACATGCA AGGCCTCTCA GGACGTGCGG AACACCGTGG CCTGGTATCA GCAGAAAACC GGCAAGGCCC CCAAGCTGCT GATCTACTCC TCCTCCTACC GGAACACCGG CGTGCCCGAC CGGTTTACCG GCTCTGGCTC CGGCACCGAC TTTACCCTGA CCATCAGCTC CCTGCAGGCC GAGGACGTGG CCGTGTACTT CTGCCAGCAG CACTACATCA CCCCCTACAC CTTCGGCGGA GGCACCAAGG TGGAAATAAA A (SEQ ID NO:23)

Vk2: GACATCGTGA TGACCCAGTC CCCCTCCAGC CTGTCCGCCT CTGTGGGCGA CAGAGTGACC ATCACATGCA AGGCCTCTCA GGACGTGCGG AACACCGTGG CCTGGTATCA GCAGAAGCCC GGCAAGGCCC CCAAGCTGCT GATCTACTCC TCCTCCTACC GGAACACCGG CGTGCCCGAC CGGTTTACCG GCTCTGGCTC CGGCACCGAC TTTACCCTGA CCATCAGCTC CCTGCAGGCC GAGGACGTGG CCGTGTACTT CTGCCAGCAG CACTACATCA CCCCCTACAC CTTCGGCGGA GGCACCAAGG TGGAAATAAA A (SEQ ID NO:24)

Vk3: GACATCCAGA TGACCCAGTC CCCCTCCAGC CTGTCCGCCT CTGTGGGCGA CAGAGTGACC ATCACATGCA AGGCCTCCCA GGACGTGCGG AACACCGTGG CCTGGTATCA GCAGAAGCCC GGCAAGGCCC CCAAGCTGCT GATCTACTCC TCCTCCTACC GGAACACCGG CGTGCCCGAC CGGTTCTCTG GCTCTGGAAG CGGCACCGAC TTTACCCTGA CCATCAGCTC CCTGCAGGCC GAGGACGTGG CCGTGTACTT CTGCCAGCAG CACTACATCA CCCCCTACAC CTTCGGCGGA GGCACCAAGG TGGAAATAAA A (SEQ ID NO:25)

Vk4: GACATCCAGA TGACCCAGTC CCCCTCCAGC CTGTCCGCCT CTGTGGGCGA CAGAGTGACC ATCACATGCA AGGCCTCTCA GGACGTGCGG AACACCGTGG CCTGGTATCA GCAGAAGCCC GGCAAGGCCC CCAAGCTGCT GATCTACTCC TCCTCCTACC GGAACACCGG CGTGCCCGAC CGGTTCTCTG

GCTCTGGAAG CGGCACCGAC TTTACCCTGA CCATCAGCTC CCTGCAGGCC
GAGGACGTGG CCGTGTACTA CTGCCAGCAG CACTACATCA CCCCCTACAC
CTTCGGCGGA GGCACCAAGG TGGAAATAAA A (SEQ ID NO:26)

[0112] Because the structure of antibodies, including the juxtaposition of CDRs and framework regions in the variable region, the structure of framework regions and the structure of heavy- and light-chain constant regions, is well-known in the art; it is well within the skill of the art to obtain related nucleic acids that encode anti-MMP-9 antibodies. Accordingly, polynucleotides comprising nucleic acid sequences having at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98% and at least 99% homology to any of the nucleotide sequences disclosed herein are also provided. Accordingly, polynucleotides comprising nucleic acid sequences having at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98% and at least 99% identity to any of the nucleotide sequences disclosed herein are also provided. In one example, the polynucleotide contains at least at or about 75 %, 80 %, 85 %, 90 %, 91 %, 92 %, 93 %, 94 %, 95 %, 96 %, 97 %, 98 %, 99 % or more sequence identity with SEQ ID NO: 21 or includes or is SEQ ID NO: 21 and/or contains at least at or about 75 %, 80 %, 85 %, 90 %, 91 %, 92 %, 93 %, 94 %, 95 %, 96 %, 97 %, 98 %, 99 % or more sequence identity with SEQ ID NO: 26 or includes or is SEQ ID NO: 26.

Pharmaceutical Compositions

[0113] MMP9 binding proteins, as well as nucleic acid (e.g., DNA or RNA) encoding MMP9 binding proteins, can be provided as a pharmaceutical composition, e.g., combined with a pharmaceutically acceptable carrier or excipient. Such pharmaceutical compositions are useful for, for example, administration to a subject in vivo or ex vivo, and for diagnosing and/or treating a subject with the MMP9 binding proteins, such as in any of the therapeutic or diagnostic methods provided herein.

[0114] Pharmaceutically acceptable carriers are physiologically acceptable to the administered patient and retain the therapeutic properties of the antibodies or peptides with which it is administered. Pharmaceutically-acceptable carriers and their formulations are and generally described in, for example, Remington' pharmaceutical Sciences (18th Edition, ed. A. Gennaro, Mack Publishing Co., Easton, PA 1990). One exemplary pharmaceutical carrier is physiological saline. Each carrier is "pharmaceutically acceptable" in the sense of being compatible with the other ingredients of the formulation and not substantially injurious to the patient.

[0115] Pharmaceutical compositions can be formulated to be compatible with a particular route of administration, systemic or local. Thus, pharmaceutical compositions include carriers, diluents, or excipients suitable for administration by various routes.

[0116] Pharmaceutical compositions can include pharmaceutically acceptable additives. Examples of additives include, but are not limited to, a sugar such as mannitol, sorbitol, glucose, xylitol, trehalose, sorbose, sucrose, galactose, dextran, dextrose, fructose, lactose and mixtures thereof. Pharmaceutically acceptable additives can be combined with pharmaceutically acceptable carriers and/or excipients such as dextrose. Additives also include surfactants such as polysorbate 20 or polysorbate 80.

[0117] The formulation and delivery methods will generally be adapted according to the site and the disease to be treated. Exemplary formulations include, but are not limited to, those suitable for parenteral administration, e.g., intravenous, intra-arterial, intramuscular, or subcutaneous administration, or oral administration.

[0118] Pharmaceutical compositions for parenteral delivery include, for example, water, saline, phosphate buffered saline, Hank's solution, Ringer's solution, dextrose/saline, and glucose solutions. The formulations can contain auxiliary substances to approximate physiological conditions, such as buffering agents, tonicity adjusting agents, wetting agents, detergents and the like. Additives can also include additional active ingredients such as bactericidal agents, or stabilizers. For example, the solution can contain sodium acetate, sodium lactate, sodium chloride, potassium chloride, calcium chloride, sorbitan monolaurate or triethanolamine oleate. Additional parenteral formulations and methods are described in Bai (1997) J. Neuroimmunol. 80:65 75; Warren (1997) J. Neurol. Sci. 152:31 38; and Tonegawa (1997) J. Exp. Med. 186:507 515. The parenteral preparation can be enclosed in ampules, disposable syringes or multiple dose vials made of glass or plastic.

[0119] Pharmaceutical compositions for intradermal or subcutaneous administration can include a sterile diluent, such as water, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid, glutathione or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates and agents for the adjustment of tonicity such as sodium chloride or dextrose.

[0120] Pharmaceutical compositions for injection include aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor ELTM (BASF, Parsippany, N.J.) or phosphate buffered saline (PBS). The carrier can be a solvent or dispersion medium containing,

for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyetheylene glycol, and the like), and suitable mixtures thereof. Fluidity 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. Antibacterial and antifungal agents include, for example, parabens, chlorobutanol, phenol, ascorbic acid and thimerosal. Isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, and sodium chloride may be included in the composition. The resulting solutions can be packaged for use as is, or lyophilized; the lyophilized preparation can later be combined with a sterile solution prior to administration.

[0121] Pharmaceutically acceptable carriers can contain a compound that stabilizes, increases, or delays absorption or clearance. Such compounds include, for example, carbohydrates, such as glucose, sucrose, or dextrans; low molecular weight proteins; compositions that reduce the clearance or hydrolysis of peptides; or excipients or other stabilizers and/or buffers. Agents that delay absorption include, for example, aluminum monostearate and gelatin. Detergents can also be used to stabilize or to increase or decrease the absorption of the pharmaceutical composition, including liposomal carriers. To protect from digestion the compound can be complexed with a composition to render it resistant to acidic and enzymatic hydrolysis, or the compound can be complexed in an appropriately resistant carrier such as a liposome. Means of protecting compounds from digestion are known in the art (see, e.g., Fix (1996) Pharm Res. 13:1760 1764; Samanen (1996) J. Pharm. Pharmacol. 48:119 135; and U.S. Pat. No. 5,391,377, describing lipid compositions for oral delivery of therapeutic agents).

[0122] Compositions of the present invention can be combined with other therapeutic moieties or imaging/diagnostic moieties as provided herein. Therapeutic moieties and/or imaging moieties can be provided as a separate composition, or as a conjugated moiety present on an MMP9 binding protein.

[0123] Formulations for in vivo administration are generally sterile. In one embodiment, the pharmaceutical compositions are formulated to be free of pyrogens such that they are acceptable for administration to human patients.

[0124] Various other pharmaceutical compositions and techniques for their preparation and use will be known to those of skill in the art in light of the present disclosure. For a detailed listing of suitable pharmacological compositions and associated administrative techniques one can refer to the detailed teachings herein, which can be further supplemented by texts such as Remington: The Science and Practice of Pharmacy 20th Ed. (Lippincott, Williams & Wilkins 2003).

[0125] Pharmaceutical compositions can be formulated based on the physical characteristics of the patient/subject needing treatment, the route of administration, and the like. Such can be packaged in a suitable pharmaceutical package with appropriate labels for the distribution to hospitals and clinics wherein the label is for the indication of treating a disorder as described herein in a subject. Medicaments can be packaged as a single or multiple units. Instructions for the dosage and administration of the pharmaceutical compositions of the present invention can be included with the pharmaceutical packages and kits described below.

Methods of Use

[0126] The MMP9 binding proteins, including anti-MMP9 antibodies and fragments thereof, of the present disclosure can be used, for example, in therapeutic and diagnostic methods, such as methods of detection of MMP9 in a sample, methods of treatment (e.g., as in methods of inhibition of angiogenesis), and methods of diagnosis and prognosis. Thus, provided are diagnostic and therapeutic methods and uses of the anti-MMP9 antibodies. Examples of methods of use are described below.

Methods of Treatment

[0127] Provided herein are methods of treatment, including methods of treating diseases and disorders associated with MMP9 expression and/or activity, as well as uses of the provided antibodies and compositions in such methods. The diseases and disorders include, but are not limited to cancer, e.g., tumors (e.g., primary or metastatic tumors), such as those that express or are disposed in a tissue which expresses MMP9, and inflammatory diseases, such as inflammatory bowel diseases, rheumatoid arthritis and inflammatory myopathies.

[0128] As used herein, "treat" or "treatment" means stasis or a postponement of development of one or more symptoms associated with a disease or disorder described herein, or ameliorating existing uncontrolled or unwanted symptoms, preventing additional symptoms, or ameliorating or preventing the underlying metabolic causes of symptoms. Thus, the terms denote that a beneficial result has been conferred on a mammalian subject with a disease or symptom, or with the potential to develop such disease or symptom. A response is achieved when the patient experiences partial or total alleviation, or reduction of signs or symptoms of illness, and can include, without limitation, prolongation of survival. The expected progression-free survival times can be measured in months to years, depending on prognostic factors including the number of relapses, stage of disease, and other factors.

[0129] Also provided are pharmaceutical compositions for use in connection with such methods, such as those containing any of the antibodies or fragments thereof described herein. Compositions can be suitable for administration locally or systemically by any suitable route.

[0130] In general, MMP9 binding proteins are administered in a therapeutically effective amount, e.g., in an amount to effect inhibition of tumor growth in a subject, to inhibit metastasis, to inhibit inflammation, to inhibit tissue destruction, to inhibit MMP9 activity, or to treat the particular disease or condition associated with MMP9.

[0131] As used herein, unless otherwise specified, the term "therapeutically effective amount" or "effective amount" refers to an amount of an agent or compound or composition that when administered (either alone or in combination with another therapeutic agent, as may be specified) to a subject is effective to prevent or ameliorate the disease condition or the progression of the disease, or result in amelioration of symptoms, e.g., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously. In one example, when in vivo administration of an anti-MMP9 antibody is employed, normal dosage amounts can vary from about 10 ng/kg to up to 100 mg/kg of mammal body weight or more per day, preferably about 1 μg/kg/day to 50 mg/kg/day, optionally about 100 μg/kg/day to 20 mg/kg/day, 500 μg/kg/day to 10 mg/kg/day, or 1 mg/kg/day to 10 mg/kg/day, depending upon the route of administration. In one embodiment, intravenous dosage range from about 1 mg/kg to about 30 mg/kg. In some embodiments, intravenous dosages range from at or about 1 mg/kg to at or about 14 mg/kg, such as from at or about 2 mg/kg to at or about 14 mg/kg, q14d, once every 14 days. In other embodiments, subcutaneous dosages range from at or about 1 mg/kg to at or about 28 mg/kg, such as from at or about 2 mg/kg to at or about 28 mg/kg, q14d, once every 14 days. In some embodiments, the effective amount of dosage is administered once every 7 to 28 days. In one embodiment, the effective amount of dosage is administered once every 7 days. In another embodiment, the effective amount of dosage is administered once every 28 days.

[0132] The selected dosage regimen will depend upon a variety of factors including the activity of the MMP9 binding protein, the route of administration, the time of administration, the rate of excretion of the particular compound being employed, the duration of the treatment, other drugs, compounds and/or materials used in combination with the particular composition

employed, the age, sex, weight, condition, general health and prior medical history of the patient being treated, and like factors well known in the medical arts.

[0133] A clinician having ordinary skill in the art can readily determine and prescribe the effective amount of the pharmaceutical composition required. For example, the physician or veterinarian can start doses of the compounds of the invention employed in the pharmaceutical composition at levels lower than that required in order to achieve the desired therapeutic effect and gradually increase the dosage until the desired effect is achieved.

[0134] In some cases, the methods of treatment include parenteral administration, e.g., intravenous, intra-arterial, intramuscular, or subcutaneous administration, or oral administration of the agent, e.g., anti-MMP9 antibody or composition containing the same.

[0135] As used herein, the term "subject" means a mammalian subject. Exemplary subjects include, but are not limited to humans, monkeys, dogs, cats, mice, rats, cows, horses, goats and sheep. In some embodiments, the subject has cancer, an inflammatory disease or condition, or an autoimmune disease or condition, and can be treated with the agent of the present invention as described below.

[0136] If needed, for treatments, methods can further include additional therapies, such as in the case of cancer, surgical removal of the cancer and/or administration of an anti-cancer agent or treatment in addition to an MMP9 binding protein. Administration of such an anti-cancer agent or treatment can be concurrent with administration of the compositions disclosed herein.

Methods of Detection of MMP9

[0137] The present disclosure also contemplates methods of detecting MMP9 in a subject, e.g., to detect tumor or tumor-associated tissue expressing MMP9, or tissue or fluid or other biological sample associated with a disease as described herein, such as autoimmune or inflammatory disease. Thus, methods of diagnosing, monitoring, staging or detecting a tumor having MMP9 activity are provided.

[0138] Samples (e.g., test biological samples) from a subject (e.g., an individual suspected of having or known to have a tumor associated with MMP9 expression, or suspected of having or known to have another disease or condition), can be analyzed for MMP9 presence, absence, expression, and/or levels. For example, such samples can be collected and analyzed by detecting the presence or absence of binding of an MMP9 binding protein, such as an antibody or fragment as described herein, to substance (e.g., protein) in the sample. In some examples, the methods further include comparing the amount of binding detected to an amount of binding to a control sample, or comparing the detected level of MMP9 to a control level of MMP9. In some

cases, the methods indicate the presence, absence, or severity of an MMP9-associated disease or condition, such as one described herein.

[0139] This analysis can be performed prior to the initiation of treatment using an MMP9 binding protein as described herein, or can be done as part of monitoring of progress of cancer treatment. In some embodiments, provided are methods of treatment, carried out by performing the detection assays and initiating, altering, or discontinuing treatment of the subject, for example, based on the results of the diagnostic assay. Such diagnostic analysis can be performed using any sample, including but not limited to tissue, cells isolated from such tissues, and the like. In some cases, the methods are performed on liquid samples, such as blood, plasma, serum, whole blood, saliva, urine, or semen. Tissue samples include, for example, formalin-fixed or frozen tissue sections.

[0140] Any suitable method for detection and analysis of MMP9 can be employed. Various diagnostic assay techniques known in the art can be adapted for such purpose, such as competitive binding assays, direct or indirect sandwich assays and immunoprecipitation assays conducted in either heterogeneous or homogeneous phases.

[0141] MMP9 binding proteins for use in detection methods can be labeled with a detectable moiety. The detectable moiety directly or indirectly produces a detectable signal. For example, the detectable moiety can be any of those described herein such as, for example, a radioisotope, such as 3H, 14C, 32P, 35S, or 125I, a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate (FITC), Texas red, cyanin, photocyan, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, β-galactosidase or horseradish peroxidase.

[0142] Detection can be accomplished by contacting a sample under conditions suitable for MMP9 binding protein binding to MMP9, and assessing the presence (e.g., level) or absence of MMP9 binding protein-MMP9 complexes. A level of MMP9 in the sample in comparison with a level of a reference sample can indicate the presence of a tumor or tumor-associated tissues having MMP9 activity. The reference sample can be a sample taken from the subject at an earlier time point or a sample from another individual.

[0143] Various aspects of the invention are further described and illustrated by way of the several examples which follow, none of which are intended to limit the scope of the invention.

EXAMPLES

Example 1A: Preparation of antibodies to human MMP-9.

[0144] The full-length human MMP9 protein without a signal peptide (SEQ ID NO. 28) was used to immunize mice. Spleen cells from immunized mice were fused with myeloma cells to generate a hybridoma library. Monoclonal cultures were prepared and screened to identify cultures expressing an anti-MMP9 monoclonal antibody.

[0145] An antibody (AB0041) was purified from one of the cultures and characterized. This antibody contained an IgG2b heavy chain and a kappa light chain. Characterization included testing for the binding of AB0041 to other human MMPs and to MMP9 proteins from other species, including cynomolgus monkey, rat and mouse. As shown in Table 2, the AB0041 antibody had greater affinity to human and cynomolgus MMP9, that it had lower affinity to rat MMP9. In addition, the AB0041 antibody did not bind to murine MMP9 or to many human non-MMP matrix metalloproteinases.

Table 2: Cross reactivity of AB0041 and AB0045

MMP Tested	Dissociation constant (Kd)	
	AB0045	AB0041
Human MMP1	>100 nM	>100 nM
Human MMP2	>100 nM	>100 nM
Mouse MMP2	>100 nM	>100 nM
Human MMP3	>100 nM	>100 nM
Human MMP7	>100 nM	>100 nM
Human MMP8	>100 nM	>100 nM
Human MMP9	0.168 ± 0.117 nM	0.133 ± 0.030 nM
Cynomolgus monkey MMP9	0.082 ± 0.022 nM	0.145 ± 0.16 nM
Mouse MMP9	>100 nM	>100 nM
Rat MMP9	0.311 ± 0.017 nM	0.332 ± 0.022 nM
Human MMP10	>100 nM	>100 nM
Human MMP12	>100 nM	>100 nM
Human MMP13	>100 nM	>100 nM

[0146] Additional characterization included assaying the binding of AB0041 to mutant mouse and human MMP9 proteins. Non-identical residues in the catalytic domain of mouse and human MMP9 proteins were identified, and forty-six non-identical amino acid residues were selected for mutagenesis. Most mutations were generated in mouse MMP9: the mouse amino acid residues were mutated to match those of human MMP9. Other mutations were generated in human MMP9: the human amino acid residues were mutated to match those of mouse MMP9. The mutated mouse or human MMP9 proteins were used in an ELISA assay.

[0147] In the ELISA assay, the AB0041 antibody was used as the primary antibody and a goat anti-mouse IgG antibody conjugated to horseradish peroxidase was used to detect the binding. The wild-type human MMP9 was used a positive control and the wild-type mouse MMP9 was used as a negative control. The results of the ELISA assay showed an arginine

residue at position 162 of the MMP9 amino acid sequence (R162) as important for the MMP9 binding of the AB0041 antibody. The results also showed the amino acid residues E111, D113, and I198 were important for the MMP9 binding of the AB0041 antibody. Based on the crystal structure of MMP9, E111, D113, R162, and I198 are grouped near each other around a Ca2+ ion binding pocket of MMP9. In this study, the AB0041 antibody was shown to specifically bind to an epitope containing amino acid residues within regions of MMP9 containing amino acid residues 104-119, 159-166, and 191-202.

[0148] In an enzymatic assay for MMP9, the AB0041 antibody was found to act as a non-competitive inhibitor of MMP9.

Example 1B: Preparation of additional antibodies to human MMP-9.

[0149] Additional hybridomas were generated, which produced antibodies having variable regions that shared identity with AB0041. One such hybridoma, designated M4, expressed an antibody containing the heavy chain (IgG2b) sequence:

[0150] MAVLVLFLCLVAFPSCVLSQVQLKESGPGLVAPSQSLSITCTVSGFSLLSYGV HWVRQPPGKGLEWLGVIWTGGSTNYNSALMSRLSISKDDSKSQVFLKMNSLQTDDTA MYYCARYYYAMDYWGQGTSVTVSS*AKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPE SVTVTWNSGSLSSSVHTFPALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPS GPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVRI SWFVNNVEVHTAQTQTHREDYNSTIRVVSALPIQHQDWMSGKEFKCKVNNKDLPSPIERTISK IKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSD GSYFIYSKLDIKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK* (SEQ ID NO:30)

[0151] (signal peptide set forth in underlined text, variable region set forth in plain text, and constant region set forth in italics), and the light chain (kappa) sequence:

[0152] MESQIQVFVFVFLWLSGVDGDIVMTQSHKFMFTSVGDRVSITCKASQDVRNT VAWYQQKTGQSPKLLIYSASYRNTGVPDRFTGSISGTDFTFTISSVQAEDLALYYCQQH YSTPYTFGGGTKLEVK*RADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSE RQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC* (signal peptide set forth in underlined text, variable region set forth in plain text, and constant region set forth in italics) (SEQ ID NO: 31).

[0153] The M4 antibody had a variable heavy chain with an amino acid sequence:

[0154] QVQLKESGPGLVAPSQSLSITCTVSGFSLLSYGVHWVRQPPGKGLEWLGVIW TGGSTNYNSALMSRLSISKDDSKSQVFLKMNSLQTDDTAMYYCARYYYAMDYWGQG TSVTVSS (CDRs 1, 2, and 3 (SEQ ID NOs: 34, 35, and 36, respectively) underlined) (SEQ ID NO: 32)

[0155] and a variable light chain with the amino acid sequence

[0156] DIVMTQSHKFMFTSVGDRVSITCKASQDVRNTVAWYQQKTGQSPKLLIYSAS YRNTGVPDRFTGSISGTDFTFTISSVQAEDLALYYCQQHYSTPYTFGGGTKLEVK (CDRs 1, 2, and 3 (SEQ ID NOs: 37, 38, and 39, respectively) underlined) (SEQ ID NO: 33).

[0157] Another such hybridoma, designated M12, expressed only a kappa chain, having the sequence:

[0158] QVFVYMLLWLSGVDGDIVMTQSQKFMSTSVGDRVSVTCKASQNVGTNVA WYQQKPGQSPKALIYSASYRFSGVPDRFTGSGSGTDFTLTISNVQSEDLAEYFCQQYNS YPYTFGGGTKLEIK*RADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQ NGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC* (signal peptide set forth in underlined text, variable region set forth in plain text, and constant region set forth in italics) (SEQ ID NO: 40).

[0159] The M12 antibody had a variable light chain with the amino acid sequence

[0160] DIVMTQSQKFMSTSVGDRVSVTCKASQNVGTNVAWYQQKPGQSPKALIYSA SYRFSGVPDRFTGSGSGTDFTLTISNVQSEDLAEYFCQQYNSYPYTFGGGTKLEIK (CDRs 1, 2, and 3 (SEQ ID NOs: 42, 43, and 44, respectively) underlined) (SEQ ID NO: 41).

[0161] A sequence comparison, showing differences between the M4 and M12 heavy and light chains as compared with AB0041 antibody is shown in Figure 4.

[0162] An enzymatic assay was carried out. The results demonstrated that the antibodies produced by the M4 and M12 hybridomas acted as non-competitive inhibitors of MMP9 (data not shown).

Example 1C: Preparation of antibodies to mouse MMP-9.

[0163] Another mouse antibody, AB0046, was generated. Using a process similar to that described in Example 1A, the MMP9-knockout mice (strain B6.FVB (Cg)- *Mmp9*^{tm1Tvu}/J) was immunized using targeted domains of the pro/catalytic domain fragment of murine MMP9. The AB0046 antibody had a kappa light chain with an amino acid sequence MSSAQFLGLLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCSASQGISNYLNWYQQKPD GTFKLLIYYTSILHSGVPSRFSGSGSGTDYSLTISNLEPEDIATYYCQQYGWLPRTFGGGT KLEIK*RADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTD QDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC* (SEQ ID NO: 45) (signal peptide set forth in underlined text, variable region set forth in plain text, and constant region set forth in italics) and an IgG1 heavy chain with an amino acid sequence MGWSSIILFLVATATGVHSQVQLQQPGSVLVRPGASVKLSCTASGYTFTSYWMNWVK QRPGQGLEWIGEIYPISGRTNYNEKFKVKATLTVDTSSSTAYMDLNSLTSEDSAVYYCA

RSRANWDDYWGQGTTLTVSS*AKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVT WNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVPRDCGC KPCICTVPEVSSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQP REEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPP KEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNVQKS NWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK* (SEQ ID NO: 46) (signal peptide set forth in underlined text, variable region set forth in plain text, and constant region set forth in italics).

[0164] The following amino acid sequence comprises the framework regions and complementarity-determining regions (CDRs) of the variable region of the IgG1 heavy chain of AB0046 (with CDRs underlined):

[0165] QVQLQQPGSVLVRPGASVKLSCTASGYTFTSYWMNWVKQRPGQGLEWIGEI YPISGRTNYNEKFKVKATLTVDTSSSTAYMDLNSLTSEDSAVYYCARSRANWDDYWG QGTTLTVSS (SEQ ID No: 47).

[0166] The following amino acid sequence comprises the framework regions and complementarity-determining regions (CDRs) of the variable region of the kappa light chain of AB0046 (with CDRs underlined):

[0167] DIQMTQTTSSLSASLGDRVTISCSASQGISNYLNWYQQKPDGTFKLLIYYTSIL HSGVPSRFSGSGSGTDYSLTISNLEPEDIATYYCQQYGWLPRTFGGGTKLEIK (SEQ ID No: 48)

[0168] Additional characterizations showed that the AB0046 antibody bound to mouse MMP9 non-competitively or its binding was not dependant on the concentration of mouse MMP9. The AB0046 antibody did not bind to human MMP9 or MMP2, mouse MMP2, 3, 7, 8, or 12. Using epitope analysis as described in Example 1A, it was shown that the proline residue at position 162 of the mouse MMP9 amino acid sequence (P162) (corresponding to R162 of human MMP9) was important for the MMP9 binding of the AB0046 antibody. The results suggested that the AB0046 antibody specifically bound to an epitope containing a residue within a portion of mouse MMP9 corresponding to the portion containing amino acids 159-166 of human MMP9. Thus, the AB0046 antibody was an inhibitory antibody specific to mouse MMP9 and had similar kinetics of binding and inhibition as those of AB0041. Because AB0046 is specific to mouse MMP9 and binds to an epitope as AB0041/AB0045, AB0046 is suitable for assays which uses either AB0041 or AB0045.

[0169] Further characterization showed that the AB0046 antibody was a murine IgG1 isotype, having a limited effector function in mouse.

[0170] Three other mouse anti-MMP9 antibodies were generated using similar methods, which were non-inhibitory and for which P162 was important for binding.

Example 2: Humanization of antibodies to human MMP9

[0171] The amino acid sequences of the heavy chain and light chain of the mouse AB0041 antibody were altered at certain locations in the framework (*i.e.*, non-CDR) portion of their variable regions to generate proteins that are less immunogenic in humans. These amino acid sequence changes were shown in Figures 1 and 2. The cross-reactivity of one humanized antibody, referred to as AB0045, is shown in Table 2A above.

[0172] The humanized variant anti-MMP9 antibody, AB0045 (humanized, modified IgG4 (S241P); see Example 2, above) contained the humanized AB0041 heavy chain variant **VH3** (having the sequence set forth in SEQ ID NO: 7

[0173] (QVQLQESGPGLVKPSETLSLTCTVSGFSLLSYGVHWVRQPPGKGLEWLGVI WTGGTTNYNSALMSRFTISKDDSKNTVYLKMNSLKTEDTAIYYCARYYYGMDYWGQ GTLVTVSS)

[0174] and the humanized AB0041 light chain variant VH4 (having the light chain sequence set forth in **Vk4** (having the sequence set forth in SEQ ID NO: 12

[0175] (DIQMTQSPSSLSASVGDRVTITCKASQDVRNTVAWYQQKPGKAPKLLIYSSS YRNTGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQHYITPYTFGGGTKVEIK)).

[0176] The heavy chain of the AB0045 antibody has the sequence set forth in SEQ ID NO: 49

(MGWSLILLFLVAVATRVHSQVQLQESGPGLVKPSETLSLTCTVSGFSLLSYGVHWVRQ PPGKGLEWLGVIWTGGTTNYNSALMSRFTISKDDSKNTVYLKMNSLKTEDTAIYYCAR YYYGMDYWGQGTLVTVSS*ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCP PCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKT KPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLP PSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKS RWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK* (signal sequence underlined; sequence of the constant region presented italics)); the light chain of the AB0045 antibody has the sequence set forth in SEQ ID NO: 50

(MRVPAQLLGLLLLWLPGARCDIQMTQSPSSLSASVGDRVTITCKASQDVRNTVAWYQ QKPGKAPKLLIYSSSYRNTGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQHYITPYT FGGGTKVEIK*RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC* (signal sequence underlined; sequence of the constant region presented italics)). The antibody contains 1312 amino acids in length, is composed of two heavy chains and two light chains, and has a

theoretical pI of about 7.90, extinction coefficient of about 1.50 AU/cm at 280 nm for 1 g/L, a molecular weight of about 144 kDa, and density of about 1 g/mL in formulation buffer (50-100 mg/mL product concentration).

[0177] Further characterization of this antibody is described in Example 3, below.

Example 3: Characterization of variant MMP9 antibody AB0045 and comparison to AB0041 and AB0046

[0178] As described above, AB0045 and AB0041 antibodies are non-competitive inhibitors of MMP9. Thus, both antibodies inhibit MMP9 enzymatic activity independently of substrate concentration. The AB0045 antibody binds to the same MMP9 epitope as the AB0041 antibody with an affinity in the 1 × 10-12 molar range, as shown by direct binding and surface plasmon resonance (SPR) assays. Both antibodies are specific for MMP9, with no significant non-specific binding observed against other purified protein targets including purified domains and full length forms of MMP enzymes. Both AB0045 and AB0041 antibodies are cross-reactive with native and recombinant human and recombinant rat and cynomolgus monkey MMP9.

[0179] The *in vitro* binding affinity, inhibition characteristics, and the specificity of the antibodies of AB0045, AB0041 and AB0046 for MMP9 of human and non-human origin were determined using Enzyme-Linked Immunosorbent Assay (ELISA) and an MMP9 enzymatic assay. SPR analysis was also used to generate dissociation constants (K_d) of AB0045 and AB0041.

[0180] In the ELISA assay, the K_d value of AB0045 and AB0041 antibodies for human, cynomolgus monkey, and rat MMP9 derived from ELISA were all found to be <400 pM. The ELISA data illustrated that both AB0045 and AB0041 antibodies cross-react with MMP9 from all the relevant toxicology species tested. The AB0046 antibody was shown to be specific to mouse MMP9 and therefore could be used as a surrogate antibody in mouse efficacy models. The results showed that the K_d value of the AB0045 antibodies for human MMP9 was 0.168 ± 0.117 nM and the and K_d value of the AB0041 antibody was 0.133 ± 0.030 nM. The results on the AB0046 antibodies showed it bound to mouse MMP9 with the K_d value of 0.218 ± 0.097 nM. In the SPR analysis, the results showed that the K_d values of AB0045 and AB0041 antibodies for human MMP9 were 8.8 pM and 0.4 pM, respectively.

[0181] The enzymatic inhibitory activities of AB0045, AB0041, and AB0046 antibodies were evaluated in an assay assessing MMP9-mediated cleavage of a fluorogenic peptide substrate Mca-PLGL-Dpa-AR-NH2. All three antibodies inhibited MMP9 enzyme activity. The IC_{50} values of AB0045 (0.691 ± 0.097 nM) and AB0041 (0.569 ± 0.185 nM) for human MMP9 were not statistically different. The IC_{50} value for the AB0046 inhibition of mouse MMP9 was

0.352 ± 0.03 nM. The value was not adjusted for the concentration of active enzyme that was generated during the preparation. Additional MMP9 enzymatic assay under steady-state conditions was used to determine IC_{50} and mode of inhibition. In this assay, the IC_{50} values of AB0045 ranged from 0.148 nM to 0.161 nM in a 20-fold range of substrate concentration, and in one example is 0.158 nmThe results showed that the MMP9 inhibitory activity of AB0045 was non-competitive.

Table 2B: Binding and Inhibitory Properties of AB0045, AB0041, and surrogate mouse antibody AB0046

	AB0045	**AB0041**	**AB0046**
ELISA			
Human MMP9 Dissociation constant	0.168 ± 0.117 nM	0.133 ± 0.030 nM	>100 nM
Cynomolgus monkey MMP9 Dissociation constant	0.082 ± 0.022 nM	0.145 ± 0.16 nM	>100 nM
Mouse MMP9 Dissociation constant	>100 nM	>100 nM	0.218±0.097 nM
Rat MMP9 Dissociation constant	0.311 ± 0.017 nM	0.332 ± 0.022 nM	>100 nM
SPR			
Human MMP9 Dissociation constant	8.8pM	0.4pM	ND
Activity Assay			
Human MMP9 IC_{50}	0.691 ± 0.097 nM	0.569 ± 0.185 nM	>100 nM
Cynomolgus monkey MMP9 IC_{50}	0.194 ± 0.048 nM*	0.189 ± 0.019 nM*	>100 nM
Rat MMP9 IC_{50}	8.23 ± 1.24 nM*	2.78 ± 1.17 nM *	>100 nM
Mouse MMP9 IC_{50}	>100 nM	>100 nM	0.352±0.03 nM*

[0182] The results confirmed that AB0045 and AB0041 have equivalent binding and inhibitory properties and that AB0046 can serve as a relevant mouse surrogate antibody, for example, in mouse models of human disease.

CLAIMS

What is claimed is:

1. An isolated antibody or fragment thereof, comprising: a heavy chain variable (VH) region having a heavy chain complementary determining region (CDR) with an amino acid sequence selected from the group consisting of SEQ ID NO: 13, SEQ ID NO: 14, and SEQ ID NO: 15.

2. The antibody or fragment of claim 1, wherein the VH region has a heavy chain CDR1 with the amino acid sequence of SEQ ID NO: 13, a heavy chain CDR2 with the amino acid sequence of SEQ ID NO: 14, and a heavy chain CDR3 with the amino acid sequence of SEQ ID NO: 15.

3. An isolated antibody or fragment thereof, comprising: a light chain variable (VL) region having a light chain complementary determining region (CDR) with an amino acid sequence selected from the group consisting of SEQ ID NO: 16, SEQ ID NO: 17, and SEQ ID NO: 18.

4. The antibody or fragment of claim 3, wherein the VL region has a light chain CDR1 with the amino acid sequence of SEQ ID NO: 16, a light chain CDR2 with the amino acid sequence of SEQ ID NO: 17, and a light chain CDR3 with the amino acid sequence of SEQ ID NO: 18.

5. The antibody or fragment of claim 3 or claim 4, wherein the antibody further comprises a VH region having a heavy chain CDR1 with the amino acid sequence of SEQ ID NO: 13, a heavy chain CDR2 with the amino acid sequence of SEQ ID NO: 14, and a heavy chain CDR3 with the amino acid sequence of SEQ ID NO: 15.

6. The antibody or fragment of any of claims 1, 2, and 5, wherein the VH region has the amino acid sequence set forth in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, or SEQ ID NO: 8.

7. The antibody or fragment of claim 6, wherein the VH region has the amino acid sequence set forth in SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, or SEQ ID NO: 8.

8. The antibody or fragment of any of claims 3-7 wherein the VL region has the amino acid sequence set forth in SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, or SEQ ID NO: 12.

9. The antibody or fragment of claim 8, wherein the VL region has the amino acid sequence set forth in SEQ ID NO: 4, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, or SEQ ID NO: 12.

10. The antibody or fragment of claim 5, wherein the VH region has the amino acid sequence set forth in SEQ ID NO: 7 and the VL region has the amino acid sequence set forth in SEQ ID NO: 12.

11. An isolated antibody or fragment thereof that competes for binding to MMP9 with an antibody having a VH region with the amino acid sequence set forth in SEQ ID NO: 7 and a VL region with the amino acid sequence set forth in SEQ ID NO: 12.

12. An isolated antibody or fragment thereof that specifically binds to an epitope of MMP9, wherein the epitope comprises an amino acid residue within a region of MMP9, the region consisting of residues 104-119, residues 159-166, or residues 191-202 of SEQ ID NO: 27.

13. The antibody or fragment of claim 12, wherein the epitope comprises an amino acid residue within a region of MMP9 consisting of residues 104-119 of SEQ ID NO: 27, an amino acid residue within a region of MMP9 consisting of residues 159-166 of SEQ ID NO: 27, and an amino acid residue within a region of MMP9 consisting of residues 191-202 of SEQ ID NO: 27.

14. The antibody or fragment of claim 12 or 13, wherein the epitope comprises E111, D113, R162, or I198 of SEQ ID NO: 27.

15. The antibody or fragment of claim 14, wherein the epitope comprises R162 of SEQ ID NO: 27.

16. The antibody or fragment of claim 14, wherein the epitope comprises E111, D113, R162, and I198 of SEQ ID NO: 27.

17. The antibody or fragment of any of claims 1-16, wherein the antibody or fragment inhibits the enzymatic activity of MMP9.

18. The antibody or fragment of claim 17, wherein the inhibition of the enzymatic activity is non-competitive.

19. The antibody or fragment of any of claims 1-18, which is human or humanized.

20. The antibody or fragment of any of claims 1-19, for use in a method of inhibiting MMP9 activity in a subject, the method comprising administering to the subject the antibody or fragment in an amount effective to inhibit MMP9 activity in the subject.

21. A method of inhibiting MMP9 activity in a subject, the method comprising administering to the subject the antibody or fragment of any of claims 1-19 in an amount effective to inhibit MMP9 activity in the subject.

22. The method of claim 21, wherein the antibody or fragment thereof is administered intravenously at a dose from about 1 mg/kg to about 14 mg/kg.

23. The method of claim 21, wherein the antibody or fragment is administered subcutaneously, at a dose of about 4 mg/kg to about 28 mg/kg.

24. The method of any of claims 21-23, wherein the antibody or fragment is administered once every 7 to 28 days.

25. An isolated nucleic acid, comprising: a nucleotide sequence encoding a heavy chain polypeptide comprising CDRs with the amino acid sequences set forth in SEQ ID NOs: 13-15 or a light chain polypeptide comprising CDRs with the amino acid sequences set forth in SEQ ID NOs: 16-18.

26. The isolated nucleic acid of claim 25, wherein the nucleotide sequence encodes the heavy chain polypeptide, which has an amino acid sequence selected from the group consisting of SEQ ID NOS: 1, 3, and 5-8.

27. The isolated nucleic acid of claim 25 or 26, wherein the nucleotide sequence encodes the light chain polypeptide, which has an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, and 9-12.

28. The isolated nucleic acid of any of claims 25-27, wherein the nucleotide sequence comprises a sequence selected from the group consisting of SEQ ID NOs: 19-26.

29. The isolated nucleic acid of any of claims 25-28, wherein the nucleotide sequence comprises SEQ ID NO: 21 and SEQ ID NO: 26.

30. A vector, comprising the isolated nucleic acid of any of claims 25-29.

31. A cell, comprising the vector of claim 30.

32. A pharmaceutical composition, comprising the antibody or fragment thereof of any of claims 1-19.

33. A pharmaceutical composition, comprising the vector of claim 30.

34. A pharmaceutical composition, comprising the cell of claim 31.

35. The pharmaceutical composition of any of claims 32-34, for use in a method of inhibiting MMP9 activity in a subject, the method comprising administering to the subject the pharmaceutical composition in an amount effective to inhibit MMP9 activity in the subject.

36. A method of inhibiting MMP9 activity in a subject, comprising administering to the subject the pharmaceutical composition of any of claims 32-34 in an amount effective to inhibit MMP9 activity in the subject.

37. A method of detecting MMP9 expression in a test sample from a subject, the method comprising:

(a) contacting the test sample with an antibody or fragment of any of claims 1-19; and

(b) detecting binding of the antibody or fragment to protein in the sample, thereby detecting the presence of MMP9.

38. The method of claim 37, further comprising comparing the amount of binding detected in the test sample with an amount of binding of the antibody or fragment to a control sample.

39. An isolated polypeptide, having an amino acid sequence consisting essentially of residues 111-198 of SEQ ID NO: 27.

40. An isolated mutant MMP9 polypeptide, comprising an amino acid sequence containing residues 111-198 of SEQ ID NO: 27 with an amino acid substitution at residue 111, 113, 162, or 198.

41. The isolated mutant MMP9 polypeptide of claim 40, wherein the amino acid sequence contains an amino acid substitution at residues 111, 113, 162, and 198 of SEQ ID NO 27.

FIGURE 1

Anti-MMP9 humanized heavy chains

AB0041	QVQLKESGPG	LVAPSQSLSI	TCTVSGFSLL	SYGVHWVRQP	PGKGLEWLGV	
VH1	QVQLQESGPG	LVKPSETLSL	TCTVSGFSLL	SYGVHWVRQP	PGKGLEWLGV	
VH2	QVQLQESGPG	LVKPSETLSL	TCTVSGFSLL	SYGVHWVRQP	PGKGLEWLGV	
VH3	QVQLQESGPG	LVKPSETLSL	TCTVSGFSLL	SYGVHWVRQP	PGKGLEWLGV	
VH4	QVQLQESGPG	LVKPSETLSL	TCTVSGFSLL	SYGVHWVRQP	PGKGLEWLGV	
AB0041	IWTGGTTNYN	SALMSRLSIS	KDDSKSQVFL	KMNSLQTDDT	AIYYCARYYY	
VH1	IWTGGTTNYN	SALMSRLTIS	KDDSKSTVYL	KMNSLKTEDT	AIYYCARYYY	
VH2	IWTGGTTNYN	SALMSRLTIS	KDDSKNTVYL	KMNSLKTEDT	AIYYCARYYY	
VH3	IWTGGTTNYN	SALMSRFTIS	KDDSKNTVYL	KMNSLKTEDT	AIYYCARYYY	
VH4	IWTGGTTNYN	SALMSRFTIS	KDDSKNTLYL	KMNSLKTEDT	AIYYCARYYY	
AB0041	GMDYWGQGTS	VTVSS	(SEQ ID NO:3)			
VH1	GNDYWGQGTS	VTVSS	(SEQ ID NO:5)			
VH2	GMDYWGQGTL	VTVSS	(SEQ ID NO:6)			
VH3	GMDYWGQGTL	VTVSS	(SEQ ID NO:7)			
VH4	GMDYWGQGTL	VTVSS	(SEQ ID NO:8)			

FIGURE 2

Anti-MMP9 humanized light chains

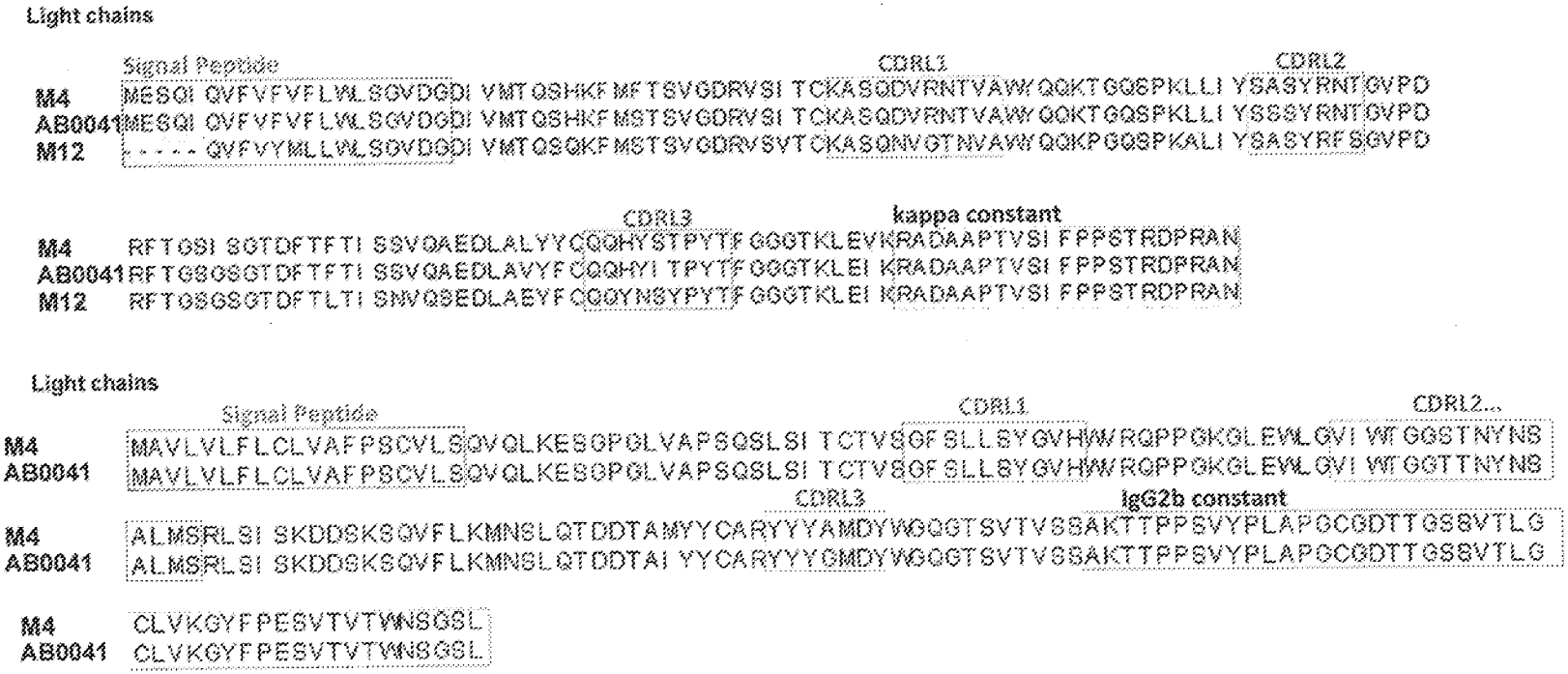
```
AB0041      DIVMTQSHKF MSTSVGDRVS ITCKASQDVR NTVAWYQQKT GQSPKLLIYS
Vk1         DIVMTQSPSF LSASVGDRVT ITCKASQDVR NTVAWYQQKT GKAPKLLIYS
Vk2         DIVMTQSPSS LSASVGDRVT ITCKASQDVR NTVAWYQQKP GKAPKLLIYS
Vk3         DIQMTQSPSS LSASVGDRVT ITCKASQDVR NTVAWYQQKP GKAPKLLIYS
Vk4         DIQMTQSPSS LSASVGDRVT ITCKASQDVR NTVAWYQQKP GKAPKLLIYS

AB0041      SSYRNTGVPD RFTGSGSGTD FTFTISSVQA EDLAVYFCQQ HYITPYTFGG
Vk1         SSYRNTGVPD RFTGSGSGTD FTLTISSLQA EDVAVYFCQQ HYITPYTFGG
Vk2         SSYRNTGVPD RFTGSGSGTD FTLTISSLQA EDVAVYFCQQ HYITPYTFGG
Vk3         SSYRNTGVPD RFSGSGSGTD FTLTISSLQA EDVAVYFCQQ HYITPYTFGG
Vk4         SSYRNTGVPD RFSGSGSGTD FTLTISSLQA EDVAVYYCQQ HYITPYTFGG

AB0041      GTKLEIK   (SEQ ID NO:4)
Vk1         GTKVEIK   (SEQ ID NO:9)
Vk2         GTKVEIK   (SEQ ID NO:10)
Vk3         GTKVEIK   (SEQ ID NO:11)
Vk4         GTKVEIK   (SEQ ID NO:12)
```

FIGURE 3

Figure 4: Comparison between AB0041, M4, and M12 heavy and light chains



INTERNATIONAL SEARCH REPORT

International application No
PCT/US2012/027160

A. CLASSIFICATION OF SUBJECT MATTER
INV. C07K16/40 C12N9/64 A61K39/395
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
C07K C12N A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
EPO-Internal, BIOSIS, Sequence Search, EMBASE, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 2009/111450 A2 (DYAX CORP [US]; DEVY LAETITIA [US]; BUCKLER DAVID [US]; COHEN EDWARD H) 11 September 2009 (2009-09-11) the whole document in particular abstract page 1, line 14 - page 12, line 21 claims 1-53; figures 1-10; examples 1-16	1-41
X A	WO 2007/094842 A2 (GENENTECH INC [US]; SIDHU SACHDEV S [US]; BIRTALAN SARA C [US]; FELLOU) 23 August 2007 (2007-08-23) the whole document in particular abstract figure 11A; sequence 413	1,19,32 2-18, 20-31, 33-41

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[X] Further documents are listed in the continuation of Box C.

[X] See patent family annex.

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"A" document defining the general state of the art which is not considered to be of particular relevance

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"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
29 October 2012	08/11/2012

Name and mailing address of the ISA/	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Ferreira, Roger

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C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

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