



US 20220324957A1

(19) **United States**(12) **Patent Application Publication**
PHILLIPS(10) **Pub. No.: US 2022/0324957 A1**(43) **Pub. Date: Oct. 13, 2022**(54) **ANTI-STEM CELL FACTOR ANTIBODIES
AND METHODS OF USE THEREOF IN
RENAL DISEASE****Publication Classification**(51) **Int. Cl.****C07K 16/24** (2006.01)**A61P 29/00** (2006.01)(52) **U.S. Cl.**CPC **C07K 16/24** (2013.01); **A61P 29/00**
(2018.01); **C07K 2317/24** (2013.01); **C07K**
2317/33 (2013.01); **C07K 2317/34** (2013.01);
C07K 2317/565 (2013.01); **C07K 2317/77**
(2013.01)(71) Applicant: **Opsidio, LLC**, Bryn Mawr, PA (US)(72) Inventor: **Martin PHILLIPS**, Bryn Mawr, PA
(US)(21) Appl. No.: **17/640,544**(22) PCT Filed: **Sep. 16, 2020**(86) PCT No.: **PCT/US20/50974**

§ 371 (c)(1),

(2) Date: **Mar. 4, 2022****Related U.S. Application Data**(60) Provisional application No. 62/900,927, filed on Sep.
16, 2019.

(57)

ABSTRACT

The disclosure relates to methods of use in renal diseases and disorders of antibodies and antigen-binding fragments thereof that bind to Stem Cell Factor (SCF). The antibodies and antigen-binding fragments thereof specifically bind to SCF248 and are useful for treating inflammatory and fibrotic renal disorders.

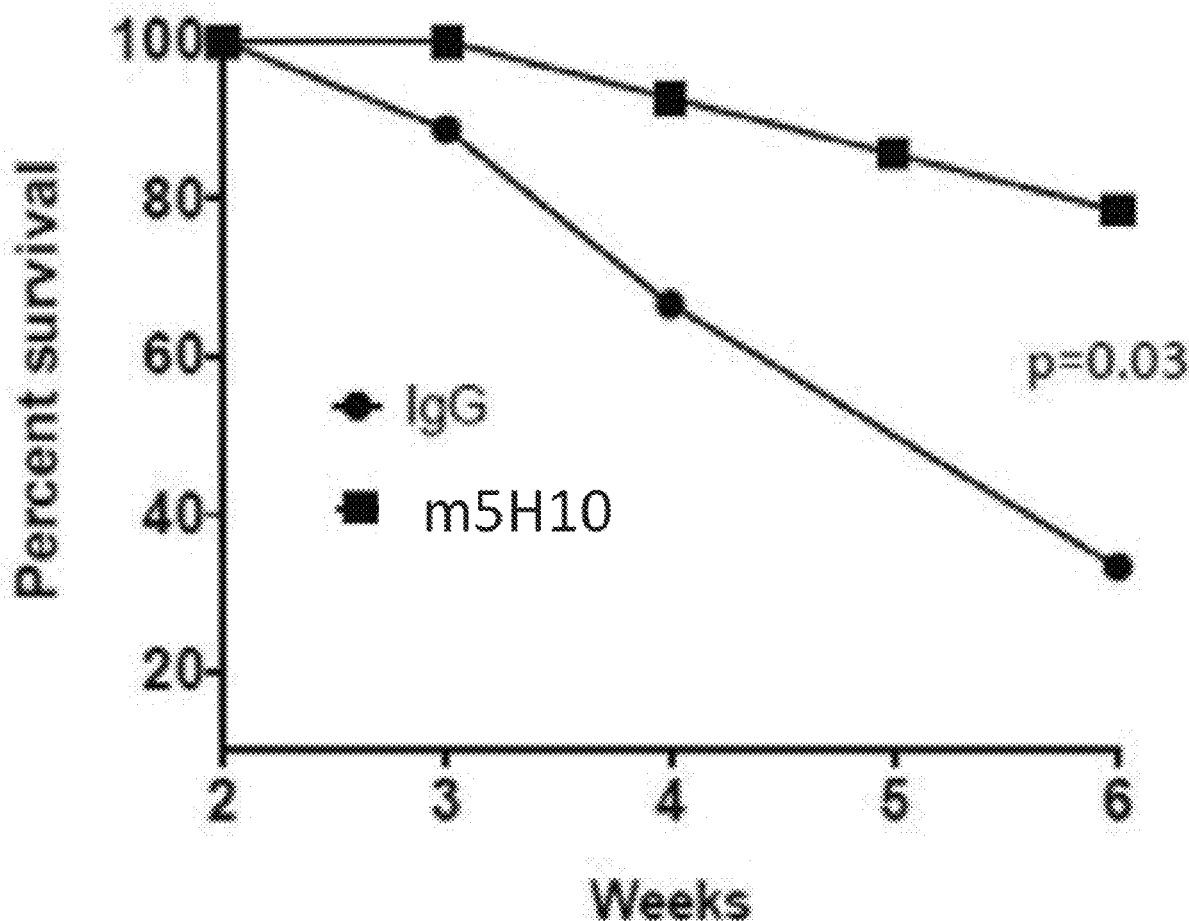
Specification includes a Sequence Listing.

Fig. 1

c-Kit⁺ Cells Promote Chronic Inflammation Feedback Loop

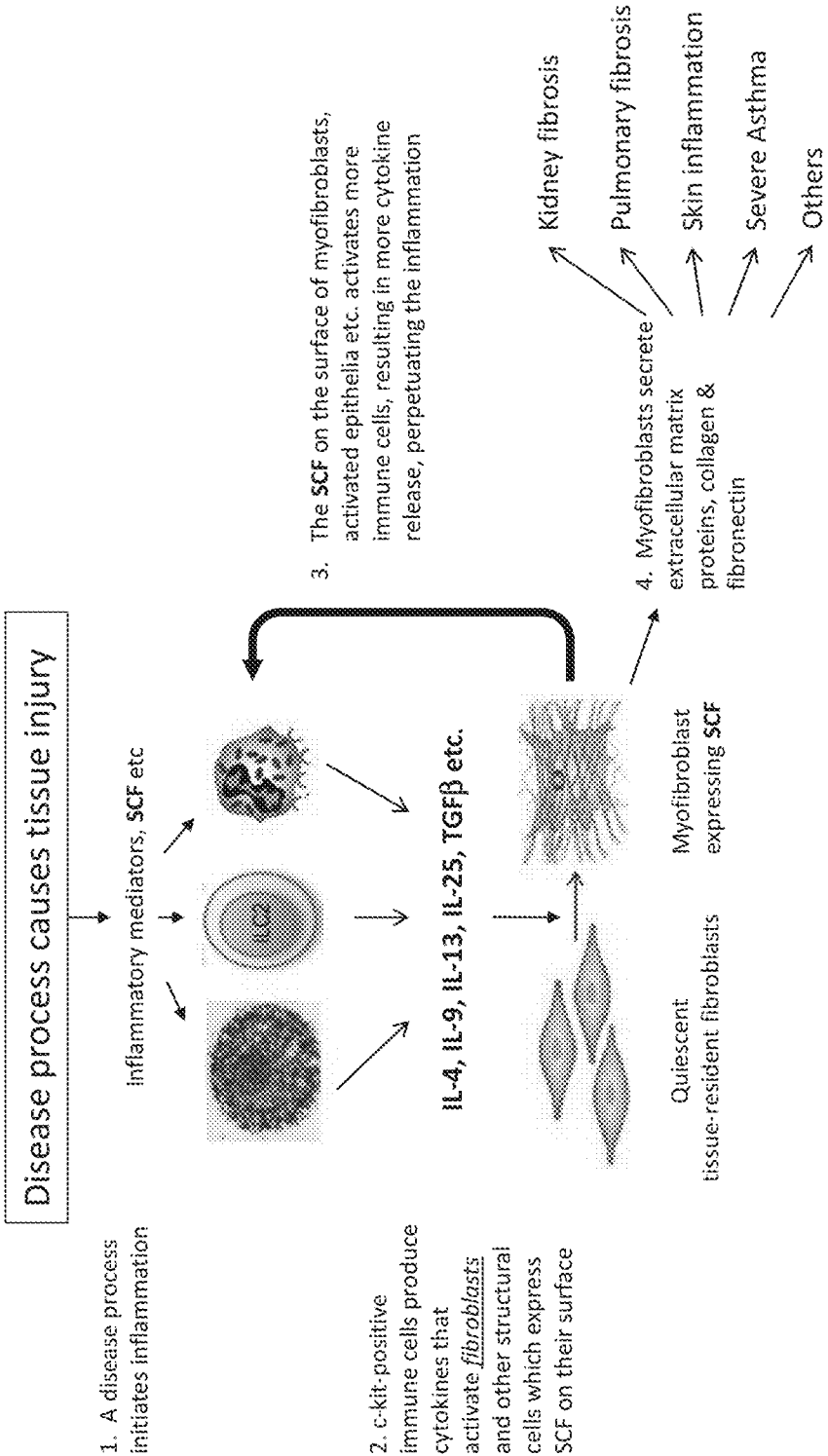


Fig. 2

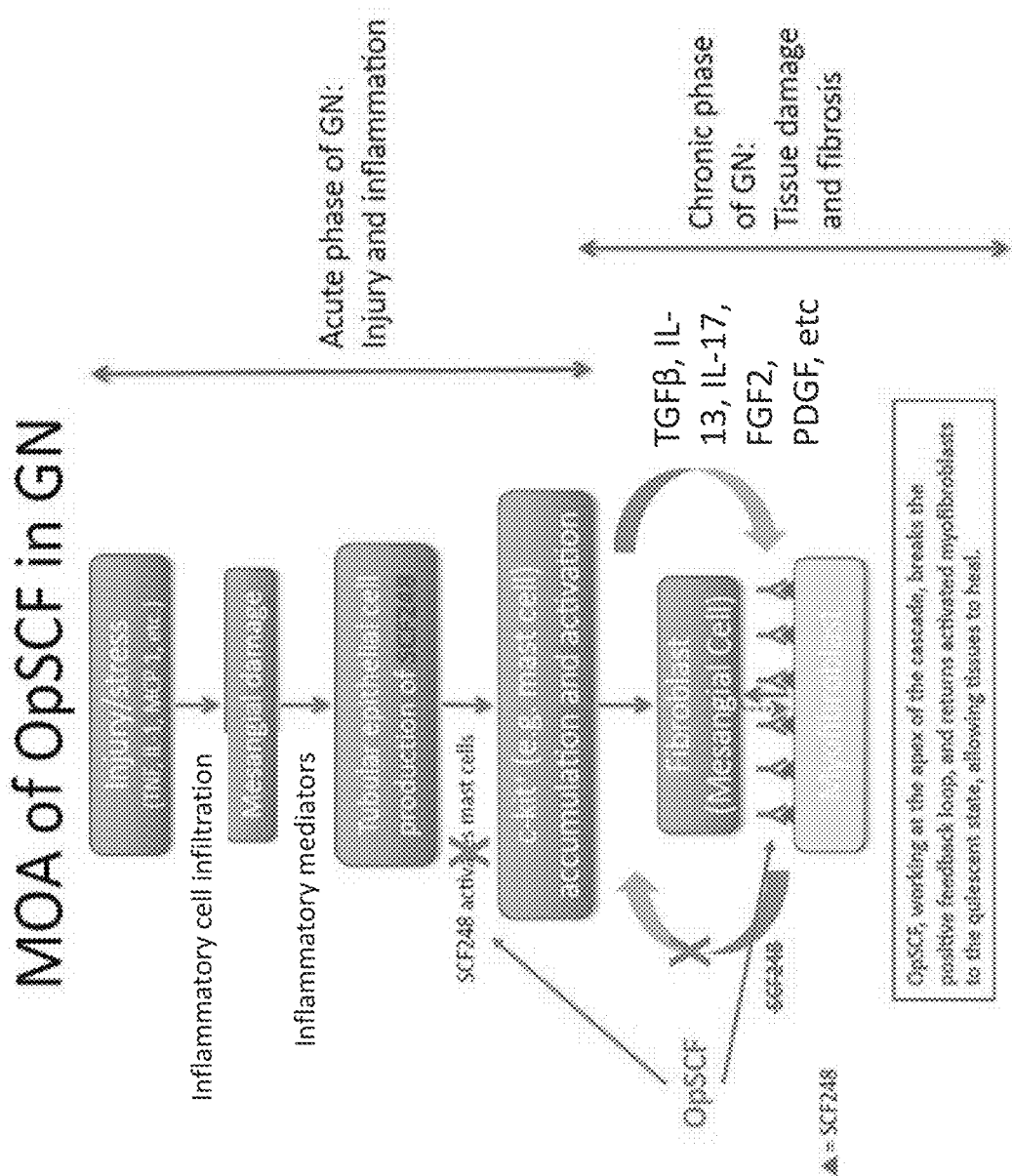


Fig. 3

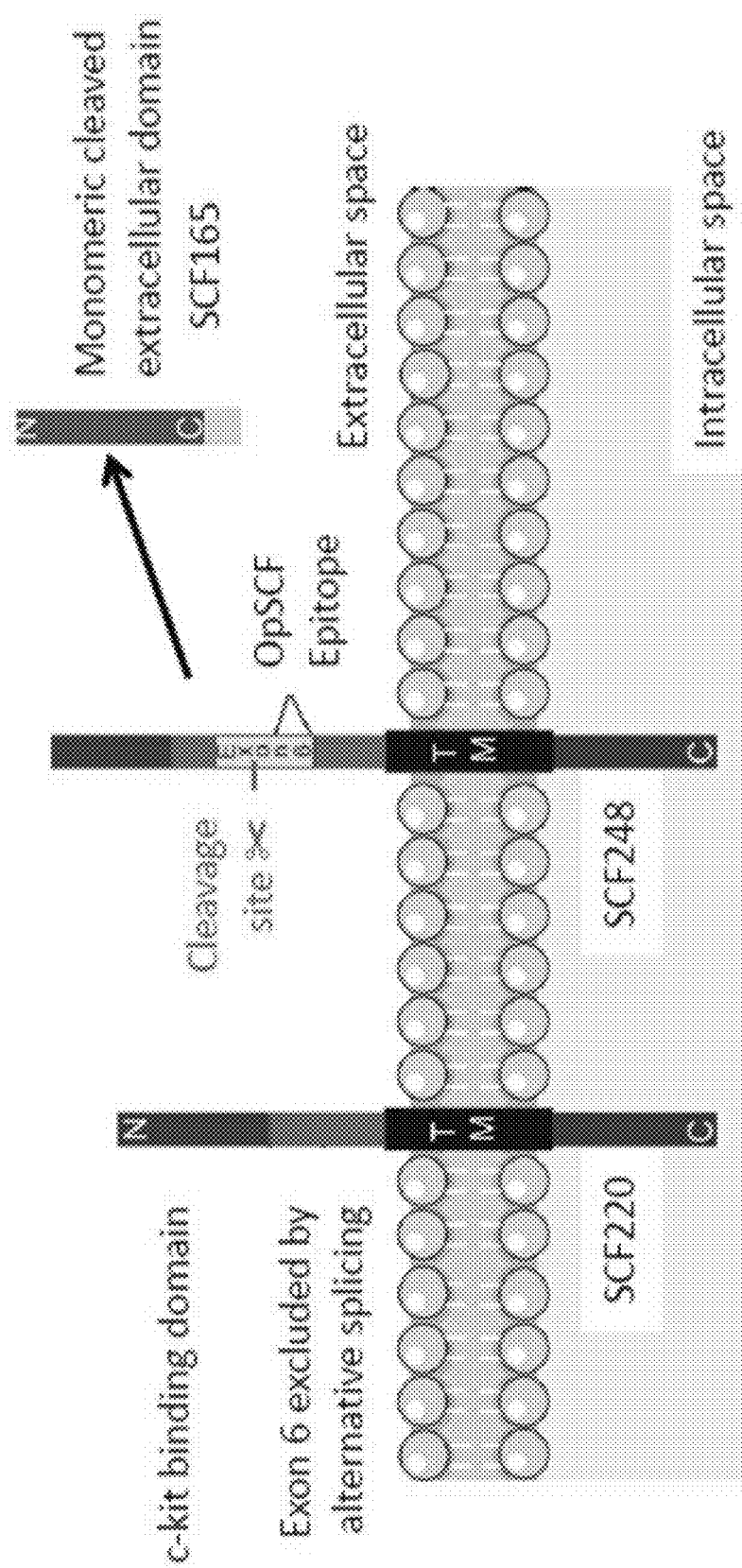


Fig. 4A

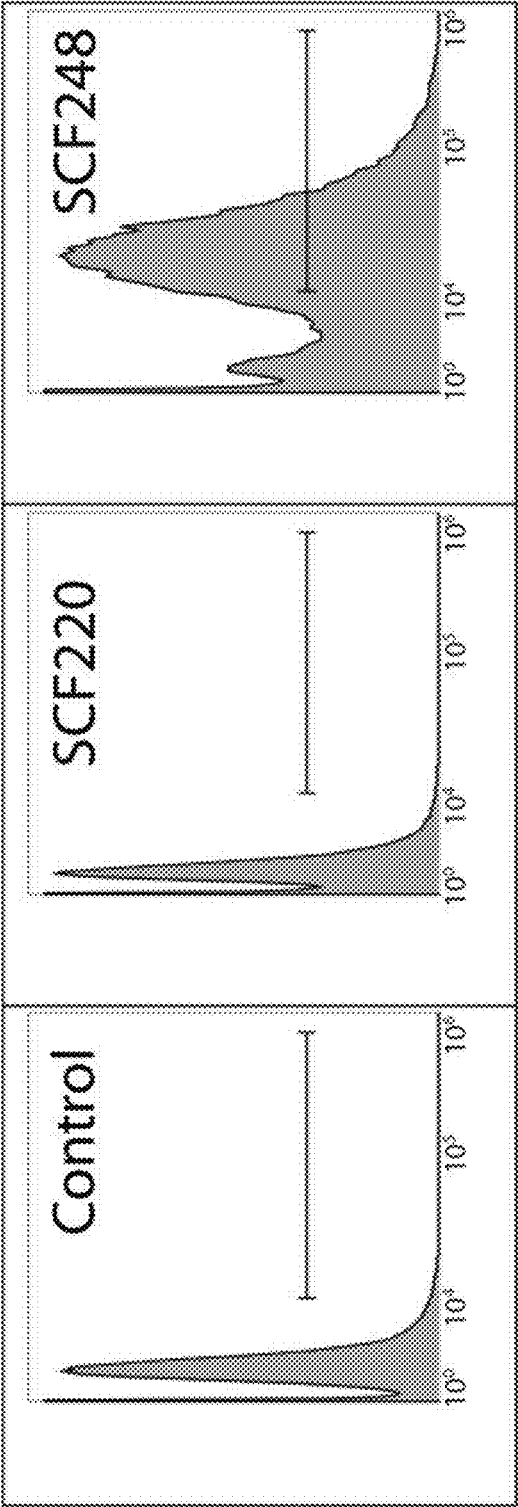


Fig. 4B

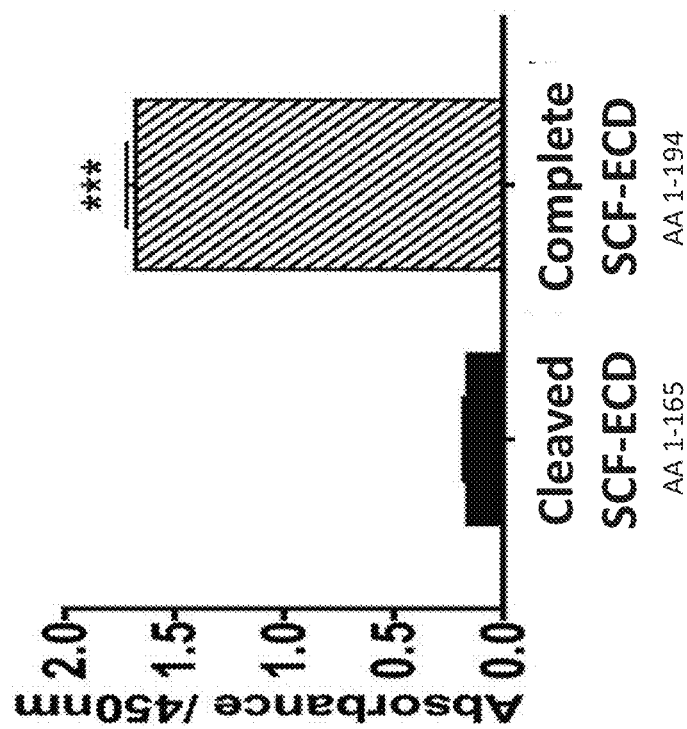


Fig. 5

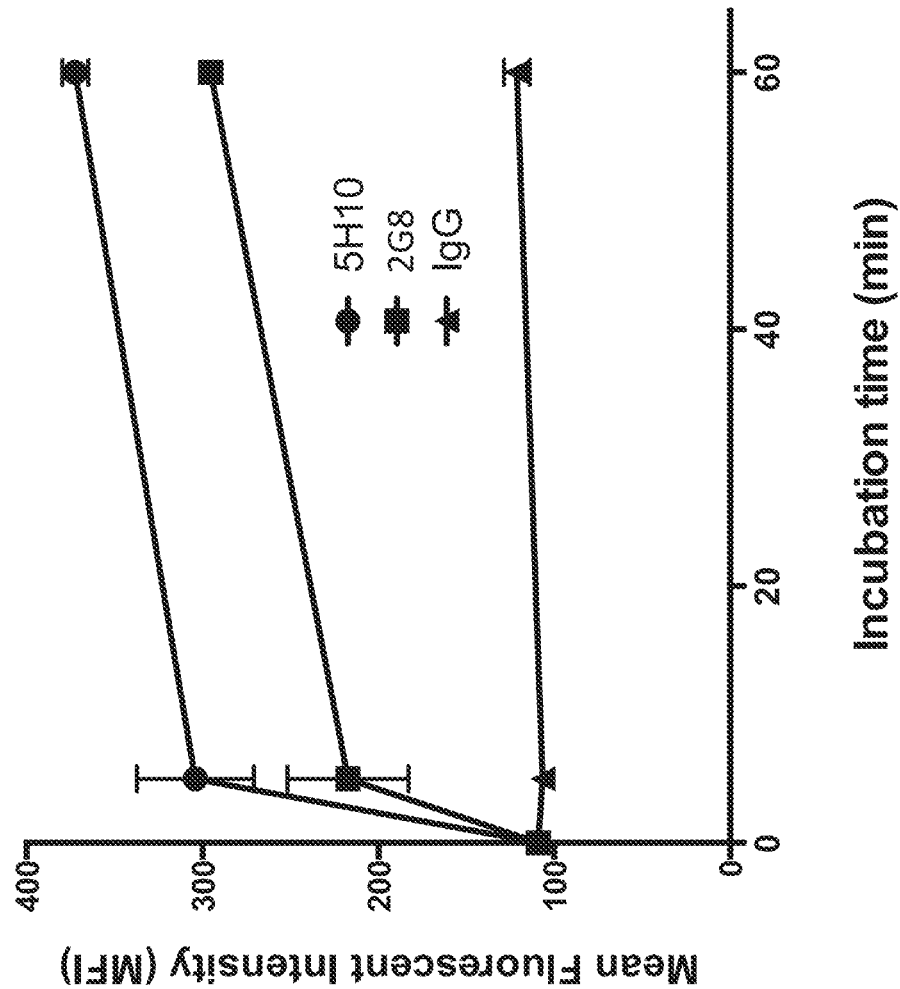


Fig. 6

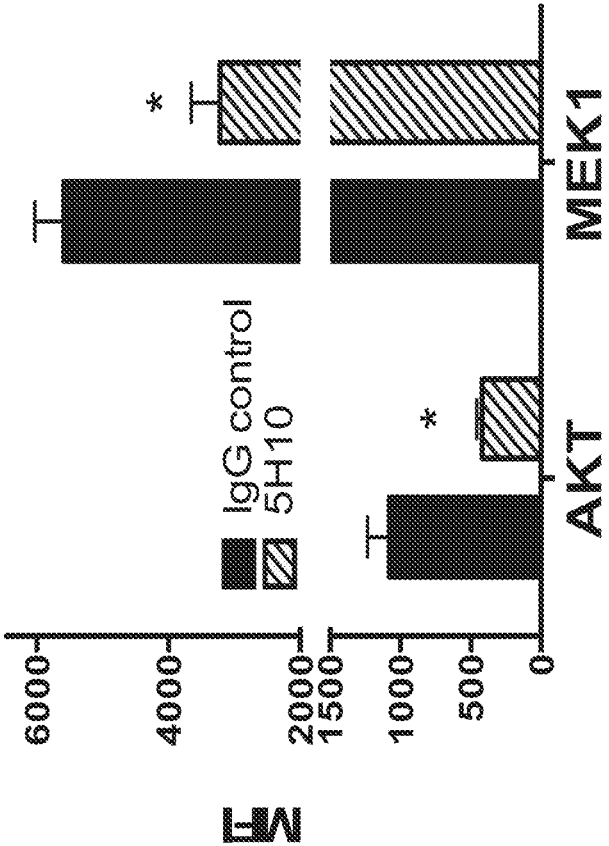


Fig. 7B

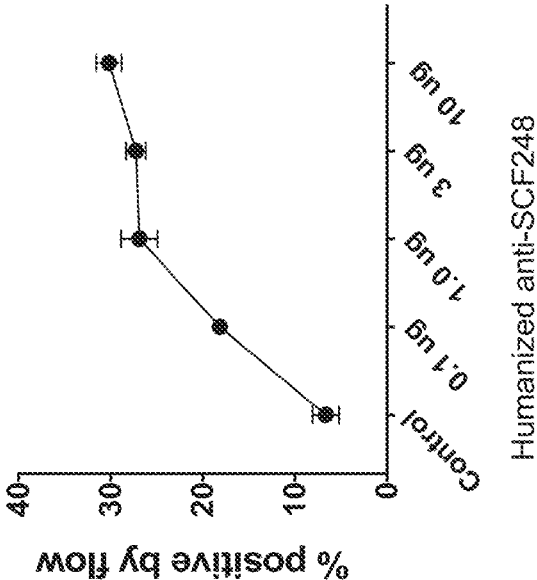


Fig. 7A

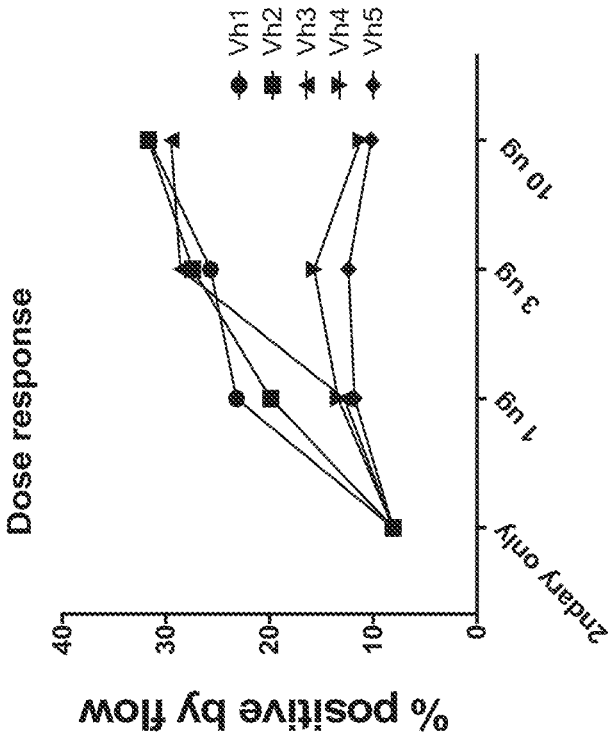


Fig. 8B

Collagen 1A1

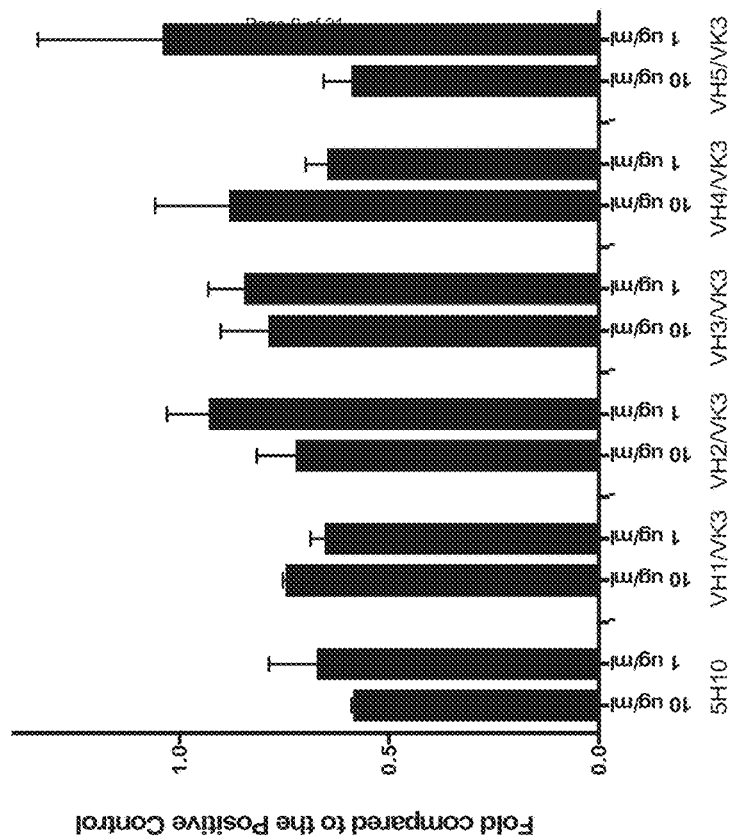


Fig. 8A

CCL11

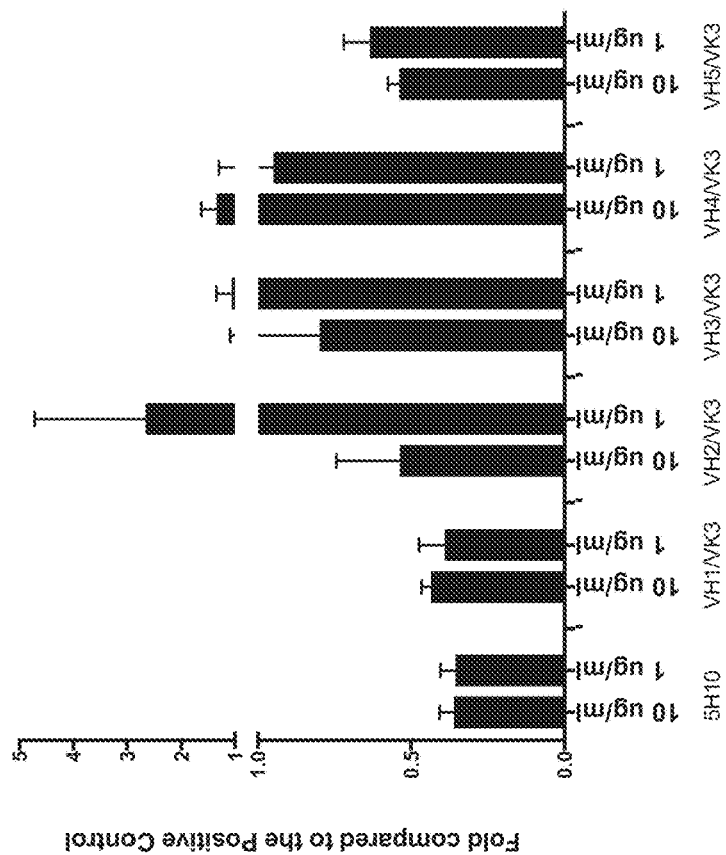


Fig. 8D

Col 3

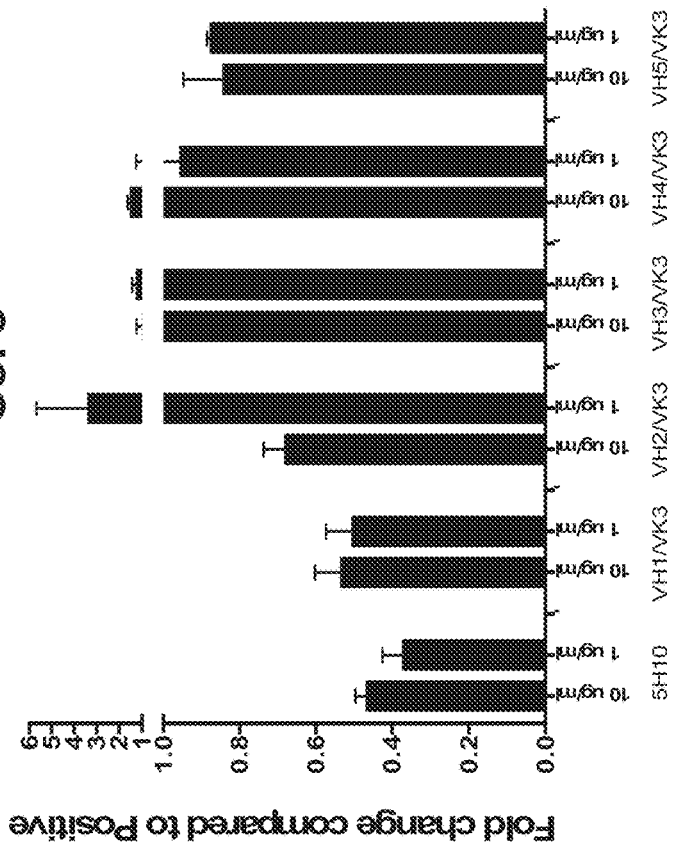


Fig. 8C

Fibronectin

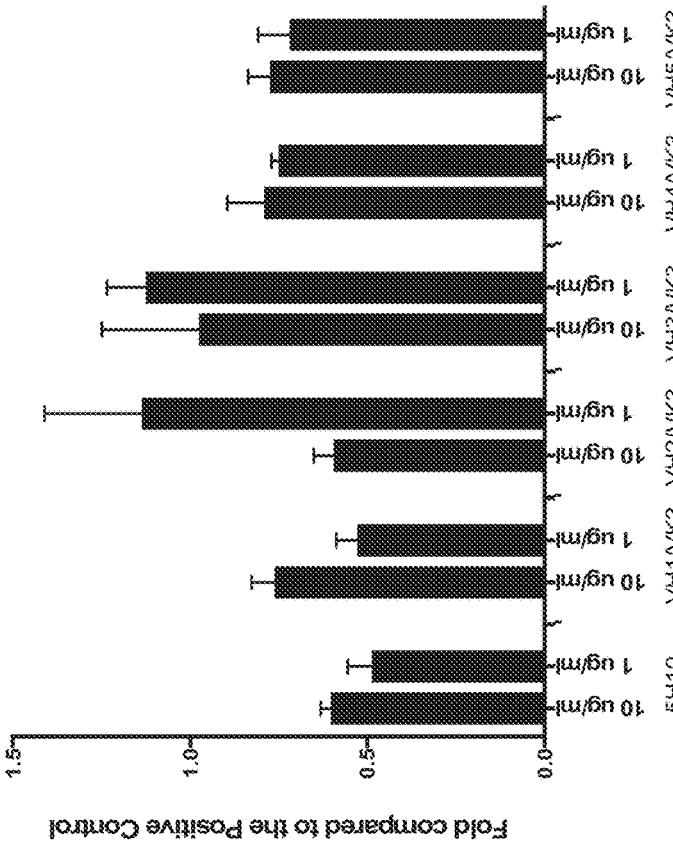


Fig. 9A

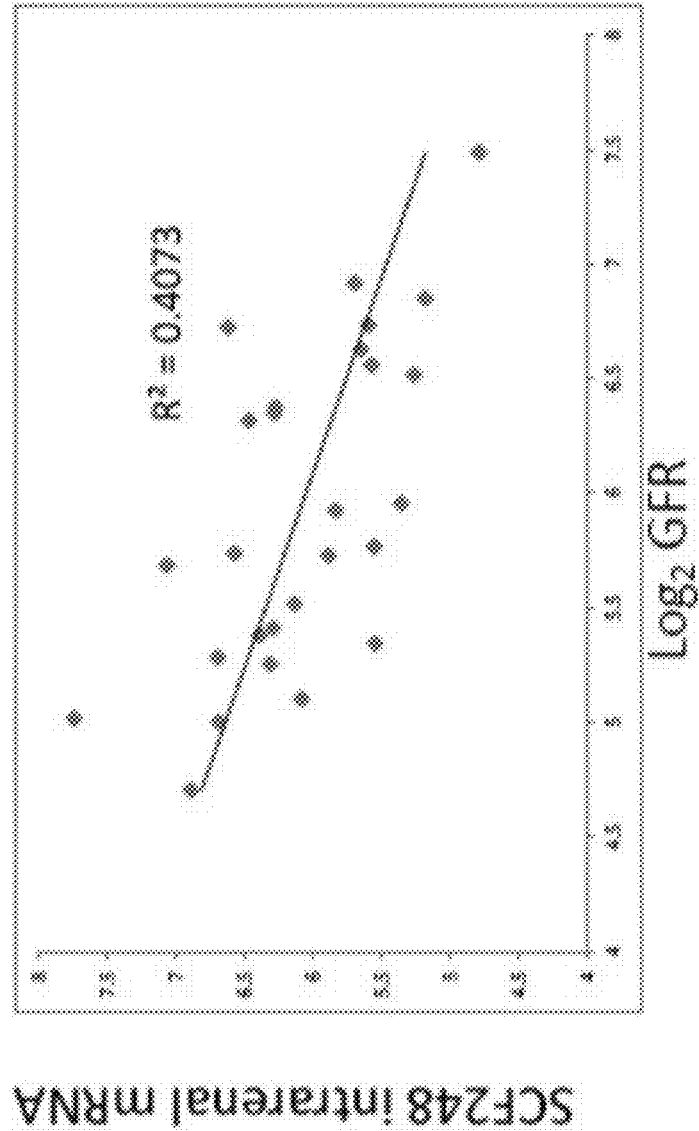


Fig. 9B

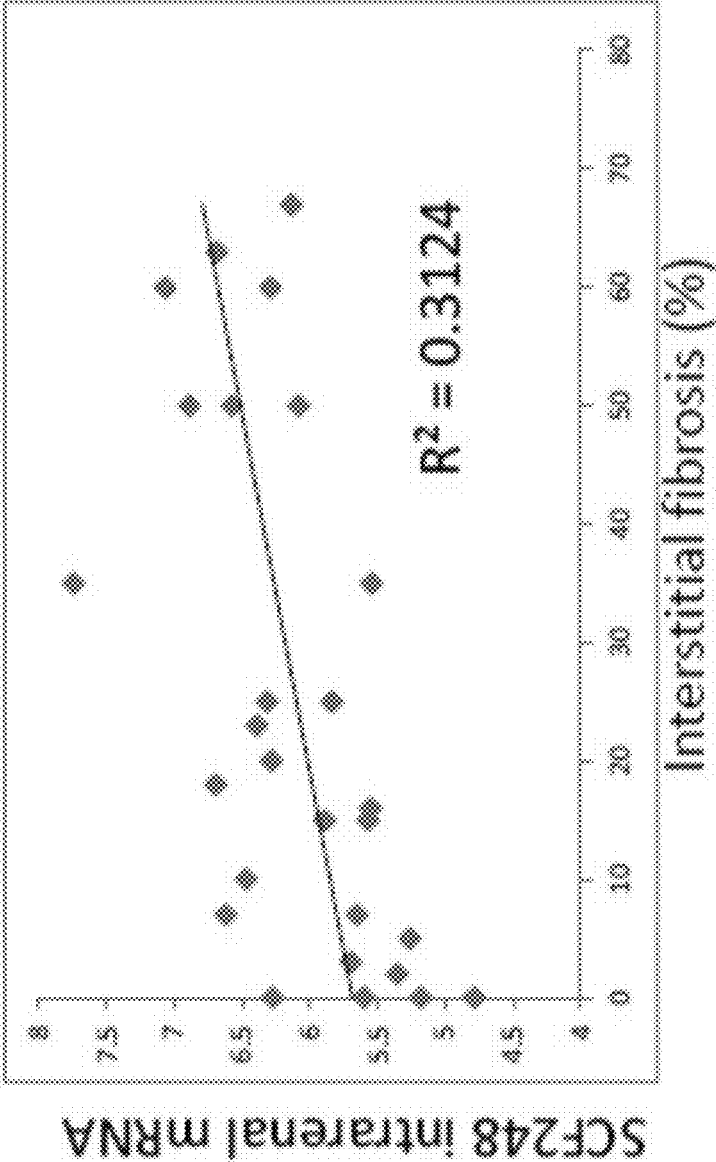


Fig. 9C

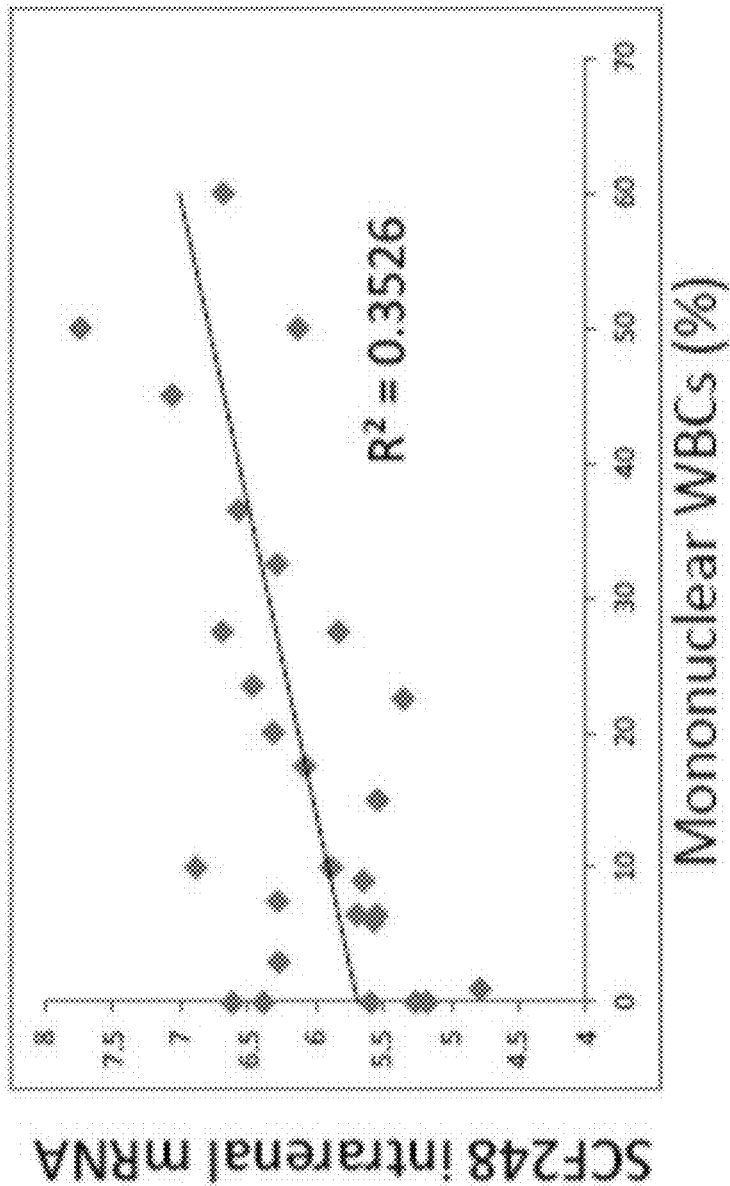


Fig. 10

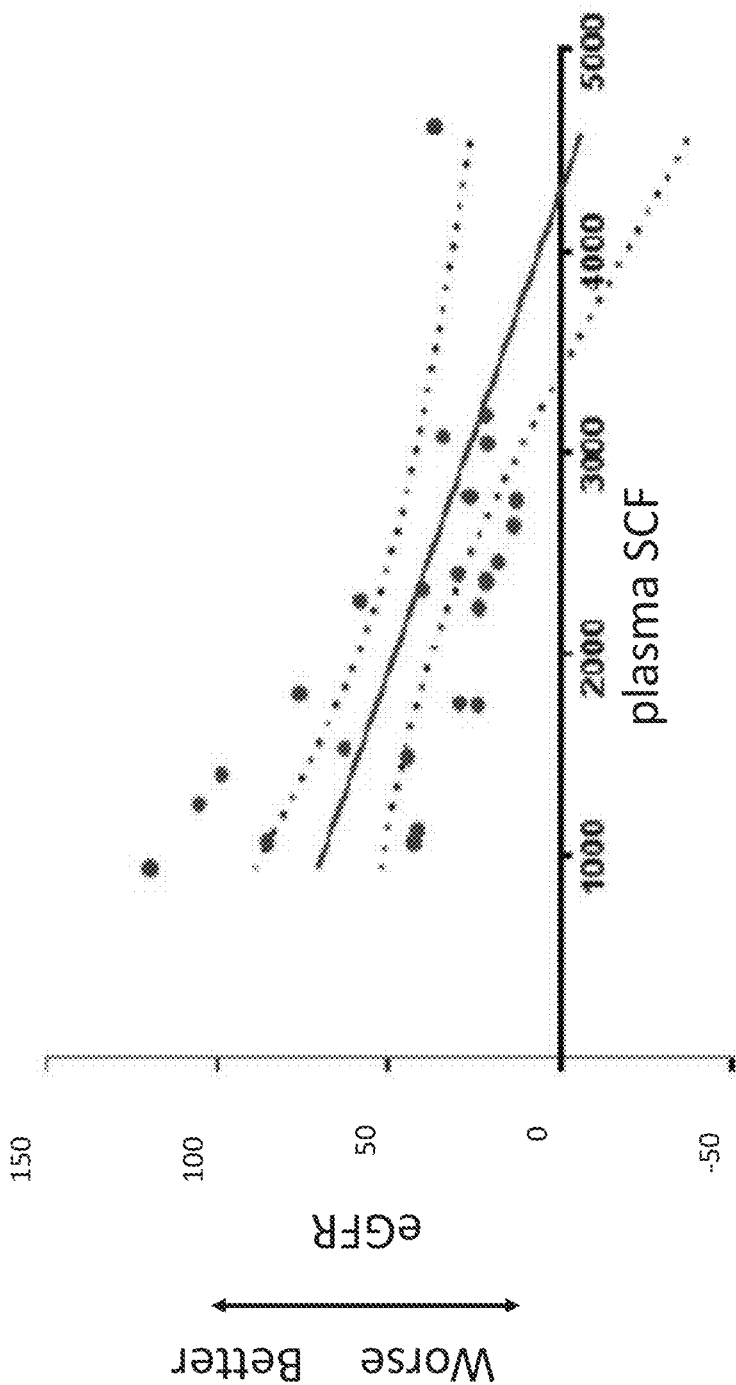


Fig. 11

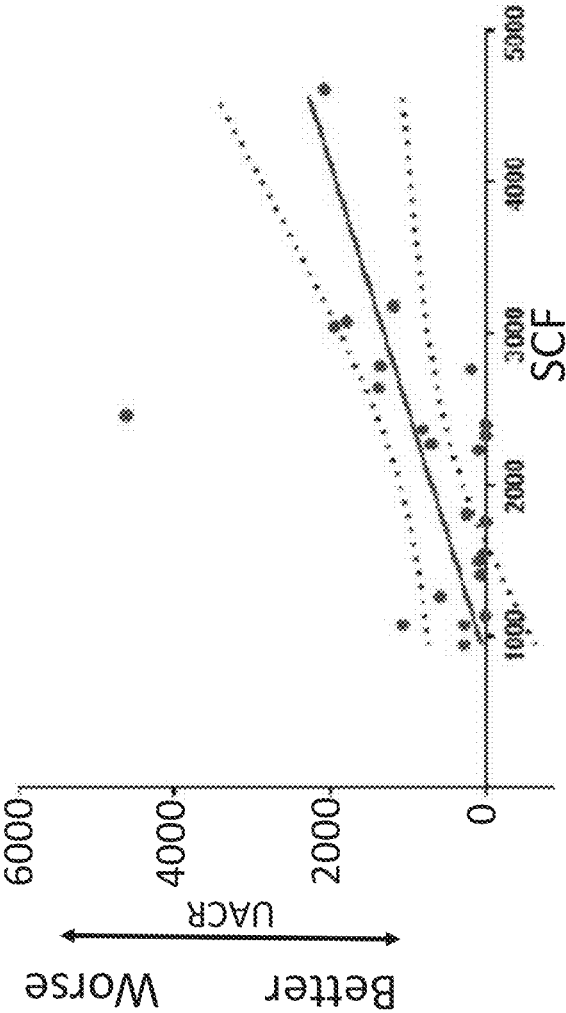


Fig. 12C

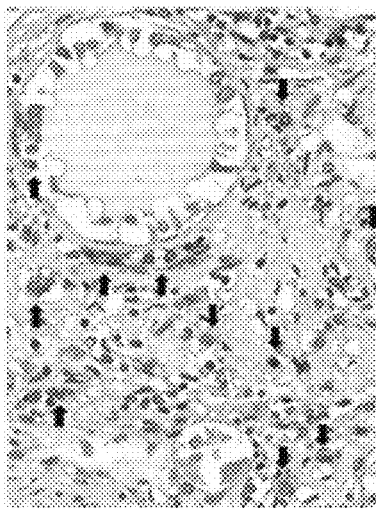


Fig. 12B

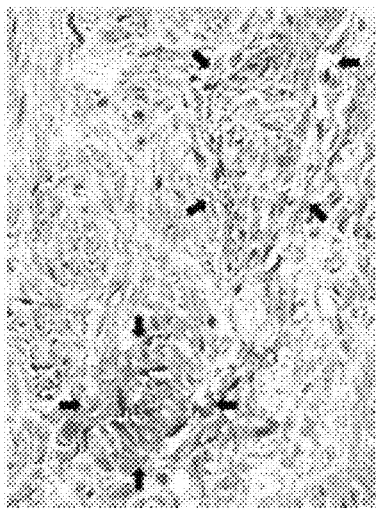
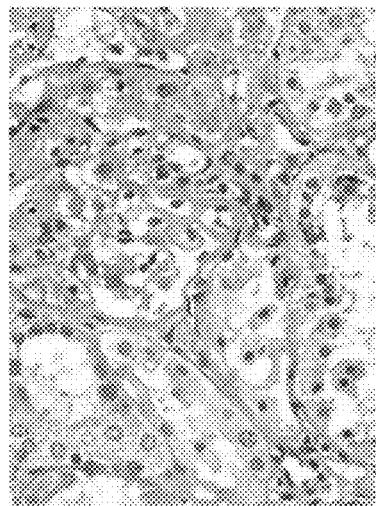


Fig. 12A



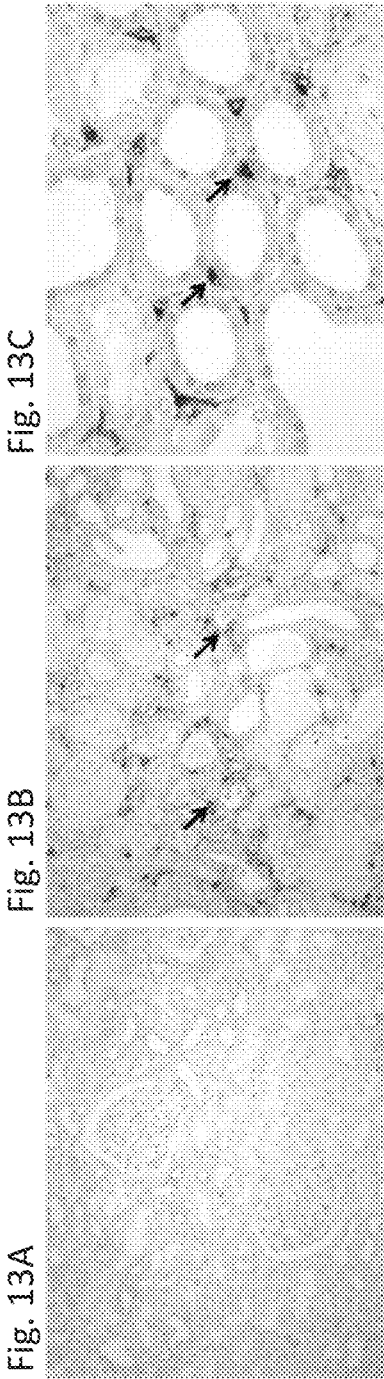


Fig. 14A

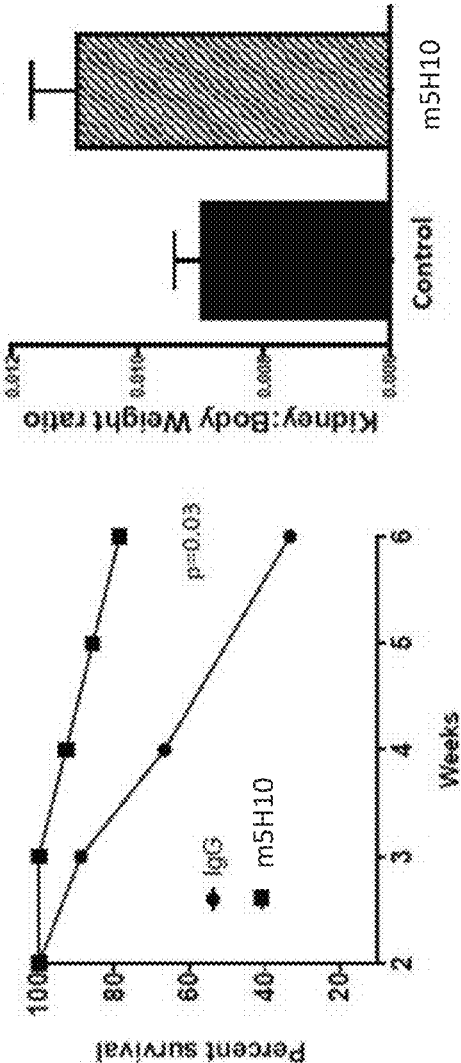


Fig. 14B

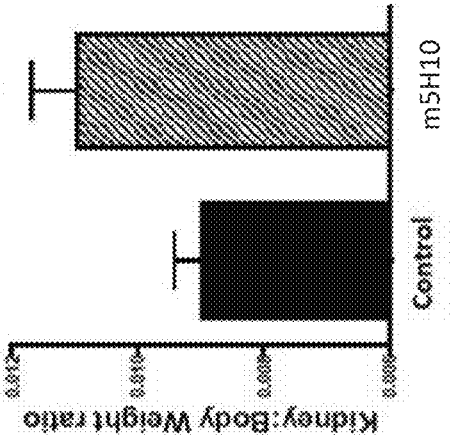


Fig. 14C

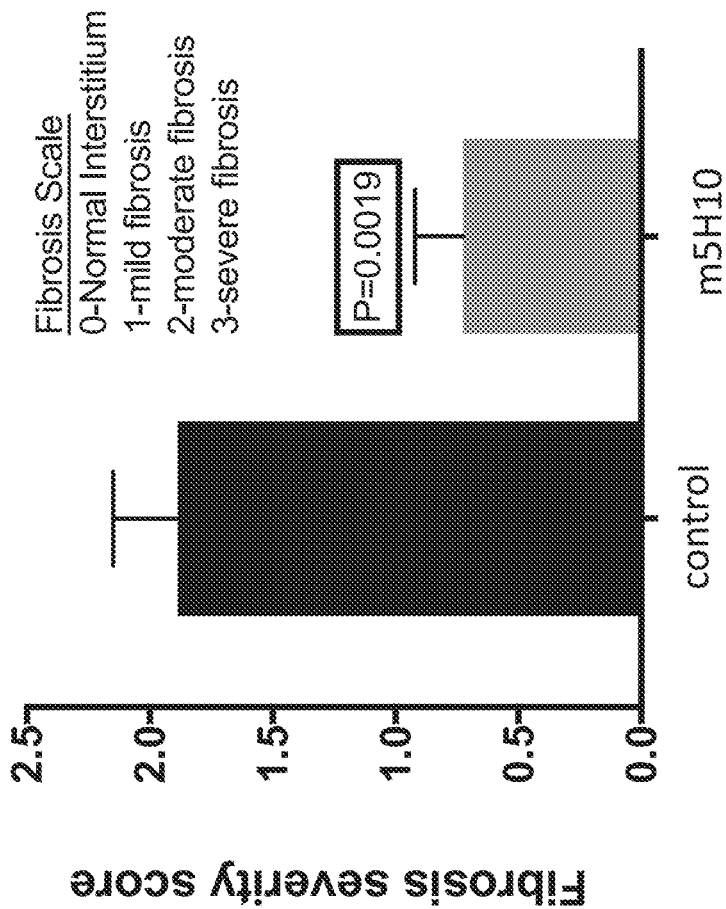


Fig. 15A

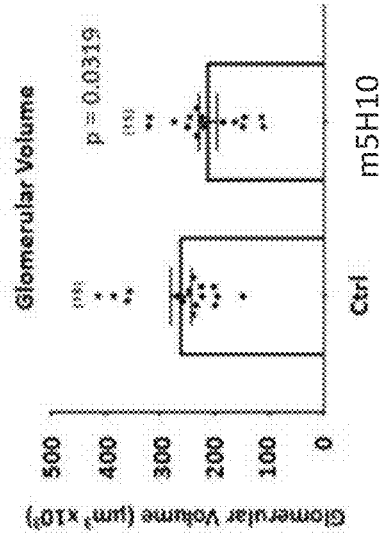


Fig. 15B

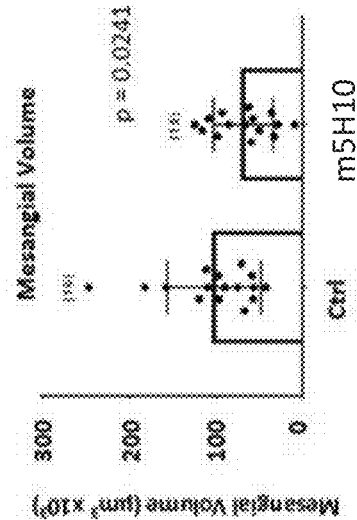
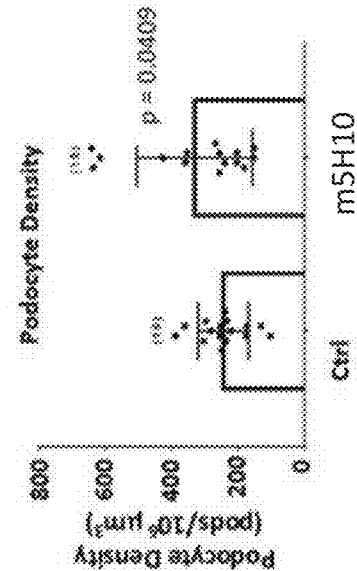
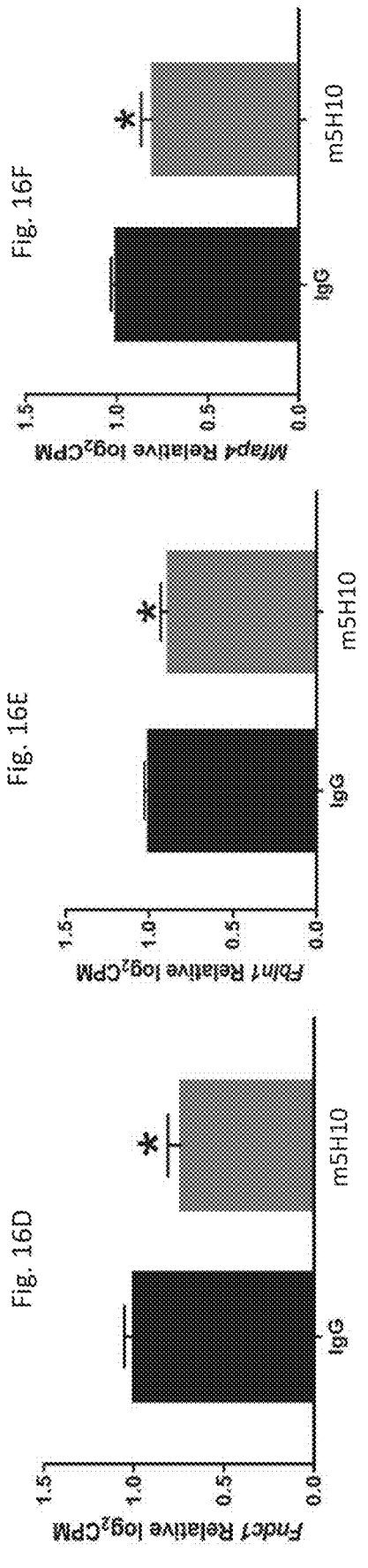
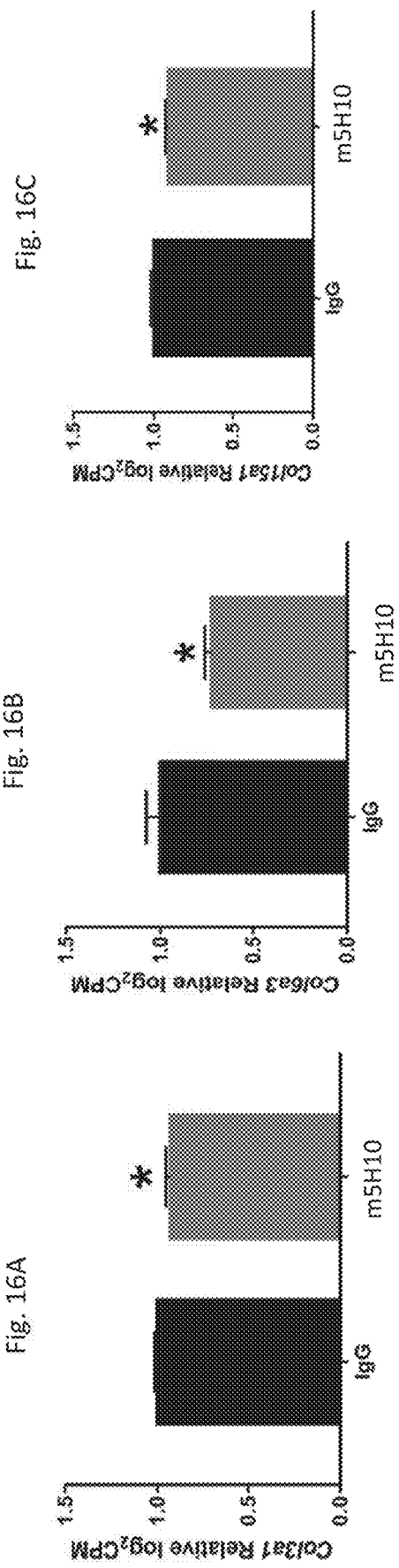


Fig. 15C





ANTI-STEM CELL FACTOR ANTIBODIES AND METHODS OF USE THEREOF IN RENAL DISEASE

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of priority to U.S. Provisional Application No. 62/900,927, filed on Sep. 16, 2019, the entire contents of which are hereby incorporated by reference.

DESCRIPTION OF THE TEXT FILE SUBMITTED ELECTRONICALLY

[0002] The content of the text file submitted electronically herewith is incorporated herein by reference in its entirety: A computer readable format copy of the Sequence Listing (filename: OPSL_001_02WO_SeqList_ST25; date recorded: Sep. 16, 2020; file size: 58 kb).

BACKGROUND

[0003] Inflammatory diseases are a major cause of morbidity and mortality worldwide. Some types of chronic inflammation can lead to fibrosis, which is the formation or development of excess fibrous connective tissue in an organ or tissue as a reparative or reactive process, as opposed to formation of fibrous tissue as a normal constituent of an organ or tissue. Chronic inflammation as well as fibrosis can affect nearly all tissues and organ systems, and fibrotic tissue remodeling can influence cancer metastasis and accelerate chronic graft rejection in transplant recipients. Chronic inflammation of the kidney can lead to fibrotic diseases with a high rate of mortality.

[0004] Stem cell factor (SCF) and its receptor c-Kit are important factors of the perpetuation of chronic inflammation and in fibrotic diseases (El-Koraie, et al., *Kidney Int.* 60: 167 (2001); Powell, et al., *Am. J. Physiol.* 289: G2 (2005); El Kossi, et al., *Am. J. Kidney Dis.* 41: 785 (2003); Powell, et al., *Am. J. Physiol.* 277: C183 (1999) Ding et al *J Pathol.* 2013 June; 230(2):205-14., Berlin et al *Lab Invest.* 2006 June; 86(6):557-65, Rasky et al *Am J Physiol Lung Cell Mol Physiol.* 2020 Jan. 1; 318(1):L200-L211). c-Kit is a type III receptor-tyrosine kinase that is present in many cell types (Orr-Urtreger et al., *Development* 109: 911 (1990). Immune cells such as mast cells, eosinophils, and innate lymphoid cells 2 and 3 (ILC2 and ILC3) are all c-Kit+ cells that may drive the chronic inflammatory process, depending on the disease and organ involved. Upon initiation of an inflammatory response, various mediators, including SCF, activate c-Kit+ immune cells, which in turn produce cytokines that cause fibroblasts to become activated myofibroblasts. Myofibroblasts secrete extracellular matrix proteins, collagen, and fibronectin, resulting in fibrosis of tissue. Activated myofibroblasts, activated epithelia, endothelia, macrophages, eosinophils, mast cells, monocytes, and other cells also express SCF on the cell surface, which activates more c-Kit+ immune cells, resulting in more cytokine release and perpetuating the inflammation.

[0005] There is a need in the art for more efficient and more specific treatments for inflammatory and fibrotic diseases of the kidney. The present disclosure addresses this and other needs.

SUMMARY OF THE DISCLOSURE

[0006] In one aspect, the present disclosure provides methods of treating renal diseases and disorders, the methods comprising administering to a patient having a renal disease or disorder an antibody or fragment thereof that specifically binds to stem cell factor (SCF). In embodiments, the renal disease or disorder is an inflammatory renal disease, a fibrotic renal disease, and/or a tissue remodeling renal disease. In embodiments, the antibodies and fragments thereof for use in the methods provided herein specifically bind to the SCF isoform SCF248. In some embodiments, the antibodies and fragments thereof for use in the methods provided herein comprise heavy chain complementarity determining regions (CDRs), wherein heavy chain CDR1 CDR2, and CDR3 comprise SEQ ID NOs: 1, 2, and 3, respectively. In some embodiments, the antibodies and fragments thereof for use in the methods provided herein comprise light chain CDRs, wherein the light chain CDR1 CDR2, and CDR3 comprise SEQ ID NOs: 4, 5, and 6, respectively. In some embodiments, the antibodies and fragments thereof for use in the methods provided herein comprise heavy chain CDR1, CDR2, and CDR3 comprising SEQ ID NOs: 1, 37, and 3, respectively. In some embodiments, the antibodies and fragments thereof comprise a heavy chain variable region comprising at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% identity to a sequence selected from the group consisting of SEQ ID NOs: 7, 8, 9, 10, 11, and 12. In some embodiments, the antibodies and fragments thereof comprise a light chain variable region comprising at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% identity to a sequence selected from the group consisting of SEQ ID NOs: 13, 14, 15, 16, and 17. In some embodiments, the antibodies and fragments thereof comprise a heavy chain variable region comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 7, 8, 9, 10, 11, and 12, and a light chain variable region comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 13, 14, 15, 16, and 17.

[0007] In some embodiments, the present disclosure provides methods for treating inflammatory and/or fibrotic diseases of the kidney, comprising administering to a subject an antibody or fragment thereof that comprises a heavy chain variable region amino acid sequence according to SEQ ID NO: 7 and a light chain variable region amino acid sequence according to SEQ ID NO: 16. In some embodiments, the antibody or fragment thereof of claim 1, wherein the antibody or fragment thereof comprises a heavy chain variable region amino acid sequence according to SEQ ID NO: 8 and a light chain variable region amino acid sequence according to SEQ ID NO: 16. In some embodiments, the antibody or fragment thereof comprises a heavy chain variable region amino acid sequence according to SEQ ID NO: 9 and a light chain variable region amino acid sequence according to SEQ ID NO: 16. In some embodiments, the antibody or fragment thereof comprises a heavy chain variable region amino acid sequence according to SEQ ID NO: 10 and a light chain variable region amino acid sequence according to SEQ ID NO: 16. In some embodiments, the antibody or fragment thereof comprises a heavy chain variable region amino acid sequence according to SEQ ID NO: 11 and a light chain variable region amino acid sequence according to SEQ ID NO: 16. In some embodiments, the antibody or fragment thereof comprises a heavy

chain variable region amino acid sequence according to SEQ ID NO: 12 and a light chain variable region amino acid sequence according to SEQ ID NO: 16.

[0008] In some embodiments, the antibody or fragment thereof is humanized. In some embodiments, the antibody is a monoclonal antibody. In some embodiments, the antibody comprises a human IgG1 domain or a human IgG4 domain. In some embodiments, the antibody is an antigen binding fragment, wherein the fragment is selected from a Fab, F(ab')₂, Fab', scFv, and single domain antibody (sdAb).

[0009] In some embodiments, the antibody or fragment thereof blocks the interaction between SCF (e.g. SCF248) and c-Kit. In some embodiments, the antibody specifically binds to SCF248. In some embodiments, the antibody does not bind to SCF220. In some embodiments, the antibody prevents the interaction of SCF248 and c-kit by causing the internalization of SCF, making it unavailable on the cell surface.

[0010] In one aspect, the present disclosure provides pharmaceutical compositions comprising the antibody or fragment thereof provided herein. In some embodiments, the pharmaceutical composition comprises a pharmaceutically acceptable carrier, diluent or excipient.

[0011] In some embodiments, the present disclosure provides isolated nucleic acid molecules encoding the antibody or fragment thereof provided herein. In some embodiments, the present disclosure provides an expression vector comprising the nucleic acid encoding the antibody or fragment thereof. In some embodiments, the present disclosure provides a recombinant host cell comprising the expression vector.

[0012] In one aspect, the present disclosure provides methods for making an antibody that specifically binds to stem cell factor isoform 248 (SCF248), the method comprising immunizing a host animal with a peptide comprising SEQ ID NO: 30 (ASSLRNDSSSSNRKAKNPPGD) or a fragment thereof, and obtaining an antibody from the immunized host animal. In some embodiments, the host animal is not a human. In some embodiments, the fragment of SEQ ID NO: 30 comprises at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, or 20 contiguous amino acids of SEQ ID NO: 30. In some embodiments, the fragment of SEQ ID NO: 30 comprises 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 contiguous amino acids of SEQ ID NO: 30. In some embodiments, the N-terminal amino acid of the fragment of SEQ ID NO: 30 is the alanine at position 1 at the N-terminus of SEQ ID NO: 30. In some embodiments, the method comprises immunizing the host animal with a peptide consisting of SEQ ID NO: 30. In some embodiments, the antibody from the immunized host animal is obtained from an immune cell isolated from the host animal. In some embodiments, the method further comprises generating a hybridoma using the immune cell. Thus, in some embodiments, the present disclosure provides hybridomas that produce monoclonal antibodies described herein.

[0013] In one aspect, the present disclosure provides an antibody or fragment thereof that specifically binds to SCF248, wherein the antibody or fragment thereof binds to an epitope comprising at least 8, at least 9, at least 10, at least 11, at least 12, or at least 13 contiguous amino acids of SEQ ID NO: 33, wherein the antibody inhibits the interaction of SCF248 with c-Kit. In further embodiments, the epitope

comprises SEQ ID NO: 33 or SEQ ID NO: 36. In yet further embodiments, the epitope consists of SEQ ID NO: 33 or SEQ ID NO: 36.

[0014] In one aspect, the present disclosure provides compositions and methods for inhibiting the interaction between SCF and c-Kit. C-kit is expressed on immune cells, hematopoietic stem cells, and some structural cells. C-kit's ligand SCF248 can be upregulated on myofibroblasts, activated epithelia, endothelia, macrophages, eosinophils, mast cells, monocytes, and others. In some embodiments, the compositions and methods specifically inhibit the interaction between SCF248 and c-Kit. For example, in some embodiments, the compositions and methods specifically inhibit the interaction between SCF248 on myofibroblasts and c-Kit on immune cells. As another example, in some embodiments, the compositions and methods provided herein specifically inhibit the interaction between SCF248 on myofibroblasts, activated epithelia, endothelia, macrophages, eosinophils, mast cells, and/or monocytes; with c-Kit on immune cells and/or structural cells. In some embodiments, the methods comprise contacting SCF248 on myofibroblasts with an antibody or fragment thereof provided herein. In some embodiments, the antibody or fragment thereof provided herein blocks binding of SCF248 to c-Kit. In some embodiments, the blocking is via steric hindrance. In some embodiments, the antibody or fragment thereof provided herein internalizes SCF248.

[0015] In some embodiments, the present disclosure provides methods for inhibiting inflammation in a subject in need thereof, the method comprising administering to the subject an antibody or fragment thereof provided herein. In some embodiments, the present disclosure provides methods for inhibiting an inflammatory disease in a subject in need thereof, the method comprising administering to the subject an antibody or fragment thereof provided herein. In further embodiments, the inflammatory disease is a chronic inflammatory disease. In some embodiments, the present disclosure provides methods for treating inflammation and/or a chronic inflammatory disease in a subject in need thereof, the method comprising administering to the subject an antibody or fragment thereof provided herein.

[0016] In some embodiments, the present disclosure provides methods for inhibiting fibrosis in a subject in need thereof, the method comprising administering to the subject an antibody or fragment thereof provided herein. In some embodiments, the present disclosure provides methods for treating a fibrotic disease in a subject in need thereof, the method comprising administering to the subject an antibody or fragment thereof provided herein. In embodiments, the method further comprises administering one or more additional therapy and/or therapeutic agent.

[0017] In some embodiments, the inflammatory renal disease or fibrotic renal disease is selected from the group consisting of renal fibrosis, Interstitial Fibrosis and Tubular Atrophy (IFTA) of the kidney, chronic kidney disease, end stage renal disease (ESRD), glomerulonephritis, chronic renal allograft rejection, nephrogenic systemic fibrosis, and nephropathy (e.g., IgA nephropathy, focal segmental glomerulosclerosis, rapidly progressive glomerulonephritis, crescentic glomerulonephritis, lupus nephritis, hypertensive nephropathy, or diabetic nephropathy).

BRIEF DESCRIPTION OF THE FIGURES

[0018] FIG. 1 provides a schematic overview of the tissue injury/inflammatory disease process.

[0019] FIG. 2 shows an exemplary mechanism of an anti-SCF248 antibody of the instant disclosure, 5H10. The 5H10 antibody is referred to in the figure as “OpSCF”.

[0020] FIG. 3 shows the isoforms of SCF, SCF220 and SCF 248; and the monomeric cleaved extracellular domain, SCF165. SCF165 is released upon cleavage of SCF248 at its cleavage site within the Exon 6 region.

[0021] FIG. 4A is a set of histograms showing the binding of murine 5H10 antibody to control cells that do not express SCF (left panel), cells that express SCF220 but not SCF248 (middle panel), and cells that express SCF248 but not SCF220 (right panel).

[0022] FIG. 4B shows the binding of murine 5H10 antibody to the 165 amino acid cleaved SCF extracellular domain (ECD) versus the complete 194 amino acid SCF ECD.

[0023] FIG. 5 shows the Mean Fluorescence Intensity (MFI) as measured by flow cytometry after contacting cultured human IPF myofibroblasts with pHrodo red-labeled 2G8, 5H10, or control IgG antibodies.

[0024] FIG. 6 shows the activation of the PI3K/AKT pathway and the MEK/ERK pathway of c-kit signaling after contacting eosinophils with an SCF248-expressing cells in the presence of 5H10 antibody or IgG control. 5H10 antibody significantly reduced activation of both pathways.

[0025] FIGS. 7A and 7B shows binding of 5H10 humanized variants at different antibody concentrations by flow cytometry to SI/SI4 hSCF248 cells. In FIG. 7A, the indicated VH is paired with VK3. In FIG. 7B, the 5H10 antibody shown is VH1/VK3.

[0026] FIG. 8A-8C show the change in mRNA level of the CCL11 (FIG. 8A), Collagen 1A1 (FIG. 8B), fibronectin (FIG. 8C), or collagen 3 (FIG. 8D) after preincubation of human IPF myofibroblasts (Mfb) with a positive control (irrelevant antibody) or the antibody indicated under each bar in the figure. The murine parent antibody is indicated as “5H10” in the figure; humanized 5H10 antibodies VH1/VK3, VH2/VK3, VH3/VK3, VH4/VK3, and VH5/VK3 were also tested as shown. Antibody concentrations tested were 1 µg/mL or 10 µg/mL.

[0027] FIG. 9A-FIG. 9C shows the correlation between SCF248 mRNA and glomerular filtration rate (FIG. 9A), interstitial fibrosis (FIG. 9B), and percentage of mononuclear white blood cells in the kidney biopsy (FIG. 9C) in patients with focal segmental glomerulosclerosis (FSGS).

[0028] FIG. 10 shows that plasma levels of SCF165 (and its derivatives) are inversely correlated with estimated glomerular filtration rate (eGFR) in patients with chronic kidney disease.

[0029] FIG. 11 shows that plasma levels of SCF165 (and its derivatives) are inversely correlated with the urinary albumin/creatinine ratio (UACR) in patients with chronic kidney disease.

[0030] FIG. 12A-FIG. 12C shows immunohistochemistry staining for SCF248 in the tubular and mesangial areas of a human glomerulonephritis kidney biopsy. FIG. 12A shows staining with control IgG; FIGS. 12B and 12C show strongly positive staining for SCF348 in the tubule-interstitium.

[0031] FIG. 13A-FIG. 13C shows immunohistochemistry staining for mast cell tryptase in a healthy kidney (FIG. 13A)

and in the kidneys of patients with diabetic nephropathy and IgA nephropathy (FIGS. 13B and 13C, respectively).

[0032] FIG. 14A-FIG. 14B shows the effect of murine 5H10 (referred to as OpSCF in the figure) treatment on survival (FIG. 14A) and kidney weight (FIG. 14B) in a TGFβ mouse model of CKD.

[0033] FIG. 15A-FIG. 15C shows the effect of murine 5H10 treatment on glomerular volume (FIG. 15A), mesangial volume (FIG. 15B), and podocyte density (FIG. 15C) kidney weight in a TGFβ mouse model of CKD.

[0034] FIG. 16A-16F show RNA sequencing demonstrating statistically significant decreases in several fibrillary matrix proteins. FIG. 16A: Collagen Type 3 alpha 1 chain; FIG. 16B: Collagen Type 6 alpha 3 chain; FIG. 16C: Collagen Type XV alpha 1 chain; FIG. 16D: Fibronectin Type III Domain containing 1; FIG. 16E: Fibulin 1; FIG. 16F: Microfibril-associated protein 4.

DETAILED DESCRIPTION

[0035] Stem Cell Factor (SCF) is a key mediator of acute and chronic inflammation, fibrotic diseases, and tissue remodeling diseases. The interaction of SCF with c-Kit on immune cells initiates and perpetuates inflammation and fibrosis. The present disclosure provides compositions and methods for treating inflammatory and fibrotic renal diseases by inhibiting the interaction of SCF with c-Kit. Thus, the present disclosure provides methods for treating chronic renal inflammatory diseases and fibrotic renal diseases such as chronic kidney disease. The methods comprise administering an antibody or fragment thereof that specifically binds to SCF to a patient suffering from an inflammatory and/or fibrotic renal disease. In embodiments, the antibodies and fragments thereof provided herein specifically bind to SCF248 and do not bind to SCF220. Thus, the present disclosure provides specific, effective methods for inhibiting inflammation and fibrosis in renal diseases and disorders, and treating inflammatory renal diseases and fibrotic renal diseases.

Definitions

[0036] As used herein, the term “antibody” refers to a binding protein having at least one antigen binding domain. The antibodies and fragments thereof of the present invention may be whole antibodies or any fragment thereof. Thus, the antibodies and fragments of the invention include monoclonal antibodies or fragments thereof and antibody variants or fragments thereof, as well as immunoconjugates. Antigen binding fragments include Fab fragments, Fab' fragments, F(ab')₂ fragments, bispecific Fab dimers (Fab₂), trispecific Fab trimers (Fab₃), Fv, single chain Fv proteins (“scFv”), bis-scFv, (scFv)₂, minibodies, diabodies, triabodies, tetrabodies, disulfide stabilized Fv proteins (“dsFv”), single-domain antibodies (sdAb, nanobody), heavy-chain only antibodies (e.g., camelid VHH, camelid nanobody, shark Ig NAR), and portions of full length antibodies responsible for antigen binding. An isolated antibody or antigen binding fragment thereof is one which has been identified and separated and/or recovered from a component of its natural environment.

[0037] In some embodiments, the antibodies and antigen binding fragments thereof are isolated antibodies and fragments thereof. Thus, the present invention provides isolated antibodies and antigen binding fragments thereof, and

nucleic acids encoding such antibodies and fragments, as well as compositions comprising such isolated antibodies, fragments, and nucleic acids. The term “isolated” refers to a compound of interest (e.g., an antibody or nucleic acid) that has been separated from its natural environment. The present invention further provides pharmaceutical compositions comprising the isolated antibodies or fragments thereof, or nucleic acids encoding such antibodies or fragments, and further comprising one or more pharmaceutically acceptable carrier. Pharmaceutically acceptable carriers include, for example, excipients, diluents, encapsulating materials, fillers, buffers, or other agents.

[0038] As used herein, the term “derived” when used to refer to a molecule or polypeptide relative to a reference antibody or other binding protein, means a molecule or polypeptide that is specific for, and capable of binding to, the same epitope as the reference antibody or other binding protein.

[0039] As used herein, the phrase “specific for” may mean that the antibody does not bind to the target due to only non-specific interactions, and this property can be determined by comparison to an isotype control or similar. Specific binding does not necessarily require, although it may include, exclusive binding to a single target. In embodiments, the antibodies provided herein specifically bind to SCF248, and do not bind SCF220.

[0040] The term “host cell” means a cell that has been transformed, or is capable of being transformed, with a nucleic acid sequence and thereby expresses a gene of interest. The term includes the progeny of the parent cell, whether or not the progeny is identical in morphology or in genetic make-up to the original parent cell, so long as the gene of interest is present.

[0041] A “variant” of a polypeptide (e.g., an antigen binding protein, or an antibody) comprises an amino acid sequence wherein one or more amino acid residues are inserted into, deleted from and/or substituted into the amino acid sequence relative to another polypeptide sequence. Variants include antibodies and fragments thereof that have a recited percent identity to an antibody or fragment provided herein or to an antibody or fragment having a recited DNA or amino acid sequence.

[0042] The term “identity” refers to a relationship between the sequences of two or more polypeptide molecules or two or more nucleic acid molecules, as determined by aligning and comparing the sequences. “Percent identity,” “percent homology,” “sequence identity,” or “sequence homology” and the like mean the percent of identical residues between the amino acids or nucleotides in the compared molecules and is calculated based on the size of the smallest of the molecules being compared. For these calculations, gaps in alignments (if any) are preferably addressed by a particular mathematical model or computer program (i.e., an “algorithm”). Methods that can be used to calculate the identity of the aligned nucleic acids or polypeptides include those described in *Computational Molecular Biology*, (Lesk, A. M., ed.), 1988, New York: Oxford University Press; *Bio-computing Informatics and Genome Projects*, (Smith, D. W., ed.), 1993, New York: Academic Press; *Computer Analysis of Sequence Data*, Part I, (Griffin, A. M., and Griffin, H. G., eds.), 1994, New Jersey: Humana Press; von Heinje, G., 1987, *Sequence Analysis in Molecular Biology*, New York: Academic Press; *Sequence Analysis Primer*, (Gribskov, M. and Devereux, J., eds.), 1991, New York: M. Stockton Press;

and Carillo et al., 1988, *SIAM J. Applied Math.* 48:1073. In calculating percent identity, the sequences being compared are typically aligned in a way that gives the largest match between the sequences.

[0043] The term “light chain” includes a full-length light chain and fragments thereof having sufficient variable region sequence to confer binding specificity. A full-length light chain includes a variable region domain and a constant region domain. The variable region domain of the light chain is at the amino-terminus of the polypeptide. Light chains include kappa chains and lambda chains.

[0044] The term “heavy chain” includes a full-length heavy chain and fragments thereof having sufficient variable region sequence to confer binding specificity. A full-length heavy chain includes a variable region domain, three constant region domains, C_{H1} , C_{H2} , and C_{H3} . The variable heavy domain is at the amino-terminus of the polypeptide, and the C_{H} domains are at the carboxyl-terminus, with the C_{H3} being closest to the carboxy-terminus of the polypeptide. Heavy chains can be of any isotype, including IgG (including IgG1, IgG2, IgG3 and IgG4 subtypes), IgA (including IgA1 and IgA2 subtypes), IgM and IgE. The term “isotype” refers to the antibody class encoded by the heavy chain constant region genes. In some embodiments, the antibodies provided herein have an IgG4 heavy chain, or an IgG4 heavy chain comprising certain amino acid mutations. For example, in some embodiments, the IgG4 comprises a mutation at position 228 (EU numbering scheme, Kabat et al. *Sequence of proteins of immunologic interest*, 5th ed Bethesda, Md., NIH 1991) to inhibit Fab arm exchange. For example, in some embodiments, the IgG4 heavy chain is an IgG4 S228P heavy chain. In some embodiments, the heavy chain comprises one or more amino acid mutations that reduce binding to Fc receptors, and thereby reduce or eliminate effector function of the antibody. For example, the heavy chain may comprise mutations at one or more of positions 233, 234, 235, 236, 237, 265, 309, 331, and 409 (EU numbering).

[0045] The term “variable region” or “variable domain” refers to a portion of the light and/or heavy chains of an antibody, typically including approximately the amino-terminal 120 to 130 amino acids in the heavy chain and about 100 to 110 amino terminal amino acids in the light chain. In certain embodiments, variable regions of different antibodies differ extensively in amino acid sequence even among antibodies of the same species. The variable region of an antibody typically determines specificity of a particular antibody for its target. The term “target,” as used herein, refers to a molecule or a portion of a molecule capable of being bound by an antigen binding protein. In certain embodiments, a target can have one or more epitopes. In certain embodiments, a target is an antigen. The use of “antigen” in the phrase “antigen binding protein” simply denotes that the protein sequence that comprises the antigen can be bound by an antibody. In this context, it does not require that the protein be foreign or that it be capable of inducing an immune response.

[0046] The term “epitope” includes any determinant capable being bound by an antigen binding protein, such as an antibody or to a T-cell receptor. An epitope is a region of an antigen that is bound by an antigen binding protein that targets that antigen, and when the antigen is a protein, includes specific amino acids that directly contact the antigen binding protein. Most often, epitopes reside on proteins,

but in some instances can reside on other kinds of molecules, such as nucleic acids. Epitope determinants can include chemically active surface groupings of molecules such as amino acids, sugar side chains, phosphoryl or sulfonyl groups, and can have specific three dimensional structural characteristics, and/or specific charge characteristics. Generally, antibodies specific for a particular target antigen will preferentially recognize an epitope on the target antigen in a complex mixture of proteins and/or macromolecules. Antibody epitopes may be linear or conformational. In embodiments, the epitope provided herein is a linear epitope.

[0047] The use of the singular includes the plural unless specifically stated otherwise. The word “a” or “an” means “at least one” unless specifically stated otherwise. The use of “or” means “and/or” unless stated otherwise. The meaning of the phrase “at least one” is equivalent to the meaning of the phrase “one or more.” Furthermore, the use of the term “including,” as well as other forms, such as “includes” and “included,” is not limiting. Also, terms such as “element” or “component” encompass both elements or components comprising one unit and elements or components comprising more than one unit unless specifically stated otherwise. As used herein, the term “about” refers to an amount more or less than the stated parameter value, for example plus or minus five or ten percent of the object that “about” modifies, or as one of skill in the art would recognize from the context (e.g., approximately 50% of the interval between values). The term “about” also includes the value referenced.

Stem Cell Factor

[0048] In humans, there are at least two forms of SCF, which have different structures and activities. SCF220 functions in several homeostatic functions, including hematopoiesis and spermatogenesis and is found in bone marrow, testis, and other tissues and organs. SCF220 is slowly cleavable and sometimes called “membrane SCF.” In contrast, SCF248 is rapidly cleavable and comprises a cleavage site in exon 6, located between the N-terminal c-kit binding domain and the transmembrane domain. SCF248 may be referred to as “soluble SCF”. Exon 6 is excluded from SCF220 via alternative splicing, and SCF220 thus lacks this cleavage site. A monomeric, extracellular domain (SCF165) is the cleavage product and serves as a biomarker in plasma for chronic inflammatory diseases. Plasma may also contain detectable levels of SCF extracellular domain that comes from SCF220, but the majority of detectable extracellular domain is expected to be SCF165. SCF248 is the isoform found on myofibroblasts, activated epithelial cells, and other cells, which activates immune cells during inflammation and contributes to perpetuation of fibrosis. More specifically, SCF248 binds to c-Kit on immune cells, initiating production of cytokines that activate fibroblasts to become myofibroblasts, which secrete extracellular matrix proteins, collagen, and fibronectin. The activated myofibroblasts as well as activated epithelia, endothelia, macrophages, eosinophils, mast cells, monocytes, and other cells also express SCF on the cell surface, activating more c-Kit+ immune cells, resulting in further cytokine release and immune activation and fibrotic responses.

[0049] The antibodies and antigen-binding fragments thereof disclosed herein are specific for SCF. In some embodiments, the antibodies and fragments thereof are specific for human SCF. In some embodiments, the antibodies and fragments thereof are specific for SCF248. In some

embodiments, the antibodies bind SCF248 and do not bind other isoforms of SCF. In some embodiments, the antibodies bind SCF248 and do not bind to SCF220. In some embodiments, the present disclosure provides methods for making an antibody or fragment thereof that is specific for SCF248. Exemplary antibodies and fragments that are specific for SCF248, as well as methods for making and using the antibodies and fragments, are provided in the present disclosure. In some embodiments, the antibodies and fragments thereof provided herein breaks the positive feedback loop between SCF248 expressed on various cell types and cKit+ immune cells, by binding to SCF248 and blocking the interaction between SCF248 and c-Kit.

Antibodies and Fragments

[0050] The present disclosure provides antibodies, including monoclonal antibodies, and fragments thereof. The antibody fragments provided herein that are specific for SCF (e.g., SCF248) are sometimes referred to herein as antigen-binding fragments, meaning that they comprise the portion of the parent antibody that is capable of binding the target antigen (SCF, e.g., SCF248). “Antibody fragment,” “antigen binding fragment” and the like are used interchangeably herein. Examples of antibody fragments include Fab fragments, Fab' fragments, F(ab)' fragments, Fv fragments, isolated CDR regions, bispecific Fab dimers (Fab2), trispecific Fab trimers (Fab3), single chain Fv proteins (“scFv”), bis-scFv, (scFv)₂, minibodies, diabodies, triabodies, tetrabodies, disulfide stabilized Fv proteins (“dsFv”), single-domain antibodies (sdAb, nanobody), heavy-chain only antibodies (e.g., camelid VHH, camelid nanobody, shark Ig NAR), and portions of full length antibodies responsible for antigen binding.

[0051] A “Fab fragment” comprises one light chain and the C_H1 and variable regions of one heavy chain. The heavy chain of a Fab molecule cannot form a disulfide bond with another heavy chain molecule. A “Fab' fragment” comprises one light chain and a portion of one heavy chain that contains the VH domain and the CHI domain and also the region between the C_H1 and C_H2 domains, such that an interchain disulfide bond can be formed between the two heavy chains of two Fab' fragments to form an F(ab')₂ molecule. A “F(ab')₂ fragment” contains two light chains and two heavy chains containing a portion of the constant region between the C_H1 and C_H2 domains, such that an interchain disulfide bond is formed between the two heavy chains. A F(ab')₂ fragment thus is composed of two Fab' fragments that are held together by a disulfide bond between the two heavy chains. A “Fv fragment” comprises the variable regions from both the heavy and light chains, but lacks the constant regions. “scFvs” are Fv molecules in which the heavy and light chain variable regions have been connected by a flexible linker to form a single polypeptide chain, which forms an antigen binding region.

[0052] In some aspects, the antibodies and fragments thereof provided herein are defined by their complementary determining regions (CDRs). CDRs are part of the variable chains in antibodies; each of the light and heavy chain variable regions comprises three CDRs, CDR1, CDR2, and CDR3. The CDRs of an antibody determine antigen specificity. In certain embodiments, definitive delineation of a CDR and identification of residues comprising the binding site of an antibody is accomplished by solving the structure of the antibody and/or solving the structure of the antibody-

ligand complex. In certain embodiments, that can be accomplished by any of a variety of techniques known to those skilled in the art, such as X-ray crystallography. In certain embodiments, various methods of analysis can be employed to identify or approximate the CDR regions. Examples of such methods include, but are not limited to, the Kabat definition, the Chothia definition, the AbM definition and the contact definition.

[0053] The Kabat definition is a standard for numbering the residues in an antibody and is typically used to identify CDR regions. See, e.g., Johnson & Wu, *Nucleic Acids Res.*, 28: 214-8 (2000). The Chothia definition is similar to the Kabat definition, but the Chothia definition takes into account positions of certain structural loop regions. See, e.g., Chothia et al., *J. Mol. Biol.*, 196: 901-17 (1986); Chothia et al., *Nature*, 342: 877-83 (1989). The AbM definition uses an integrated suite of computer programs produced by Oxford Molecular Group that model antibody structure. See, e.g., Martin et al., *Proc Natl Acad Sci (USA)*, 86:9268-9272 (1989); “AbM™, A Computer Program for Modeling Variable Regions of Antibodies,” Oxford, UK; Oxford Molecular, Ltd. The AbM definition models the tertiary structure of an antibody from primary sequence using a combination of knowledge databases and ab initio methods, such as those described by Samudrala et al., “Ab Initio Protein Structure Prediction Using a Combined Hierarchical Approach,” in *PROTEINS, Structure, Function and Genetics Suppl.*, 3:194-198 (1999). The contact definition is based on an analysis of the available complex crystal structures. See, e.g., MacCallum et al., *J. Mol. Biol.*, 5:732-45 (1996).

[0054] Antibodies and fragments thereof may also include recombinant polypeptides, fusion proteins, and bi-specific antibodies. The anti-SCF antibodies and fragments thereof disclosed herein may be of an IgG1, IgG2, IgG3, or IgG4 isotype. In one embodiment, the anti-SCF antibodies and fragments thereof disclosed herein are of an IgG1 or an IgG4 isotype. The anti-SCF antibodies and fragments thereof of the present invention may be derived from any species including, but not limited to, mouse, rat, rabbit, primate, llama, camel, goat, shark, chicken, and human. The SCF antibodies and fragments thereof may be chimeric, humanized, or fully human antibodies. In one embodiment, the anti-SCF antibodies are murine antibodies. In another embodiment, the anti-SCF antibodies are chimeric antibodies.

In a further embodiment, the chimeric antibodies are mouse-human chimeric antibodies. In another embodiment, the antibodies are derived from mice and are humanized. [0055] A “chimeric antibody” is an antibody having at least a portion of the heavy chain variable region and at least a portion of the light chain variable region derived from one species; and at least a portion of a constant region derived from another species. For example, in one embodiment, a chimeric antibody may comprise murine variable regions and a human constant region. [0056] A “humanized antibody” is an antibody containing complementarity determining regions (CDRs) that are derived from a non-human antibody; and framework regions as well as constant regions that are derived from a human antibody. For example, the anti-SCF antibodies provided herein may comprise CDRs derived from one or more murine antibodies and human framework and constant regions. Thus, in one embodiment, the humanized antibody provided herein binds to the same epitope on SCF as the murine antibody from which the antibody’s CDRs are derived. [0057] In some embodiments, the antibodies and fragments thereof provided herein comprise a heavy and light chain, each of which comprises three CDRs. The amino acid sequences of exemplary heavy chain CDR1, CDR2, and CDR3 (HCDR1, HCDR2, and HCDR3, respectively) and light chain CDR1, CDR2, and CDR3 (LCDR1, LCDR2, and LCDR3, respectively) are provided below in Table 1. Table 1 also provides the amino acid sequences of exemplary heavy and light chain variable regions. In some embodiments, the present disclosure provides antibodies referred to herein as “5H10” and “2G8”. The heavy chain variable regions of humanized 5H10 or 2G8 are referred to herein as VH1, VH2, VH3, VH4, and VH5. 5H10 VH0 is the variable heavy chain of the murine parent antibody generated via the methods described herein. VH1, VH2, VH3, VH4, and VH5 are each humanized heavy chain variable regions derived from 5H10 VH0 or 2G8 VH0. The 5H10 antibody comprises a kappa light chain. The murine parent antibody variable light chain is referred to herein as 5H10 VK0. VK1, VK2, VK3, and VK4 are each humanized light chain variable regions derived from VK0. The 2G8 antibody comprises a lambda light chain. The murine parent antibody variable light chain is referred to herein as 2G8 VL0. VL1, VL2, VL3, and VL4 are each humanized light chain variable regions derived from VL0.

TABLE 1

Exemplary anti-SCF antibody sequences	
SEQ ID NO	Description
1	5H10 Heavy chain CDR1 SYWMN
2	5H10 Heavy chain CDR2 QIYPGDGDTHYNGKFKG
3	5H10 Heavy chain CDR3 SNWVGSY
4	5H10 Light chain CDR1 KSSQSLLLESDGKTYLN

TABLE 1-continued

Exemplary anti-SCF antibody sequences	
SEQ ID NO	Description
5	5H10 Light chain CDR2
	LVSRLDS
6	5H10 Light chain CDR3
	WQGTSLPQT
7	5H10 Heavy chain variable region VH0 (murine parent)
	QVQLVQSGAELVPRGSSVKISCKSSGYAFSSYWMNVKQRPQG LEWIGQIYPGDGDTHYNGKFKGKATLTADKSSSTAYMQLSRLTS EDSAVYFCSSSNWVGSYWGQGLTVTVSA
8	5H10 Heavy chain variable region VH1 (humanized)
	QVQLVQSGAELKPGSSVKISCKSSGYAFSSYWMNVKQRPQG LEWIGQIYPGDGDTHYNGKFKGKATLTADKSTSTAYMELSSLTS EDSAVYFCSSSNWVGSYWGQGLTVTVSS
9	5H10 Heavy chain variable region VH2 (humanized)
	QVQLVQSGAEVKKPGSSVKISCKSSGYAFSSYWMNVKQRPQG LEWIGQIYPGDGDTHYNGKFKGKATLTADKSTSTAYMELSSLRS EDTAVYFCSSSNWVGSYWGQGLTVTVSS
10	5H10 Heavy chain variable region VH3 (humanized)
	QVQLVQSGAEVKKPGSSVKISCKSSGYAFSSYWMNVKQRPQG LEWIGQIYPGDGDTHYNGKFKGKATLTADKSTSTAYMELSSLRS EDTAVYFCSSSNWVGSYWGQGLTVTVSS
11	5H10 Heavy chain variable region VH4 (humanized)
	QVQLVQSGAEVKKPGSSVKISCKSSGYAFSSYWMNVKQRPQG LEWIGQIYPGDGDTHYNGKFKGKATLTADKSTSTAYMELSSLRS EDTAVYFCSSSNWVGSYWGQGLTVTVSS
12	5H10 Heavy chain variable region VH5 (humanized)
	QVQLVQSGAEVKKPGSSVKISCKSSGYAFSSYWMNVKQRPQG LEWIGQIYPGDGDTHYNGKFKGKATLTADKSTSTAYMELSSLRS EDTAVYFCSSSNWVGSYWGQGLTVTVSS
13	5H10 Light chain variable region VK0 (murine parent)
	DVVMQTPTPLTSLVTIGQTASISCKSSQSLLES DGKTYLNWLSQR PGQSPKRLIYLVSRLD SGVPDRFTGSGSGTDFTLKISRVEAEDL GVYYCWQGTSLPQTFGGG TKLEIK
14	5H10 Light chain variable region VK1 (humanized)
	DVVMQTSPPLTSLVTLGQPASISCKSSQSLLES DGKTYLNWLQQR PGQSPRRLIYLVSRLD SGVPDRFTGSGSGTDFTLKISRVEAEDV GVYYCWQGTSLPQTFGGG TKVEIK
15	5H10 Light chain variable region VK2 (humanized)
	DVVMQTSPPLSLPVTLGQPASISCKSSQSLLES DGKTYLNWLQQR PGQSPRRLIYLVSRLD SGVPDRFTGSGSGTDFTLKISRVEAEDV GVYYCWQGTSLPQTFGGG TKVEIK
16	5H10 Light chain variable region VK3 (humanized)
	DVVMQTSPPLSLPVTLGQPASISCKSSQSLLES DGKTYLNWLQQR PGQSPRRLIYLVSRLD SGVPDRFTGSGSGTDFTLKISRVEAEDV GVYYCWQGTSLPQTFGGG TKVEIK
17	5H10 Light chain variable region VK4 (humanized)
	DVVMQTSPPLSLPVTLGQPASISCKSSQSLLES DGKTYLNWLQQR PGQSPRRLIYLVSRLD SGVPDRFTGSGSGTDFTLKISRVEAEDV GVYYCWQGTSLPQTFGGG TKVEIK
37	5H10 VH5 CDR2
	QIYPGDGDTHYNGKFKG

[0058] The skilled person will understand that the variable heavy and variable light chains may be independently selected, or mixed and matched, from the antibodies provided herein. Thus, in some embodiments, the antibodies and fragments thereof provided herein comprise heavy and light chain combinations selected from the group consisting of VH0/VK0, VH0/VK1, VH0/VK2, VH0/VK3, VH0/VK4, VH1/VK0, VH1/VK1, VH1/VK2, VH1/VK3, VH1/VK4, VH2/VK0, VH2/VK1, VH2/VK2, VH2/VK3, VH2/VK4, VH3/VK0, VH3/VK1, VH3/VK2, VH3/VK3, VH3/VK4, VH4/VK0, VH4/VK1, VH4/VK2, VH4/VK3, VH4/VK4, VH5/VK0, VH5/VK1, VH5/VK2, VH5/VK3, and VH5/VK4.

[0059] In some embodiments, the present disclosure provides antibodies or fragments comprising amino acid sequences having at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% homology to an amino acid sequence selected from the group consisting of SEQ ID NOs: 7-12. In some embodiments, the present disclosure provides antibodies or fragments thereof comprising a heavy chain variable region according to a sequence selected from the group consisting of SEQ ID NOs: 7-12. In some embodiments, the present disclosure provides antibodies or fragments comprising amino acid sequences having at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% homology to an amino acid sequence selected from the group consisting of SEQ ID NOs: 7-11, wherein the antibody or fragment comprises a heavy chain CDR1, CDR2, and CDR3 identical to SEQ ID NOs: 1, 2, and 3, respectively. In some embodiments, the present disclosure provides antibodies or fragments comprising amino acid sequences having at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% homology to an amino acid sequence of SEQ ID NO: 12, wherein the antibody or fragment comprises a heavy chain CDR1, CDR2, and CDR3 identical to SEQ ID NOs: 1, 37, and 3, respectively.

[0060] In some embodiments, the present disclosure provides antibodies or fragments comprising amino acid sequences having at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% homology to an amino acid sequence selected from the group consisting of SEQ ID NOs: 13-17. In some embodiments, the present disclosure provides antibodies or fragments thereof comprising a light chain variable region according to a sequence selected from the group consisting of SEQ ID NOs: 13-17. In some embodiments, the present disclosure provides antibodies or fragments comprising amino acid sequences having at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% homology to an amino acid sequence selected from the group consisting of SEQ ID NOs: 13-17, wherein the antibody or fragment comprises a light chain CDR1, CDR2, and CDR3 identical to SEQ ID NOs: 4, 5, and 6, respectively.

[0061] In some embodiments, the present disclosure provides antibodies or fragments comprising amino acid sequences having at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% homology to: SEQ ID NO: 7 and SEQ ID NO: 13; SEQ ID NO: 7 and SEQ ID NO: 14; SEQ ID NO: 7 and SEQ ID NO: 15; SEQ ID NO: 7 and SEQ ID NO: 16; SEQ ID NO: 7 and SEQ ID NO: 17; SEQ ID NO: 7 and SEQ ID NO: 13; SEQ ID NO: 7 and SEQ ID NO: 14; SEQ ID NO: 7 and SEQ ID NO: 15; SEQ ID NO: 7 and SEQ ID NO: 16; SEQ ID NO: 7 and SEQ ID NO: 17; SEQ ID NO: 8 and SEQ ID NO: 13; SEQ ID NO: 8 and SEQ ID NO:

NO: 14; SEQ ID NO: 8 and SEQ ID NO: 15; SEQ ID NO: 8 and SEQ ID NO: 16; SEQ ID NO: 8 and SEQ ID NO: 17; SEQ ID NO: 9 and SEQ ID NO: 13; SEQ ID NO: 9 and SEQ ID NO: 14; SEQ ID NO: 9 and SEQ ID NO: 15; SEQ ID NO: 9 and SEQ ID NO: 16; SEQ ID NO: 9 and SEQ ID NO: 17; SEQ ID NO: 10 and SEQ ID NO: 13; SEQ ID NO: 10 and SEQ ID NO: 14; SEQ ID NO: 10 and SEQ ID NO: 15; SEQ ID NO: 10 and SEQ ID NO: 16; SEQ ID NO: 10 and SEQ ID NO: 17; SEQ ID NO: 11 and SEQ ID NO: 13; SEQ ID NO: 11 and SEQ ID NO: 14; SEQ ID NO: 11 and SEQ ID NO: 15; SEQ ID NO: 11 and SEQ ID NO: 16; SEQ ID NO: 11 and SEQ ID NO: 17; SEQ ID NO: 12 and SEQ ID NO: 13; SEQ ID NO: 12 and SEQ ID NO: 14; SEQ ID NO: 12 and SEQ ID NO: 15; SEQ ID NO: 12 and SEQ ID NO: 16; or SEQ ID NO: 12 and SEQ ID NO: 17.

[0062] In particular embodiments, the antibodies and fragments thereof comprise heavy and light chain combinations selected from the group consisting of VH1/VK1, VH1/VK2, VH1/VK3, VH2/VK1, VH2/VK2, VH2/VK3, VH3/VK1, VH3/VK2, VH3/VK3, VH4/VK1, VH4/VK2, VH4/VK3, VH5/VK1, VH5/VK2, and VH5/VK3. In some embodiments, the antibodies comprise an amino acid sequence having at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% sequence identity to SEQ ID NO: 8 or SEQ ID NO: 9; and an amino acid sequence having at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% sequence identity to SEQ ID NO: 16. In some embodiments, the antibody, or fragment thereof, comprises an amino acid sequence having at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% sequence identity to SEQ ID NO: 8 or SEQ ID NO: 9; and an amino acid sequence having at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% sequence identity to SEQ ID NO: 16; wherein the antibody or fragment comprises a heavy chain CDR1, CDR2, and CDR3 identical to SEQ ID NOs: 1, 2, and 3, respectively, and a light chain CDR1, CDR2, and CDR3 identical to SEQ ID NOs: 4, 5, and 6, respectively. In some embodiments, the antibody, or fragment thereof, comprises an amino acid sequence having at least 95% or at least 99% sequence identity to SEQ ID NO: 8 or SEQ ID NO: 9; and an amino acid sequence having at least 95% or at least 99% sequence identity to SEQ ID NO: 16; wherein the antibody or fragment comprises a heavy chain CDR1, CDR2, and CDR3 identical to SEQ ID NOs: 1, 2, and 3, respectively, and a light chain CDR1, CDR2, and CDR3 identical to SEQ ID NOs: 4, 5, and 6, respectively. The antibody or fragment thereof may specifically bind to SCF248 but may not bind to SCF220. In some embodiments, the antibodies comprise a heavy chain variable region according to SEQ ID NO: 8 and a light chain variable region according to SEQ ID NO: 16. In some embodiments, the antibodies comprise a heavy chain variable region according to SEQ ID NO: 9 and a light chain variable region according to SEQ ID NO: 16.

[0063] In some embodiments, the antibodies and fragments provided herein comprise a heavy chain variable region amino acid sequence according to SEQ ID NO: 7, 8, 9, 10, 11, or 12, or a variant thereof; and/or comprise a light chain variable region amino acid sequence according to SEQ ID NO: 13, 14, 15, 16, or 17, or a variant thereof. Variants may comprise 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acid substitutions or deletions, or a combination thereof. In some embodiments, the amino acid substitutions are conservative substitutions. The anti-SCF antibodies disclosed herein having one or more amino acid substitution, insertion, deletion,

or combination thereof in the CDR or variable light or heavy chain region retain the biological activity of the corresponding anti-SCF antibody that does not have an amino acid substitution, insertion, or deletion relative to the sequences provided herein. Thus, the variant anti-SCF antibodies provided herein retain specific binding to SCF248. The terms percent homology, sequence identity, sequence homology, and the like are used interchangeably herein and refer to the number of identical amino acid sequences shared by two reference sequences, divided by the total number of amino acid positions, multiplied by 100.

[0064] In some embodiments, the present invention provides antibodies that bind to the same epitope as any one of the exemplary antibodies disclosed herein. Thus, in some embodiments, the present invention provides antibodies that compete for binding to SCF with the exemplary antibodies provided herein. For example, in some embodiments, the present disclosure provides antibodies that specifically bind to a region of the amino acid sequence provided herein as SEQ ID NO: 29. In some embodiments, antibodies provided herein specifically bind to an epitope comprising the amino acid sequence of SEQ ID NO: 33 (ASSLRNDSSSSNRK) or SEQ ID NO: 36 ASSLRNDSSSSNR. In some embodiments, the present disclosure provides antibodies that specifically bind to an epitope consisting of an amino acid sequence according to SEQ ID NO: 33 or SEQ ID NO: 36. In some embodiments, the present disclosure provides antibodies that specifically bind to an epitope comprising at least 5, at least 6, at least 7, at least 8, at least 9, or at least 10 contiguous amino acids of SEQ ID NO: 33.

[0065] In some embodiments, the antibodies and fragments thereof provided herein comprise the HCDR1, HCDR2, HCDR3, LCDR1, LCDR2, and/or LCDR3 of the heavy and light chain variable regions provided herein, or variants thereof. Thus, in some embodiments, the antibodies and fragments thereof provided herein include antibodies wherein the HCDRs are the HCDRs of SEQ ID NO: 7, 8, 9, 10, 11, or 12; and/or wherein the LCDRs are the LCDRs of SEQ ID NOs: 13, 14, 15, 16, or 17. For example, in some embodiments, the antibodies and fragments thereof comprise amino acids 31-35, 50-65, and 95-102 of any one of the heavy chain variable regions provided herein, as defined by the Kabat numbering scheme. In some embodiments, the antibodies and fragments thereof comprise amino acids 24-34, 50-56, and 89-97 of any one of the light chain variable regions provided herein, as defined by the Kabat numbering scheme.

[0066] Exemplary humanized antibodies are provided herein. Additional anti-SCF antibodies comprising the heavy and light chain CDRs provided herein, or variants thereof, may be generated using any human framework sequence, and are also encompassed in the present invention. In one embodiment, framework sequences suitable for use in the present invention include those framework sequences that are structurally similar to the framework sequences provided herein. Further modifications in the framework regions may be made to improve the properties of the antibodies provided herein. Such further framework modifications may include chemical modifications; point mutations to reduce immunogenicity or remove T cell epitopes; or back mutation to the residue in the original germline sequence.

[0067] In some embodiments, such framework modifications include those corresponding to the mutations exemplified herein, including backmutations to the germline

sequence. For example, in one embodiment, one or more amino acids in the human framework regions of the VH and/or VL of the humanized antibodies provided herein are back mutated to the corresponding amino acid in the parent murine antibody. The present invention also encompasses humanized antibodies that bind to SCF (e.g., SCF248) and comprise framework modifications corresponding to the exemplary modifications described herein with respect to any suitable framework sequence, as well as other framework modifications that otherwise improve the properties of the antibodies. In other embodiments, the antibodies provided herein comprise one or more mutations to improve stability, improve solubility, alter glycosylation, and/or reduce immunogenicity, such as, for example, by targeted amino acid changes that reduce deamidation or oxidation, reduce isomerization, optimize the hydrophobic core and/or charge cluster residues, remove hydrophobic surface residues, optimize residues involved in the interface between the variable heavy and variable light chains, and/or modify the isoelectric point.

[0068] The anti-SCF antibodies and fragments thereof provided herein may further comprise Fc region modifications to alter effector functions. Fc modifications may be amino acid insertions, deletions, or substitutions, or may be chemical modifications. For example, Fc region modifications may be made to increase or decrease complement binding, to increase or decrease antibody-dependent cellular cytotoxicity, or to increase or decrease the half-life of the antibody. Some Fc modifications increase or decrease the affinity of the antibody for an Fcγ receptor such as FcγRI, FcγRII, FcγRIII, or FcRn. Various Fc modifications have been described in the art, for example, in Shields et al., *J Biol. Chem* 276; 6591 (2001); Tai et al. *Blood* 119; 2074 (2012); Spiekermann et al. *J Exp. Med* 196; 303 (2002); Moore et al. *mAbs* 2:2; 181 (2010); Medzihradsky *Methods in Molecular Biology* 446; 293 (2008); Mannan et al. *Drug Metabolism and Disposition* 35; 86 (2007); and Idusogie et al. *J Immunol* 164; 4178 (2000). In some embodiments, Fc region glycosylation patterns are altered. In other embodiments, the Fc region is modified by pegylation (e.g., by reacting the antibody or fragment thereof with polyethylene glycol (PEG). Exemplary Fc modifications include modifications at one or more amino acid position selected from the group consisting of 228, 233, 234, 235, 236, 241, 248, 265, 297, 309, 331, and 409 (Kabat numbering; Kabat et al., *Sequences of Immunological Interest*, Fifth Edition, National Institute of Health, Bethesda, Md. (1991)). In embodiments, the antibody has modifications to reduce or abolish effector function. In embodiments, the antibody is an IgG1 antibody having one or more Fc modification selected from the group consisting of E233P, L234V, L234A, L235V, L235A, G236 (deleted), D265A, D270A, N297A and N297Q. In embodiments, the antibody is an IgG4 antibody having one or more Fc modification selected from the group consisting of S228P, E233P, F234A, F234V, L235A, L235V, S241P, L248E, D265A, D265T, L309L, and R409K. In embodiments, the anti-SCF antibodies provided herein comprise a S241P mutation and an L248E mutation.

[0069] In embodiments, the present disclosure provides antibodies provided herein that comprise a human IgG4 constant region according to SEQ ID NOs: 40 and 41. In embodiments, the present disclosure provides antibodies comprising at least about 80%, at least about 85%, at least about 90%, at least about 95%, or about 99% sequence

identity to SEQ ID NO: 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50. In embodiments, the present disclosure provides antibodies comprising a heavy chain according to SEQ ID NO: 40 and a light chain according to SEQ ID NO: 41. In embodiments, the present disclosure provides antibodies comprising a heavy chain according to SEQ ID NO: 42, 43, 44, 45, or 46 and a light chain according to SEQ ID NO: 47, 48, 49, or 50. In embodiments, the present disclosure provides an antibody comprising a heavy chain according to SEQ ID NO: 42 and a light chain according to SEQ ID NO: 49. In embodiments, the present disclosure provides an antibody comprising a heavy chain according to SEQ ID NO: 43 and a light chain according to SEQ ID NO: 49. In embodiments, the present disclosure provides an antibody comprising a heavy chain according to SEQ ID NO: 44 and a light chain according to SEQ ID NO: 49. In embodiments, the present disclosure provides an antibody comprising a heavy chain according to SEQ ID NO: 45 and a light chain according to SEQ ID NO: 49. In embodiments, the present disclosure provides an antibody comprising a heavy chain according to SEQ ID NO: 46 and a light chain according to SEQ ID NO: 49.

[0070] In some embodiments, the antibodies provided herein are specific for SCF248 and do not bind to SCF220. Thus, the antibodies provided herein are capable of specifically inhibiting the interaction between SCF248 and c-Kit that induces and perpetuates chronic inflammatory responses and fibrosis in inflammatory and fibrotic renal diseases. Moreover, the antibodies provided herein are capable of specifically inducing the internalization of SCF and thereby reducing the interaction between SCF248 and c-Kit. Accordingly, in some embodiments the present disclosure provides methods for treating inflammatory and fibrotic renal diseases comprising administering to patients in need thereof antibodies that are specific for SCF248, and are safe and effective in various inflammatory and fibrotic renal diseases discussed herein and known in the art.

[0071] For preparation of monoclonal antibodies, any technique that provides for the production of antibody molecules by continuous cell lines in culture may be used (see e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.). These include, but are not limited to, the hybridoma technique originally developed by Kohler and Milstein and the trioma technique, the human B-cell hybridoma technique (See, e.g., Kozbor et al., *Immunol. Today*, 4:72 (1983)), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole et al., in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96 (1985)). Alternatively, the antibodies may be made by recombinant DNA methods. In some embodiments, antibodies in accordance with the present disclosure may be made by isolating monoclonal antibodies from phage display libraries using the techniques described, for example, in Clackson et al., *Nature* 352:624-28 (1991) and Marks et al., *J. Mol. Biol.* 222(3):581-97 (1991). In some embodiments, the antibodies are fully human antibodies constructed by combining Fv clone variable domain sequence(s) selected from human-derived phage display or yeast display libraries with known human constant domain sequence(s).

[0072] In some embodiments provided herein, the antibodies are prepared from a hybridoma. Using the hybridoma method, a mouse, hamster, or other appropriate host animal, is immunized by injecting an immunizing peptide to elicit

the production by lymphocytes of antibodies that will specifically bind to an immunizing antigen. Alternatively, lymphocytes can be immunized in vitro. Following immunization, the lymphocytes are isolated and fused with a suitable myeloma cell line using, for example, polyethylene glycol, to form hybridoma cells that can then be selected away from unfused lymphocytes and myeloma cells. Hybridomas that produce monoclonal antibodies directed specifically against a chosen antigen as determined by immunoprecipitation, immunoblotting, or by an in vitro binding assay such as radioimmunoassay (RIA) or enzyme-linked immunosorbent assay (ELISA) can then be propagated in vitro (e.g., in culture) using standard methods (Goding, *Monoclonal Antibodies: Principles and Practice*, Academic Press, 1986) or in vivo as ascites tumors in an animal. The monoclonal antibodies can then be purified from the culture medium or ascites fluid as described for polyclonal antibodies above.

[0073] In some embodiments, the antibodies provided herein are generated using the murine hybridoma system. Hybridoma production in the mouse is a well-established procedure. Immunization protocols and techniques for isolation of immunized splenocytes for fusion are known in the art. Fusion partners (e.g., murine myeloma cells) and fusion procedures are also known. Embodiments of the technology herein provide antibodies (e.g., monoclonal antibodies) produced from a hybridoma prepared by immunizing mice with a peptide that is a portion or fragment of the SCF protein.

[0074] In some embodiments, the antibodies specific for SCF248 provided herein are generated by immunizing mice with a peptide having an amino acid sequence that is largely or exclusively within exon 6. For example, the immunizing peptide comprises any stretch of 5 or more amino acids within SEQ ID NO: 34. As another example, the immunizing peptide comprises any stretch of 5 or more amino acids beginning at amino acid position 20 of SEQ ID NO: 29. As another example, the immunizing peptide comprises a stretch of 5 or more amino acids beginning at amino acid position 20 of SEQ ID NO: 29 and ending at any one of positions 25 to 38 of SEQ ID NO: 29. Thus, in some embodiments, the immunizing peptide comprises the amino acid sequence of exon 6 after the cleavage site, and is either fully contained within exon 6 or comprises only 1, 2, 3, 4, or 5 amino acids of exon 7. In some embodiments, the immunizing peptide comprises or consists of SEQ ID NO: 30. In some embodiments, the immunizing peptide comprises any of the peptides provided herein or conservative variants thereof. Conservative variants may comprise 1, 2, 3, 4, or 5 amino acid substitutions or deletions, or a combination thereof. As provided above, in some embodiments, the antibodies generated using the immunizing peptides provided herein have an epitope that falls entirely or largely within exon 6. By "largely within" it is meant that at least 75%, at least 80%, at least 85%, at least 90%, or at least 95% of the peptide falls within exon 6. In some embodiments, the epitope begins at the cleavage site of exon 6 (i.e., between the alanines at amino acid positions 19 and 20 of SEQ ID NO: 29 and extends to the end of exon 6. In some embodiments, the epitope begins at the cleavage site of exon 6 and extends to the 1st, 2nd, 3rd, 4th or 5th n-terminal amino acid of the transmembrane domain. In some embodiments, the epitope comprises or consists of SEQ ID NO: 33. In some embodiments, the antibody referred to herein as 5H10

(including the murine, chimeric, and humanized 5H10 antibodies) binds to an epitope of SCF comprising or consisting of SEQ ID NO: 33.

[0075] In some embodiments, methods provided herein were used to generate antibodies referred to herein as 5H10. In some embodiments, the antibody “5H10” is also referred to herein as “OpSCF.” Antibody 5H10 advantageously binds SCF248 with high specificity and does not bind SCF220. The amino acid sequences of the murine parent antibody 5H10, as well as humanized variants thereof, are provided herein (see, Table 1).

[0076] In one embodiment, the present invention provides methods of use of bispecific or multispecific antibodies specific for SCF and at least one other antigen or epitope. The anti-SCF antibodies and fragments thereof provided herein may be tested for binding to SCF using the binding assays provided herein, or any other binding assay known in the art.

[0077] Unless otherwise stated, the practice of the present invention employs conventional molecular biology, cell biology, biochemistry, and immunology techniques that are well known in the art and described, for example, in *Methods in Molecular Biology*, Humana Press; *Molecular Cloning: A Laboratory Manual*, second edition (Sambrook et al., 1989), *Current Protocols in Immunology* (J. E. Coligan et al., eds., 1991); *Immunobiology* (C. A. Janeway and P. Travers, 1997); *Antibodies* (P. Finch, 1997); *Antibodies: a practical approach* (D. Catty., ed., IRL Press, 1988-1989); *Monoclonal antibodies: a practical approach* (P. Shepherd and C. Dean, eds., Oxford University Press, 2000); *Phage display: a laboratory manual* (C. Barbas III et al, Cold Spring Harbor Laboratory Press, 2001); and *Using antibodies: a laboratory manual* (E. Harlow and D. Lane (Cold Spring Harbor Laboratory Press, 1999).

Methods of Treatment

[0078] As used herein, the terms “treatment” or “treating” refers to both therapeutic treatment and prophylactic or preventive measures. Subjects in need of treatment include those subjects that already have the disease or condition, as well as those that may develop the disease or condition and in whom the object is to prevent, delay, or diminish the disease or condition. As used herein, the term “subject” denotes a mammal, such as a rodent, a feline, a canine, and a primate. Preferably, a subject according to the invention is a human. The term “therapeutically effective amount,” as used herein, refers to the amount of a compound or composition that is necessary to provide a therapeutic and/or preventative benefit to the subject.

[0079] In one aspect the present invention provides methods for treating a subject for an inflammatory and/or fibrotic renal disease. In one aspect, the present disclosure provides antibodies that are for use as a medicament useful for treating renal diseases, such as inflammatory and/or fibrotic renal diseases. In one aspect, the present disclosure provides antibodies for use in a method of treatment of a renal disease such as an inflammatory and/or fibrotic renal disease. In some embodiments, the inflammatory renal disease is a chronic inflammatory renal disease. Exemplary inflammatory and/or fibrotic renal diseases include, for example, renal fibrosis, renal cirrhosis, Interstitial fibrosis and tubular atrophy (IFTA) of the kidney, chronic kidney disease, end stage renal disease (ESRD), Goodpasture’s syndrome, glomerulonephritis, membranoproliferative glomerulonephritis

(MPGN), chronic renal allograft rejection, nephrogenic systemic fibrosis, and nephropathy (e.g., IgA nephropathy, focal segmental glomerulosclerosis, rapidly progressive glomerulonephritis, crescentic glomerulonephritis, lupus nephritis, hypertensive nephropathy, or diabetic nephropathy).

[0080] In some embodiments, the antibodies and fragments thereof disclosed herein may be administered to the subject by at least one route selected from parenteral, subcutaneous, intramuscular, intravenous, intrarticular, intrabronchial, intraabdominal, intracapsular, intracartilaginous, intracavitary, intracelial, intracerebellar, intracerebroventricular, intracolic, intracervical, intragastric, intrahepatic, intramyocardial, intraosteal, intrapelvic, intrapericardiac, intraperitoneal, intrapleural, intraprostatic, intrapulmonary, intrarectal, intrarenal, intraretinal, intraspinal, intrasynovial, intrathoracic, intratympanic, intrauterine, intravesical, intravitreal, bolus, subconjunctival, oral, vaginal, rectal, buccal, sublingual, intranasal, intratumoral, and transdermal.

[0081] In embodiments, the antibodies and fragments thereof disclosed herein may be administered to a subject in need thereof in combination with one or more additional therapy. The one or more additional therapy may be a procedure such as a surgical procedure or dialysis, or may be a therapeutic agent, such as an agent designed to mitigate or reduce symptoms of a disease or disorder associated with renal fibrosis and/or inflammation.

[0082] The present invention is further illustrated by reference to the following Examples. However, it should be noted that these Examples, like the embodiments described above, are illustrative and are not to be construed as restricting the scope of the invention in any way.

EXAMPLES

[0083] The following examples are given for the purpose of illustrating various embodiments of the disclosure and are not meant to limit the present disclosure in any fashion. Changes therein and other uses which are encompassed within the spirit of the disclosure, as defined by the scope of the claims, will be recognized by those skilled in the art.

[0084] An overview of the tissue injury/disease process is summarized in FIG. 1. A disease process initiates inflammation. c-Kit⁺ immune cells produce cytokines that cause fibroblasts to change into activated myofibroblasts which express SCF248 on their surface. The expression of SCF248 on the surface of myofibroblasts and other cells activates more immune cells, resulting in cytokine release of IL-4, IL-9, IL-13, IL-25, TGFβ, and other cytokines, perpetuating inflammation. Myofibroblasts secrete extracellular matrix proteins, collagen, and fibronectin, leading to fibrosis diseases such as chronic kidney disease and others. An exemplary mechanism of an antibody of the instant disclosure which targets SCF248 in glomerulonephritis (GN) as an exemplary renal disease (said antibody referred to herein as OpSCF and/or as 5H10) is summarized in FIG. 2.

[0085] As provided above, SCF has two isoforms which result from alternative splicing: SCF248 and SCF220. SCF248 and SCF220 differ by exon 6. SCF220 is associated with homeostatic functions, and SCF248 is associated with inflammation and fibrosis. SCF248 activates immune cells during inflammation and is sometimes called “soluble SCF.” SCF248 is expressed on various cell types including myofibroblasts, activated epithelia, endothelia, macrophages, eosinophils, mast cells, and monocytes (FIG. 3). The

SCF248 isoform results in cleavage of monomeric cleaved extracellular domain, called SCF165. The amino acid sequence of exon 6 is provided herein as SEQ ID NO: 34.

Example 1: Production of Anti-SCF mAbs Utilizing Hybridoma Technology

[0086] A peptide comprising ASSLRNDSSSSNRKAKNPPGD (SEQ ID NO: 30) was used to generate antibodies that bind to SCF248. The immunization peptide comprised a portion of exon 6, i.e. the SCF248 isoform of stem cell factor. In particular, the immunization peptide comprised a portion of exon 6 that begins after a cleavage site as defined herein. Mice were immunized with a peptide according to SEQ ID NO: 30 with a standard protocol. The determination of high titer serum antibodies indicated the appropriate immunization and fusion hybridomas were made. Culture supernatants were analyzed from individual clones for SCF-specific antibodies and chosen based upon specificity. Hybridomas producing specific monoclonal antibodies against the peptide were propagated and the monoclonal with the highest titer was subsequently tested in biologically relevant cultures. Antibody 5H10 had high specificity for SCF248 and no cross-reactivity with SCF220. No other monoclonal antibodies produced by the hybridomas had high specificity for SCF248 without cross-reactivity with SCF220. Thus, 5H10 was selected for further characterization, development, and chimerization and subsequent humanization.

Example 2. 5H10 Binding to SCF248 Complete Extracellular Domain

[0087] The murine 5H10 antibody obtained as described in Example 1 was directly conjugated with a fluorescent marker and the labeled antibody was incubated with SI/S14 hSCF248 cells, which express SCF248; SI/S14 hSCF220 cells, which express SCF220; or control cells that do not express SCF. Binding of the labeled antibody to the cells was assessed by flow cytometry. The specificity of 5H10 for SCF248 and lack of crossreactivity with SCF220 is shown in FIG. 4A.

[0088] Binding of the murine 5H10 antibody to the cleaved extracellular domain (ECD) containing only amino acids 1-165 of SCF, vs the complete ECD containing amino acids 1-194 of SCF, was assessed by an ELISA method. The antibody bound to the complete SCF ECD but not to the cleaved SCF ECD (FIG. 4B), demonstrating that the antibody is specific for the complete extracellular domain and does not bind to the monomeric cleaved ECD that circulates in blood.

[0089] To assess the ability of 2G8 and 5H10 antibodies to internalize SCF248 on myofibroblasts, antibodies were labeled with pHrodo red, which is colorless at neutral pH and fluoresces red at the low pH within an endosome. Labeled antibodies were incubated with cultured human IPF myofibroblasts for 45 minutes and red fluorescence was visualized by microscopy. As shown in FIG. 5, the dye-labeled antibodies, but not control IgG, were rapidly internalized. 5H10 was internalized more rapidly and resulted in higher fluorescence compared to 2G8.

[0090] SCF triggers c-kit to signal by two distinct pathways: the MEK/ERK pathway and the PI3K/AKT pathway. A study was conducted to determine whether the murine 5H10 antibody inhibits intracellular signaling in c-kit posi-

tive cells in either or both of these pathways. Eosinophils were incubated with SCF248-expressing cell lines, in the presence of either 5H10 or IgG control, and phospho-protein expression was measured with a BioRad Bio-Plex assay system. 5H10 significantly decreased the phospho-MEK and phosphor-AKT levels, indicating that the antibody significantly reduced c-kit mediated intracellular signaling (FIG. 6).

[0091] Taken together, the results of these studies indicated that antibody 5H10 binds specifically to and internalizes SCF248, and does not cross-react with the SCF220 isoform or the cleaved ECD. Moreover, 5H10 significantly inhibits the intracellular signaling pathways in c-kit positive cells that perpetuate inflammation.

Example 3. Humanized 5H10

[0092] Chimeric antibodies derived from 5H10 were produced by subcloning the variable domains of the heavy and light chains into a vector with a human IgG4 backbone. Chimeric antibodies were expressed and purified using standard protocols. 2G8 is a previously developed antibody that binds to SCF248 and SCF220, and contains a lambda light chain. The chimeric heavy and light chains of 2G8 were named VH0 and VL0, respectively. 5H10, the SCF248-specific antibody provided herein, contains a kappa light chain. The chimeric heavy and light chains of 5H10 were named VH0 and VK0, respectively.

[0093] The chimeric antibodies were humanized. Humanized heavy chains retained the same complementarity-determining regions (CDRs) but more “human-like” framework regions, and several humanized variants of each of 2G8 and 5H10 variable heavy chains, referred to herein as VH1, VH2, VH3, VH4, and VH5, were generated. Humanized kappa light chain variants of 5H10, referred to herein as VK1, VK2, VK3, and VK4, were also generated. Humanized lambda light chains of 2G8 were named VL1, VL2, VL3, and VL4. The 2G8 and 5H10 combinations of chimeric and humanized light chains and heavy chains tested are shown in Table 2 and Table 3, respectively. As shown in Table 2, certain heavy and light chain combinations of the 5H10 antibody variants resulted in high binding to hSCF248.

TABLE 2

Binding score for 2G8 chimeric and humanized clones to SI/S14 hSCF248 cells	
2G8 mAb	Binding Score
VH0/VL0	high
VH1/VL1	Moderate high
VH1/VL3	moderate
VH1/VL4	Moderate
VH2/VL1	Moderate
VH2/VL4	Moderate
VH3/VL1	Moderate
VH3/VL4	Moderate
VH4/VL1	Moderate
VH4/VL2	Moderate
VH5/VL1	Moderate high
VH5/VL4	Moderate

TABLE 3

Binding score for 5H10 chimeric and humanized clones to S1/S14 hSCF248 cells	
5H10 mAb	Binding Score
VH0/VK0	high
VH1/VK1	High
VH1/VK2	High
VH1/VK3	High
VH1/VK4	No binding
VH2/VK2	Moderate high
VH2/VK3	high
VH3/VK2	Moderate
VH3/VK3	Moderate
VH4/VK2	Moderate low
VH4/VK3	Moderate low
VH5/VK2	Low
VH5/VK3	low

[0094] Binding affinity was also assessed using a BiaCore analysis. BiaCore data showed that the affinity for immobilized SCF248 peptide antigen of all humanized 5H10 antibodies having the VK1, VK2, or VK3 light chain was very similar to the binding affinity of the parental murine 5H10 using this assay. Humanized 5H10 antibodies having a VK4 light chain did not bind to the peptide.

TABLE 4

Biacore data					
	VK0	VK1	VK2	VK3	VK4
VH0	1.00	0.91			
VH1	0.92	0.99	0.97	0.94	—
VH2		0.98	0.99	0.94	—
VH3		1.15	1.16	1.10	—
VH3		1.27	1.32	0.85	—
VH5		1.07	0.93	1.09	—

[0095] 5H10 clones VH1/VK3, VH12/VK3, VH13/VK3, VH14/VK3, and VH15/VK3 were assessed by flow cytometry for binding to the SCF248-expressing cell line. As shown in FIGS. 7A and 7B, VH1/VK3 and VH12/VK3 exhibited high binding, maximized at 1 µg/mL. The negative control was secondary antibody only. No binding was observed with the control SCF220-expressing cell line (not shown).

Example 4. In Vitro Blockade of the Interaction of SCF and c-Kit

[0096] The humanized 5H10 antibodies were tested for their capacity to inhibit the SCF-c-kit interaction and the inflammation feed-forward loop in vitro. Cultured human IPF myofibroblasts (Mfb), which express surface SCF248, were overlaid with LAD2 mast cells, an SCF-responsive cell line. Absent any other intervention, the Mfb stimulate the LAD2 cells, which produce cytokines to stimulate Mfb to produce additional cytokines and extracellular matrix proteins. In this assay, the readout for inflammation and the feed-forward loop is mRNA for CCL11, collagens 1 and 3, and fibronectin.

[0097] Murine 5H10 and humanized (VH1/VK3, VH2/VK3, VH3/VK3, VH4/VK3, and VH5/VK3) 5H10 antibodies were pre-incubated with Mfb at concentrations of 1 µg/mL and 10 µg/mL to assess their capacity to inhibit the feed-forward loop. Results are shown in FIGS. 8A-8D. The

humanized VH1/VK3 antibody consistently demonstrated inhibition of the SCF—c-kit interaction, even at the lower concentration.

Example 5. Correlation Between SCF248 in Kidney Biopsies and Disease Progression

[0098] RNAseq was performed to quantitate SCF248 mRNA from kidney biopsies from patients with focal segmental glomerulosclerosis (FSGS). A significant inverse correlation of SCF248 mRNA with glomerular filtration rate was observed as shown in FIG. 9A. A positive correlation of SCF248 mRNA with the % interstitial fibrosis was also observed, as shown in FIG. 9B. Further, a positive correlation of SCF248 mRNA with the percentage of mononuclear white blood cells in the kidney biopsy was identified, as shown in FIG. 9C. Together, these data suggest an association of SCF248 with markers of inflammation and progressive renal insufficiency.

[0099] Moreover, a chronic kidney disease subject's plasma level of cleaved stem cell factor extracellular domain, SCF165, was significantly inversely correlated with estimated glomerular filtration rate (eGFR) (FIG. 10); and correlated with the urinary albumin/creatinine ratio (UACR) (FIG. 11), in chronic kidney disease.

Example 6. 5H10 Effectively Treats Disease in a Model of Chronic Kidney Disease

[0100] In areas of human renal fibrosis, SCF248 is expressed. In comparison to samples stained by immunohistochemistry with control IgG (FIG. 12A), samples stained with murine 5H10 antibody were strongly positive for SCF248 in the tubulo-interstitium (FIG. 12B and FIG. 12C). Additionally, staining for mast cell tryptase revealed the presence of mast cells in the kidneys of patients with diabetic nephropathy and IgA nephropathy (FIG. 13B and FIG. 13C), but not in a healthy patient's kidney. (FIG. 13A).

[0101] A mouse model of chronic kidney disease (CKD) was used to investigate the effect of 5H10 on disease progression and survival. C57/Black 6 TGFβ1 transgenic mice (TGFβ mice) overexpress TGFβ1 in the liver under the control of the albumin promoter, which leads to an increase in circulating TGFβ that promotes tissue fibrosis. TGFβ mice experience progressive glomerular and mesangial expansion and decreased podocyte density. Progressive interstitial fibrosis results in loss of kidney weight and death.

[0102] TGFβ mice were given either 5H10 or control antibody for four weeks starting at two weeks of age at a dose of 20 mg/kg, twice a week. The experiment was terminated at week six due to mortality. In comparison to mice treated with control IgG antibody, mice treated with 5H10 had a significantly improved survival (p=0.03) and a reduced loss in kidney weight (p=0.03) (FIG. 14A and FIG. 14B). The kidneys were scored in a masked fashion by an experienced nephropathologist, and the kidneys in the 5H10-treated group had significantly less fibrosis (FIG. 14C).

[0103] In order to evaluate kidney histology during disease progression, TGFβ mice were dosed at 5 mg/kg, twice a week with 5H10 or control antibody starting at two weeks of age and autopsied after two weeks during CKD disease progression. In comparison to control IgG, glomerular volume and mesangial volume increased less with 5H10 treatment, suggesting less tissue damage. Early in the course of CKD, glomerular volume and mesangial volume increase

with the influx of inflammatory cells and the extracellular matrix. The podocyte density was maintained with 5H10 therapy, indicating less podocyte dropout and less glomerular swelling (FIG. 15A, FIG. 15B, FIG. 15C). RNA sequencing demonstrated statistically significant decreases in matrix proteins Collagen Type 3 Alpha 1 chain (FIG. 16A), Collagen Type 6 Alpha 3 chain (FIG. 16B), Collagen Type XV Alpha 1 chain (FIG. 16C), Fibronectin Type III Domain containing 1 (FIG. 16D), Fibulin 1 (FIG. 16E), and Microfibril-associated protein 4 (FIG. 16F), in animals treated with m5H10. Thus, the administration of 5H10 antibody in a model of chronic kidney disease significantly reduced kidney fibrosis and improved survival, indicating that the antibody is useful as a treatment for kidney disease.

[0104] Publications, patents and patent applications cited herein are specifically incorporated by reference in their entireties. While the described invention has been described with reference to the specific embodiments thereof it should be understood by those skilled in the art that various changes may be made and equivalents may be substituted without departing from the true spirit and scope of the invention. In addition, many modifications may be made to adopt a particular situation, material, composition of matter, process, process step or steps, to the objective spirit and scope of the described invention. All such modifications are intended to be within the scope of the claims appended hereto.

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 50

<210> SEQ ID NO 1

<211> LENGTH: 5

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 1

Ser Tyr Trp Met Asn
1 5

<210> SEQ ID NO 2

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 2

Gln Ile Tyr Pro Gly Asp Gly Asp Thr His Tyr Asn Gly Lys Phe Lys
1 5 10 15

Gly

<210> SEQ ID NO 3

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 3

Ser Asn Trp Val Gly Ser Tyr
1 5

<210> SEQ ID NO 4

<211> LENGTH: 16

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 4

Lys Ser Ser Gln Ser Leu Leu Glu Ser Asp Gly Lys Thr Tyr Leu Asn
1 5 10 15

<210> SEQ ID NO 5

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 5

Leu Val Ser Arg Leu Asp Ser

-continued

1 5

<210> SEQ ID NO 6
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 6

Trp Gln Gly Thr His Leu Pro Gln Thr
1 5

<210> SEQ ID NO 7
<211> LENGTH: 116
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 7

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser
1 5 10 15

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

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Gln Ile Tyr Pro Gly Asp Gly Asp Thr His Tyr Asn Gly Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Ser Asn Trp Val Gly Ser Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ala
115

<210> SEQ ID NO 8
<211> LENGTH: 116
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Humanized 5H10 Heavy chain variable region VH1

<400> SEQUENCE: 8

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

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

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Gln Ile Tyr Pro Gly Asp Gly Asp Thr His Tyr Asn Gly Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Ser Asn Trp Val Gly Ser Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

-continued

Thr Val Ser Ser
115

<210> SEQ ID NO 9
<211> LENGTH: 116
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Humanized 5H10 Heavy chain variable region VH2

<400> SEQUENCE: 9

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15
Ser Val Lys Ile Ser Cys Lys Ser Ser Gly Tyr Ala Phe Ser Ser Tyr
20 25 30
Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Gln Ile Tyr Pro Gly Asp Gly Asp Thr His Tyr Asn Gly Lys Phe
50 55 60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95
Ser Ser Ser Asn Trp Val Gly Ser Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110
Thr Val Ser Ser
115

<210> SEQ ID NO 10
<211> LENGTH: 116
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Humanized 5H10 Heavy chain variable region VH3

<400> SEQUENCE: 10

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ser Ser Gly Tyr Ala Phe Ser Ser Tyr
20 25 30
Trp Met Asn Trp Val Arg Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Gln Ile Tyr Pro Gly Asp Gly Asp Thr His Tyr Asn Gly Lys Phe
50 55 60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95
Ser Ser Ser Asn Trp Val Gly Ser Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110
Thr Val Ser Ser
115

<210> SEQ ID NO 11
<211> LENGTH: 116
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

-continued

<220> FEATURE:

<223> OTHER INFORMATION: Humanized 5H10 Heavy chain variable region VH4

<400> SEQUENCE: 11

```

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1           5           10           15
Ser Val Lys Val Ser Cys Lys Ser Ser Gly Tyr Ala Phe Ser Ser Tyr
20           25           30
Trp Met Asn Trp Val Arg Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35           40           45
Gly Gln Ile Tyr Pro Gly Asp Gly Asp Thr His Tyr Asn Gly Lys Phe
50           55           60
Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65           70           75           80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
85           90           95
Ser Ser Ser Asn Trp Val Gly Ser Tyr Trp Gly Gln Gly Thr Leu Val
100          105          110
Thr Val Ser Ser
115

```

<210> SEQ ID NO 12

<211> LENGTH: 116

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Humanized 5H10 Heavy chain variable region VH5

<400> SEQUENCE: 12

```

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1           5           10           15
Ser Val Lys Val Ser Cys Lys Ser Ser Gly Tyr Ala Phe Ser Ser Tyr
20           25           30
Trp Met Asn Trp Val Arg Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35           40           45
Gly Gln Ile Tyr Pro Gly Asp Gly Asp Thr His Tyr Asn Gly Lys Phe
50           55           60
Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65           70           75           80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85           90           95
Ser Ser Ser Asn Trp Val Gly Ser Tyr Trp Gly Gln Gly Thr Leu Val
100          105          110
Thr Val Ser Ser
115

```

<210> SEQ ID NO 13

<211> LENGTH: 112

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 13

```

Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Val Thr Ile Gly
1           5           10           15
Gln Thr Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Glu Ser
20           25           30

```

-continued

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Ser Gln Arg Pro Gly Gln Ser
35 40 45

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

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Leu Pro Gln Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> SEQ ID NO 14

<211> LENGTH: 112

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Humanized 5H10 Light chain variable region VK1

<400> SEQUENCE: 14

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Glu Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Leu Val Ser Arg Leu Asp Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Leu Pro Gln Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> SEQ ID NO 15

<211> LENGTH: 112

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Humanized 5H10 Light chain variable region VK2

<400> SEQUENCE: 15

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Glu Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Leu Val Ser Arg Leu Asp Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Leu Pro Gln Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

-continued

100 105 110
 <210> SEQ ID NO 16
 <211> LENGTH: 112
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Humanized 5H10 Light chain variable region VK3

<400> SEQUENCE: 16

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
 1 5 10 15
 Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Glu Ser
 20 25 30
 Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln Arg Pro Gly Gln Ser
 35 40 45
 Pro Arg Arg Leu Ile Tyr Leu Val Ser Arg Leu Asp Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly
 85 90 95
 Thr His Leu Pro Gln Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105 110

<210> SEQ ID NO 17
 <211> LENGTH: 112
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Humanized 5H10 Light chain variable region VK4

<400> SEQUENCE: 17

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
 1 5 10 15
 Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Glu Ser
 20 25 30
 Asp Gly Lys Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
 35 40 45
 Pro Arg Arg Leu Ile Tyr Leu Val Ser Arg Leu Asp Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly
 85 90 95
 Thr His Leu Pro Gln Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105 110

<210> SEQ ID NO 18
 <211> LENGTH: 348
 <212> TYPE: DNA
 <213> ORGANISM: Mus musculus

<400> SEQUENCE: 18

cagggttcagc tgcagcagtc tggggctgag ctcgtgaggc ctgggtcctc agtgaagatt 60
 tcctgcaagt cttctggcta tgcattcagt agctactgga tgaactgggt gaagcagagg 120

-continued

cctggacagg gtcttgagtg gattggacag atttatcctg gagatgggtga tactcactac	180
aatggaaagt tcaagggcaa agccacactg actgcagaca aatcctccag cacagcctac	240
atgcagctca gcaggctaac atctgaggac tctgcggtct atttctgttc aagttcaaac	300
tgggtcggga gttactgggg ccaagggact ctggtcaccg tctcctca	348

<210> SEQ ID NO 19
<211> LENGTH: 348
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Humanized heavy chain variable region VH1

<400> SEQUENCE: 19

cagggtccagc tgggtgcaatc tggggctgag ctgaagaagc ctgggtcctc ggtgaagatt	60
tcctgcaagt cttctggata tgcattcagc agctattgga tgaactgggt gaagcagagg	120
cctggacaag ggcttgagtg gattggacag atctatcctg gagatgggtga tactcactac	180
aatggaaagt tcaagggcaa agccacgctg accgcggaca aatccacgag cacagcctac	240
atggagctga gcagcctgac atctgaggac tctgcggtgt atttctgttc aagttcaaac	300
tgggtcggga gttactgggg ccaaggaacc ctggtcaccg tctcctca	348

<210> SEQ ID NO 20
<211> LENGTH: 348
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Humanized heavy chain variable region VH2

<400> SEQUENCE: 20

cagggtccagc tgggtgcaatc tggggctgag gtgaagaagc ctgggtcctc ggtgaagatt	60
tcctgcaagt cttctggata tgcattcagc agctattgga tgaactgggt gaagcagagg	120
cctggacaag ggcttgagtg gattggacag atctatcctg gagatgggtga tactcactac	180
aatggaaagt tcaagggcaa agccacgctg accgcggaca aatccacgag cacagcctac	240
atggagctga gcagcctgag atctgaggac acggccgtgt atttctgttc aagttcaaac	300
tgggtcggga gttactgggg ccaaggaacc ctggtcaccg tctcctca	348

<210> SEQ ID NO 21
<211> LENGTH: 348
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Humanized heavy chain variable region VH3

<400> SEQUENCE: 21

cagggtccagc tgggtgcaatc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtt	60
tcctgcaagt cttctggata tgcattcagc agctattgga tgaactgggt gcgacagagg	120
cctggacaag ggcttgagtg gattggacag atctatcctg gagatgggtga tactcactac	180
aatggaaagt tcaagggcaa agccacgctg accgcggaca aatccacgag cacagcctac	240
atggagctga gcagcctgag atctgaggac acggccgtgt atttctgttc aagttcaaac	300
tgggtcggga gttactgggg ccaaggaacc ctggtcaccg tctcctca	348

<210> SEQ ID NO 22

-continued

```

<211> LENGTH: 348
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Humanized heavy chain variable region VH4

<400> SEQUENCE: 22
caggtccagc tgggtgcaatc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtt      60
tcctgcaagt cttctggata tgcattcagc agctattgga tgaactgggt gcgacagagg      120
cctggacaag ggcttgagtg gattggacag atctatcctg gagatgggtga tactcactac      180
aatggaaagt tcaagggcag agtcacgatt accgcggaca aatccacgag cacagcctac      240
atggagctga gcagcctgag atctgaggac acggccgtgt attctgttc aagttcaaac      300
tgggtcggga gttactgggg ccaaggaacc ctggtcaccg tctcctca      348

<210> SEQ ID NO 23
<211> LENGTH: 348
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Humanized heavy chain variable region VH5

<400> SEQUENCE: 23
caggtccagc tgggtgcaatc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtt      60
tcctgcaagt cttctggata tgcattcagc agctattgga tgaactgggt gcgacagagg      120
cctggacaag ggcttgagtg gattggacag atctatcctg gagatgggtga tactcactac      180
aatggaaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac      240
atggagctga gcagcctgag atctgaggac acggccgtgt attactgttc aagttcaaac      300
tgggtcggga gttactgggg ccaaggaacc ctggtcaccg tctcctca      348

<210> SEQ ID NO 24
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 24
gatgttgtga tgaccagac tccactcact ttgtcggtta ccattggaca aacagcctcc      60
atctcttgca agtcaagtca gaccccttta gaaagtgatg gaaagacata tttgaattgg      120
ttgtcacaga ggccaggcca gtctccaaag cgcctaattc atctggtgtc tagactggac      180
tctggagtcc ctgacagggt cactggcagt ggatcaggga cagatttcac actgaaaatc      240
agcagagtgg aggetgagga tttgggagtt tattattggt ggcaaggcac acatcttcct      300
cagacgttcg gtggaggcac caagctggag atcaaaa      336

<210> SEQ ID NO 25
<211> LENGTH: 336
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Humanized light chain variable region VK1

<400> SEQUENCE: 25
gatgttgtga tgactcagtc tccactcact ctgtcggtca cccttggaca gccggcctcc      60
atctcctgca agtctagtca aagcctotta gaaagtgatg gaaagaccta cttgaattgg      120

```

-continued

ttgcagcaga ggccaggcca atctccaagg cgcctaattt atctggtttc tagactggac	180
tctgggggtcc cagacagatt cactggcagt gggtcaggca ctgatttcac actgaaaatc	240
agcaggggtgg aggctgagga tgttgggggtt tattactgct ggcaaggcac acatcttcct	300
cagactttcg gcggaggggac caaggtggag atcaaaa	336

<210> SEQ ID NO 26
 <211> LENGTH: 336
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Humanized light chain variable region VK2

<400> SEQUENCE: 26

gatgttgtga tgactcagtc tccactctcc ctgcccgtca cccttgaca gccggcctcc	60
atctcctgca agtctagtc aagcctctta gaaagtgatg gaaagaccta cttgaattgg	120
ttgcagcaga ggccaggcca atctccaagg cgcctaattt atctggtttc tagactggac	180
tctgggggtcc cagacagatt cactggcagt gggtcaggca ctgatttcac actgaaaatc	240
agcaggggtgg aggctgagga tgttgggggtt tattactgct ggcaaggcac acatcttcct	300
cagactttcg gcggaggggac caaggtggag atcaaaa	336

<210> SEQ ID NO 27
 <211> LENGTH: 336
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Humanized light chain variable region VK3

<400> SEQUENCE: 27

gatgttgtga tgactcagtc tccactctcc ctgcccgtca cccttgaca gccggcctcc	60
atctcctgca agtctagtc aagcctctta gaaagtgatg gaaagaccta cttgaattgg	120
ttgcagcaga ggccaggcca atctccaagg cgcctaattt atctggtttc tagactggac	180
tctgggggtcc cagacagatt cagcggcagt gggtcaggca ctgatttcac actgaaaatc	240
agcaggggtgg aggctgagga tgttgggggtt tattactgct ggcaaggcac acatcttcct	300
cagactttcg gcggaggggac caaggtggag atcaaaa	336

<210> SEQ ID NO 28
 <211> LENGTH: 336
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Humanized light chain variable region VK4

<400> SEQUENCE: 28

gatgttgtga tgactcagtc tccactctcc ctgcccgtca cccttgaca gccggcctcc	60
atctcctgca agtctagtc aagcctctta gaaagtgatg gaaagaccta cttgaattgg	120
tttcagcaga ggccaggcca atctccaagg cgcctaattt atctggtttc tagactggac	180
tctgggggtcc cagacagatt cagcggcagt gggtcaggca ctgatttcac actgaaaatc	240
agcaggggtgg aggctgagga tgttgggggtt tattactgct ggcaaggcac acatcttcct	300
cagactttcg gcggaggggac caaggtggag atcaaaa	336

<210> SEQ ID NO 29

-continued

<211> LENGTH: 40
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 29

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

Pro Val Ala Ala Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg
20 25 30

Lys Ala Lys Asn Pro Pro Gly Asp
35 40

<210> SEQ ID NO 30
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 30

Ala Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Lys
1 5 10 15

Asn Pro Pro Gly Asp
20

<210> SEQ ID NO 31
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 31

Ser Ser Asn Arg Lys Ala Lys Asn
1 5

<210> SEQ ID NO 32
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 32

Ser Ser Ser Ser Asn Arg Lys Ala Lys Asn Pro Pro Gly Asp
1 5 10

<210> SEQ ID NO 33
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 33

Ala Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys
1 5 10

<210> SEQ ID NO 34
<211> LENGTH: 29
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 34

Asp Ser Arg Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala
1 5 10 15

Ala Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg
20 25

-continued

<210> SEQ ID NO 35
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 35

Ser Asn Arg Lys Ala Lys Asn
1 5

<210> SEQ ID NO 36
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 36

Ala Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg
1 5 10

<210> SEQ ID NO 37
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: VH5 CDR2

<400> SEQUENCE: 37

Gln Ile Tyr Pro Gly Asp Gly Asp Thr His Tyr Asn Gly Lys Phe Gln
1 5 10 15

Gly

<210> SEQ ID NO 38
<211> LENGTH: 443
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: VH0 IgG4 heavy chain

<400> SEQUENCE: 38

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser
1 5 10 15

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

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Gln Ile Tyr Pro Gly Asp Gly Asp Thr His Tyr Asn Gly Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Ser Ser Ser Asn Trp Val Gly Ser Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

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

Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu
130 135 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145 150 155 160

-continued

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

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

Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr
195 200 205

Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
210 215 220

Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro
225 230 235 240

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

Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
260 265 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
275 280 285

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
290 295 300

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
305 310 315 320

Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
325 330 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
340 345 350

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
355 360 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
370 375 380

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

Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
405 410 415

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
420 425 430

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440

<210> SEQ ID NO 39
<211> LENGTH: 219
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: VKO Kappa light chain

<400> SEQUENCE: 39

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

Gln Thr Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Glu Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Ser Gln Arg Pro Gly Gln Ser
35 40 45

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

-continued

```

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly
85          90          95

Thr His Leu Pro Gln Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100         105         110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115         120         125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130         135         140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145         150         155         160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165         170         175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180         185         190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195         200         205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210         215

```

```

<210> SEQ ID NO 40
<211> LENGTH: 327
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: heavy chain constant region

<400> SEQUENCE: 40

```

```

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1      5      10      15

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

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35     40     45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50     55     60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65     70     75     80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
85     90     95

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
100    105    110

Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
115    120    125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
130    135    140

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145    150    155    160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
165    170    175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
180    185    190

```

-continued

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
195 200 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
210 215 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225 230 235 240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
245 250 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
260 265 270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
275 280 285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
290 295 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305 310 315 320

Leu Ser Leu Ser Leu Gly Lys
325

<210> SEQ ID NO 41
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 41

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1 5 10 15

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
20 25 30

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65 70 75 80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> SEQ ID NO 42
<211> LENGTH: 443
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: 5H10 VH1 Heavy Chain

<400> SEQUENCE: 42

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

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

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

-continued

Gly	Gln	Ile	Tyr	Pro	Gly	Asp	Gly	Asp	Thr	His	Tyr	Asn	Gly	Lys	Phe
50					55						60				
Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Thr	Ser	Thr	Ala	Tyr
65					70					75					80
Met	Glu	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys
			85						90					95	
Ser	Ser	Ser	Asn	Trp	Val	Gly	Ser	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val
			100					105					110		
Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala
			115				120					125			
Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu
	130					135					140				
Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly
145					150					155					160
Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser
				165					170					175	
Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu
			180					185					190		
Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr
		195					200					205			
Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro
	210					215					220				
Cys	Pro	Ala	Pro	Glu	Phe	Glu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro
225					230					235					240
Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr
				245					250					255	
Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn
			260					265					270		
Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg
		275					280					285			
Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val
	290					295					300				
Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser
305					310					315					320
Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys
				325					330					335	
Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu
			340					345					350		
Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe
		355						360				365			
Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu
	370					375					380				
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe
385					390					395					400
Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly
				405					410					415	
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
				420				425					430		
Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys					
		435						440							

-continued

```

<210> SEQ ID NO 43
<211> LENGTH: 443
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: 5H10 VH2 Heavy Chain

<400> SEQUENCE: 43

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

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

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35          40          45

Gly Gln Ile Tyr Pro Gly Asp Gly Asp Thr His Tyr Asn Gly Lys Phe
50          55          60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65          70          75          80

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

Ser Ser Ser Asn Trp Val Gly Ser Tyr Trp Gly Gln Gly Thr Leu Val
100         105         110

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

Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu
130         135         140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145         150         155         160

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

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

Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr
195         200         205

Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
210         215         220

Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro
225         230         235         240

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

Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
260         265         270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
275         280         285

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
290         295         300

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
305         310         315         320

Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
325         330         335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
340         345         350

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe

```

-continued

355	360	365
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu		
370	375	380
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe		
385	390	395 400
Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly		
405	410	415
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr		
420	425	430
Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys		
435	440	

<210> SEQ ID NO 44
 <211> LENGTH: 443
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: 5H10 VH3 Heavy Chain

<400> SEQUENCE: 44

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

-continued

260					265					270					
Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg
	275						280					285			
Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val
	290					295					300				
Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser
305					310					315				320	
Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys
			325					330					335		
Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu
		340					345					350			
Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe
	355					360					365				
Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu
	370					375					380				
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe
385					390					395				400	
Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly
			405					410					415		
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
		420					425					430			
Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys					
	435					440									

<210> SEQ ID NO 45
 <211> LENGTH: 443
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: 5H10 VH4 Heavy Chain

<400> SEQUENCE: 45

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ser
1			5						10				15		
Ser	Val	Lys	Val	Ser	Cys	Lys	Ser	Ser	Gly	Tyr	Ala	Phe	Ser	Ser	Tyr
		20						25				30			
Trp	Met	Asn	Trp	Val	Arg	Gln	Arg	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile
	35					40						45			
Gly	Gln	Ile	Tyr	Pro	Gly	Asp	Gly	Asp	Thr	His	Tyr	Asn	Gly	Lys	Phe
	50					55					60				
Lys	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Lys	Ser	Thr	Ser	Thr	Ala	Tyr
65				70					75					80	
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Phe	Cys
			85					90					95		
Ser	Ser	Ser	Asn	Trp	Val	Gly	Ser	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val
			100					105					110		
Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala
	115					120						125			
Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu
	130					135				140					
Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly
145				150					155				160		
Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser

-continued

165					170					175					
Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu
	180						185					190			
Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr
	195					200					205				
Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro
	210					215					220				
Cys	Pro	Ala	Pro	Glu	Phe	Glu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro
	225					230					235				240
Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr
				245					250					255	
Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn
			260					265					270		
Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg
	275						280					285			
Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val
	290					295					300				
Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser
	305					310					315				320
Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys
				325					330					335	
Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu
			340					345					350		
Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe
	355						360					365			
Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu
	370					375					380				
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe
	385					390					395				400
Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly
				405					410					415	
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
			420					425					430		
Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys					
	435						440								

<210> SEQ ID NO 46

<211> LENGTH: 443

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: 5H10 VH5 Heavy Chain

<400> SEQUENCE: 46

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ser
1			5					10					15		
Ser	Val	Lys	Val	Ser	Cys	Lys	Ser	Ser	Gly	Tyr	Ala	Phe	Ser	Ser	Tyr
		20						25				30			
Trp	Met	Asn	Trp	Val	Arg	Gln	Arg	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile
	35					40					45				
Gly	Gln	Ile	Tyr	Pro	Gly	Asp	Gly	Asp	Thr	His	Tyr	Asn	Gly	Lys	Phe
	50					55					60				
Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Lys	Ser	Thr	Ser	Thr	Ala	Tyr

-continued

65	70	75	80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys	85	90	95
Ser Ser Ser Asn Trp Val Gly Ser Tyr Trp Gly Gln Gly Thr Leu Val	100	105	110
Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala	115	120	125
Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu	130	135	140
Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly	145	150	155
Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser	165	170	175
Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu	180	185	190
Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr	195	200	205
Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro	210	215	220
Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro	225	230	235
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr	245	250	255
Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn	260	265	270
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg	275	280	285
Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val	290	295	300
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser	305	310	315
Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys	325	330	335
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu	340	345	350
Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe	355	360	365
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu	370	375	380
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe	385	390	395
Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly	405	410	415
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr	420	425	430
Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys	435	440	

<210> SEQ ID NO 47

<211> LENGTH: 219

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

-continued

<220> FEATURE:

<223> OTHER INFORMATION: 5H10 VK1 Light Chain

<400> SEQUENCE: 47

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

<210> SEQ ID NO 48

<211> LENGTH: 219

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: 5H10 VK2 Light Chain

<400> SEQUENCE: 48

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

```

      100              105              110
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
      115              120              125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
      130              135              140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
      145              150              155              160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
      165              170              175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
      180              185              190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
      195              200              205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
      210              215

<210> SEQ ID NO 49
<211> LENGTH: 219
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: 5H10 VK3 Light Chain

<400> SEQUENCE: 49

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Glu Ser
      20              25              30

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln Arg Pro Gly Gln Ser
      35              40              45

Pro Arg Arg Leu Ile Tyr Leu Val Ser Arg Leu Asp Ser Gly Val Pro
      50              55              60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly
      85              90              95

Thr His Leu Pro Gln Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
      100              105              110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
      115              120              125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
      130              135              140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
      145              150              155              160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
      165              170              175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
      180              185              190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
      195              200              205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
      210              215

```

-continued

```

<210> SEQ ID NO 50
<211> LENGTH: 219
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: 5H10 VK4 Light Chain

<400> SEQUENCE: 50

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Glu Ser
20          25          30

Asp Gly Lys Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
35          40          45

Pro Arg Arg Leu Ile Tyr Leu Val Ser Arg Leu Asp Ser Gly Val Pro
50          55          60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly
85          90          95

Thr His Leu Pro Gln Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100         105         110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115         120         125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130         135         140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145         150         155         160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165         170         175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180         185         190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195         200         205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210         215

```

1. A method for treating an inflammatory or fibrotic renal disease in a subject in need thereof, the method comprising administering to the subject an antibody or antigen binding fragment thereof that specifically binds to stem cell factor (SCF), wherein the antibody or antigen binding fragment thereof comprises heavy chain CDR1, CDR2, and CDR3 comprising SEQ ID NOs: 1, 2, and 3, respectively; and light chain CDR1, CDR2, and CDR3 according to SEQ ID NOs: 4, 5, and 6, respectively.

2. The method of claim 1, wherein the antibody or fragment thereof comprises a heavy chain variable region having at least 80% identity to a sequence selected from SEQ ID NOs: 7, 8, 9, 10, and 11.

3. The method of claim 1, wherein the antibody or fragment thereof comprises a heavy chain variable region having at least 90% identity to a sequence selected from SEQ ID NOs: 7, 8, 9, 10, and 11.

4. The method of claim 1, wherein the antibody or fragment thereof comprises a light chain variable region

having at least 80% identity to a sequence selected from SEQ ID NOs: 13, 14, 15, and 16.

5. The method of claim 1, wherein the antibody or fragment thereof comprises a light chain variable region having at least 90% identity to a sequence selected from SEQ ID NOs: 13, 14, 15, and 16.

6. The method of claim 1, wherein the antibody or fragment thereof comprises a heavy chain variable region amino acid sequence selected from SEQ ID NOs: 7, 8, 9, 10, and 11; and a light chain variable region amino acid sequence selected from SEQ ID NOs: 13, 14, 15, and 16.

7. The method of claim 1, wherein the antibody or fragment thereof comprises a heavy chain variable region amino acid sequence according to SEQ ID NO: 7 and a light chain variable region amino acid sequence according to SEQ ID NO: 16.

8. The method of claim 1, wherein the antibody or fragment thereof comprises a heavy chain variable region

amino acid sequence according to SEQ ID NO: 8 and a light chain variable region amino acid sequence according to SEQ ID NO: 16.

9. The method of claim 1, wherein the antibody or fragment thereof comprises a heavy chain variable region amino acid sequence according to SEQ ID NO: 9 and a light chain variable region amino acid sequence according to SEQ ID NO: 16.

10. The method of claim 1, wherein the antibody or fragment thereof comprises a heavy chain variable region amino acid sequence according to SEQ ID NO: 10 and a light chain variable region amino acid sequence according to SEQ ID NO: 16.

11. The method of claim 1, wherein the antibody or fragment thereof comprises a heavy chain variable region amino acid sequence according to SEQ ID NO: 11 and a light chain variable region amino acid sequence according to SEQ ID NO: 16.

12. The method of claim 1, wherein the antibody or fragment thereof is humanized.

13. The method of claim 1, wherein the antibody is a monoclonal antibody.

14. The method of claim 13, wherein the antibody comprises a human IgG4 domain.

15. The method of claim 14, wherein the IgG4 domain comprises a S241P mutation at amino acid residue 241 and

an L248E mutation at amino acid residue 248, wherein the numbering of the residues is that of the Kabat numbering system.

16. The method of claim 13, wherein the antibody comprises a heavy chain according to SEQ ID NO: 42 and a light chain according to SEQ ID NO: 49.

17. The method of claim 13, wherein the antibody comprises a heavy chain according to SEQ ID NO: 43 and a light chain according to SEQ ID NO: 49.

18. The method of claim 1, wherein the antibody or fragment thereof specifically binds to SCF248.

19. The method of claim 1, wherein the antibody does not bind to SCF220.

20. The method of claim 1, wherein the inflammatory or fibrotic renal disease is selected from the group consisting of chronic kidney disease (CKD), end stage renal disease (ERSD), renal fibrosis, glomerulonephritis, and nephropathy.

21. The method of claim 20, wherein the nephropathy or glomerulonephritis is IgA nephropathy, diabetic nephropathy, focal segmental glomerulosclerosis, rapidly progressive glomerulonephritis, crescentic glomerulonephritis, lupus nephritis, hypertensive nephropathy, or diabetic nephropathy.

* * * * *